

# **Annual Report 2014**

**Centre for Image Analysis**

**Centrum för bildanalys**

*Cover:* Illustrations from the seven PhD theses presented at CBA during 2014. Further information in Section 4.2.

**Top, left**

*Andreas Kårsnäs* — Automatic detection of sub-cellular structures in breast tumour tissue for the quantification of sub-cellular protein expression levels.

**Top, left**

*Erik Wernersson* — Selection of a wood fibre from a paper sheet for further characterisation.

**Top, left**

*Jimmy Azar* — Multi-instance based feature descriptor of a tissue image: automatic extraction of lumen areas and profiling of surrounding regions by means of a progressively expanding set of neighborhood sampling rings.

**Top, left**

*Lennart Svensson* — The image series shows exploration of template matching results in an electron microscopy volume image. Left and center images: two example registrations of a template IgG molecule. Right image: visualization of the template to volume correlation for different rotations of the template.

**Top, left**

*Gustaf Kylberg* — Examples of classes in the Kylberg Texture Dataset. The texture samples are intensity normalized to have the same mean and standard deviation.

*Cover design:*

Anton Axelsson

*Edited by:*

Gunilla Borgefors, Omer Ishaq, Filip Malmberg, Lena Nordström, Ingela Nyström, Ida-Maria Sintorn, Robin Strand

Centre for Image Analysis, Uppsala, Sweden



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# 1 Introduction

The Centre for Image Analysis (CBA) carries out research and graduate education in computerised image analysis and perceptualisation. Our work ranges from the pure theory to methods, algorithms and systems for applications primarily in biomedicine and forest industry.

## 1.1 General background

CBA is collaboration between Uppsala University (UU) and the Swedish University of Agricultural Sciences (SLU), which started in 1988. This means that CBA celebrated 25 years in 2013! From an organizational point of view, CBA was an independent entity within our host universities until 2010.

At UU, we are hosted by the Disciplinary Domain of Science and Technology and today belong to one of five divisions within the Dept. of Information Technology (IT), the Division of Visual Information and Interaction (Vi2). At SLU, we today belong to the Dept. of Forest Genetics and Plant Physiology in Umeå. The organizational matters are outlined in Section 2. The re-organizations have not prevented us from continuing and expanding our research. We foresee opportunities for collaborations among our close colleagues at UU and SLU.

During 2013, a total of 39 persons were working at CBA: 18 researchers, 19 PhD students, one technical staff, and one administrator. Additionally, 17 Master thesis students completed their thesis work with supervision from CBA. This does not mean, however, that we have had more than 50 full-time persons at CBA: many have split appointments, part time at CBA and part time elsewhere, adding up to approximately 30 full-time employments. Having world class scientists visiting CBA and CBA staff visiting their groups, for longer or shorter periods, is an important ingredient of our activities.

Most of us at CBA also undertake some undergraduate teaching. Previously this has been organised by other divisions, but with the organizational changes our new division now handles undergraduate education.

We can conclude that the activities remain high. On average, three PhD dissertations are produced each year at CBA. Nevertheless, in 2013 there was no PhD exam. On the other hand, we expect as many as eight (8!) PhD theses to be defended in 2014. In 2013, we published 50 internationally reviewed papers, more than any year before in the history of CBA. There are several reasons for this. The main reason is that so many of our PhD students are at the end of their studies, which is when they publish most. Another reason is that we have more researchers than before and are involved in more co-operation projects.

We had continued support from the Disciplinary Domain of Medicine and Pharmacy, the Science for Life Laboratory (SciLifeLab), and strategic resources within the Dept. of IT. The strong economy has led to recruitments of new PhD students and researchers during the year. A successful example of collaboration we have is with the Dept. of Radiology, Oncology, and Radiation Sciences; Section of Radiology, where two of our staff members work part time in order to be close to radiology researchers.

In 2013, we have established ourselves within the field of automatic reading of old hand-written documents, referred to as HTR (Hand-written Text Recognition). The framework project is funded by VR, with support from the Vice Chancellor, and is truly multi-disciplinary, with partners from the Humanities and Social Sciences, and the Uppsala University Library.

An outreach activity that was particularly important was the 11th International Symposium on Mathematical Morphology (ISMM 2013) held in Uppsala in May with 69 participants. See <http://www.cb.uu.se/ismm2013>. Researchers from both universities were active in the arrangements.

Another outreach activity we have is our participation in the annual symposium on image analysis, arranged by the Swedish Society for Automated Image Analysis in March. In 2013, it was held in Gothenburg and CBA accounted for about a quarter of the participants with 20 registrations.

Image processing is highly inter- and multi-disciplinary, with foundations in mathematics, statistics, physics, signal processing and computer science, and with applications in many diverse fields. We are working in a wide range of application areas, most of them related to life sciences and usually in close collaboration with domain experts. Our collaborators are found locally as well as nationally and internationally. For a complete list of our 45 national and 30 international collaborators see Section 5.6.

Ingela Nyström, our director, continues to coordinate the strategic research programme in the e-science field, eSSENCE. She terminated her position on the board of the Swedish University Computer Network, SUNET, during 2013.

We are very active in international and national societies. Both Ewert Bengtsson and Gunilla Borgefors are elected members of the Royal Society of Sciences in Uppsala and the Royal Swedish Academy of Engineering Sciences (IVA). Ingela Nyström is elected member of the Royal Society of Arts and Sciences of Uppsala. Gunilla Borgefors is Editor in Chief for the journal Pattern Recognition Letters and Cris Luengo is Area Editor for the same journal. Ewert Bengtsson is associate editor of Computer Methods and Programs in Biomedicine. Ingela Nyström serves as Secretary of the International Association of Pattern Recognition, IAPR. Researchers at CBA also served on several other journal editorial boards, scientific organization boards, conference committees, and PhD dissertation committees. In addition, we took a very active part in reviewing grant applications and scientific papers submitted to conferences and journals.

In addition to the more common ways of spreading information about our activities and work, such as seminar series, publications, web-pages, etc., we have our “CBA TV”. Short “trailers” on our projects and activities are presented on an LCD monitor facing the main entrance stairway where students and colleagues from other groups pass by.

This annual report is also available on the CBA webpage, see [http://www.cb.uu.se/annual\\_report/AR2013.pdf](http://www.cb.uu.se/annual_report/AR2013.pdf)

## 1.2 Summary of research

The objective of CBA is to carry out research and education in computerised image analysis and perceptualisation. We are pursuing this objective through a large number of research projects, ranging from fundamental mathematical methods development, to application-tailored development and testing, the latter mainly in biomedicine and forest industry. We are also developing new methods for perceptualisation, combining computer graphics, haptics, and image processing. Our research is organised in a large number of projects (53) of varying size, ranging in effort from a few person months to many person years. There is a lot of interaction between different researchers: generally, a person is involved in several different projects in different constellations with internal and external partners. In this context, the university affiliation of the particular researchers seldom is of importance.

On the theoretical side, most of our work is based on discrete mathematics with fundamental work on sampling grids, fuzzy methods, skeletons, distance functions, and tessellations, in three and more dimensions.

Several projects deal with light microscopy, developing tools for modern quantitative biology and clinical cancer detection and grading. We are collaborating with local biologists and pathologists, research centers in the US and India, and a Danish company. We have close collaboration with the strategic project programme SciLifeLab through which a research platform in quantitative microscopy is formed.

We also work with electron microscopy (EM) images; one application is focused on finding viruses in EM images. Since the texture of the virus particles is an important feature in identification of the different virus types, this project has also led to basic research on texture analysis.

New techniques are creating 3D images on microscopic scales. We have been analyzing electron microscope tomography images of protein molecules for several years. We are also involved in optical projection tomography, where we image zebrafish embryos. Another technique is X-ray microtomography; we are developing methods to use such images to study the internal structure of paper, wood fibre composites and bone, and bone-implant integration.

On a macroscopic scale, we are working with interactive segmentation of 3D CT and MR images by use of haptics. We have developed a segmentation toolbox, WISH, which is publicly available. Applications of this toolbox are for facial surgery planning and measurements of CT wrist images.

Over the last several years, we have expanded our activities in perceptualisation under leadership of Guest Professor Ingrid Carlbom, with the goal of creating a system in which you can see, feel, and manipulate virtual 3D objects as if they were real. We have created a unique haptic system where virtual objects can be grabbed and manipulated. This project has obvious synergy with the Human-Computer Interaction research performed within the Division Vi2.

See Section 5 for details on all our research projects.

An activity bridging research and education is the supervision of master thesis projects. This year we completed 18 such projects. In Section 3.2, we describe these theses.

### 1.3 How to contact CBA

CBA maintains a home page (<http://www.cb.uu.se/>) both in English and in Swedish. The main structure contains links to a brief presentation, staff, vacant positions (if any), etc. It also contains information on courses, seminars (note that our Monday 14:15 seminar series is open to anyone interested), a layman introduction to image analysis, this annual report (as .html and .pdf versions), lists of all publications since CBA was created in 1988, and other material.

In addition, all staff members have their own home page, which are linked to from the CBA “Staff” page. On these, you can usually find detailed course and project information, etc.

Centre for Image Analysis (Centrum för bildanalys, CBA) can be contacted in the following ways:

*Visiting address:* Lägerhyddsvägen 2  
Polacksbacken, building 2, floor 1  
Uppsala

*Postal address:* Box 337  
SE-751 05 Uppsala  
Sweden

*Telephone:* +46 18 471 3460  
*Fax:* +46 18 511925  
*E-mail:* cb@cb.uu.se

## 2 Organisation

From the start in 1988 until the end of 2010, CBA was an independent entity belonging equally to Uppsala University (UU) and Swedish University of Agricultural Sciences (SLU), administered through UU. After decisions by the host universities this was changed and from 2011 the UU part of CBA became a division within the Dept. of Information Technology. Within the Dept. of IT, there was a review of the division structure, so from 2012 CBA together with the previous Division for Human-Computer Interaction forms the Division for Visual Information and Interaction (Vi2). Ingela Nyström is head of Vi2 and also head of CBA. At SLU, the Dept. of Forest Genetics and Plant Physiology was appointed as host department where the SLU staff is employed.

Since 2011, there is a three-year agreement between the Vice Chancellors of the two universities, according to which CBA continues as a collaboration with joint activities administered by UU. The long term strategic planning of CBA is handled by a joint council with two representatives from each university. All personnel is employed at a department at one of the two universities, and everyday management of CBA is the responsibility of the head of the division of the Dept. of IT at UU to which CBA belongs.

The appointed members of the joint council *Centrumråd* are:

- Gunilla Borgefors, deputy chair, S-Faculty, SLU
- Elna-Marie Larsson, Faculty of Medicine, UU
- Cris Luengo, S-Faculty, SLU
- Ingela Nyström, chair, TN-Faculty, UU

One component of the close integration between image analysis research at the two universities is that the SLU Professor Gunilla Borgefors is a full-time Guest Professor in computerised image processing at UU since 2012, with full financing from SLU.

The many organizational changes in the past few years have of course affected us all, to varying degrees. We hope that the current organization will allow us to continue our successful joint research and to develop new branches with new colleagues. As seen in this report, we have been able to keep up a high activity despite a turbulent period.

### 2.1 Finances

After the re-organization, where CBA at UU now is part of the Division of Visual Information and Interaction (Vi2) at the Dept. of Information Technology, the CBA economy is not separate. In fact, Vi2 has been formed to become integrated in activities as well as organization. Hence, we report how this is financed as a whole. The total expenditure for Vi2 was 39.1 million SEK for 2013. To cover this, 40% came from UU, 8% from SLU, 32% from external sources, and 20% from undergraduate education.

The largest cost in our budget is personnel, which is 59% of the total cost. Over the years, the number of people working at CBA has varied considerably. During 2013, about 39 people were working at CBA. Most of the personnel is employed by UU, the rest by SLU. Within the whole division Vi2, we counted more than 50 persons during the year (but not 50 full-time equivalents).

Even though CBA itself does not organise undergraduate education, Vi2 offers undergraduate education with several courses in Human-Computer Interaction themes. In addition, we have inherited the courses on Image Analysis, Computer Graphics, and Scientific Visualization previously organised by the Division of Scientific Computing and given by teachers from CBA. Most of us teach 10–20%, while some Senior Lecturers teach more. The economy in Table 1 below summarises the overall economy for Vi2 in 2013. This summary is based on joining the two accounts from UU and SLU (after clearing

internal transactions between the universities). The numbers are rounded to the nearest 1000 SEK. The same numbers for income and costs are also given as pie charts in Figure 1. Who finances each project can be ascertained in Section 5, where all projects are listed. Project grants that have been received but not used are directly balanced to next year, and are thus not included in the income–cost tables.

Table 1: Vi2 income and costs for 2014 in kSEK.

<b>Income</b>		<b>Costs</b>	
UU	167991	Personnel	25081
SLU	2529	Equipment	99
UU undergraduate education	6476	Operating exp. <sup>4</sup>	3175
Governmental grants <sup>1</sup>	8541	Rent	1880
Non-governmental grants <sup>2</sup>	1253	University overhead	9481
Contracts <sup>3</sup>	4800		
Financial netto	44		
<b>Total income</b>	<b>38012</b>	<b>Total cost</b>	<b>39080</b>

<sup>1</sup> The Swedish Research Council, Vinnova – Swedish Governmental Agency for Innovation Systems

<sup>2</sup> Research foundations, EU

<sup>3</sup> Internal invoices from UU and compensations

<sup>4</sup> Including travel and conferences

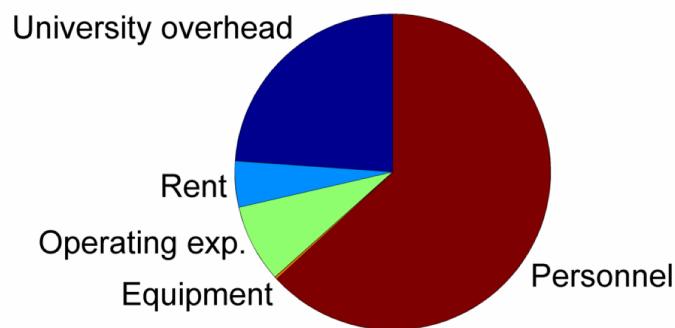
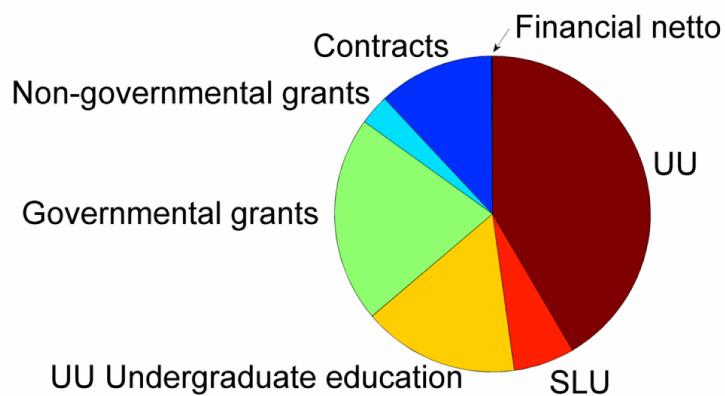


Figure 1: Vi2 income (top) and costs (below) for 2014.

## 2.2 Staff, CBA

Christophe Avenel, Post Doc., UU  
Jimmy Azar, Graduate Student –141031, UU  
Ewert Bengtsson, Professor, UU  
Gunilla Borgefors, Professor, UU  
Anders Brun, PhD, Researcher, UU  
Ingrid Carlbom, Professor, UU  
Ginevra Castellano, Associate Senior Lecturer, 140701–  
Vladimir Curic, Graduate Student –140831, UU  
Olle Eriksson, PhD, Senior Lecturer, (part time) UU  
Azadeh Fakhrzadeh, Graduate Student, SLU  
Anders Hast, Docent and Excellent Teacher, Lecturer, UU  
Omer Ishaq, Graduate Student, UU  
Gustaf Kylberg, Graduate Student –140331, UU  
Andreas Kårsnäs, Industrial Graduate Student –140430, (part time) UU and Visiopharm, Hørsholm, Denmark  
Elisabeth Linnér, Graduate Student, UU  
Fei Liu, Graduate Student, University of Gävle  
Cris Luengo, Docent, Researcher, SLU  
Kristina Lidayova, Graduate Student, UU  
Patrik Malm, Graduate Student –140228, UU  
Filip Malmberg, PhD, Researcher, UU  
Damian Matuszewski, Graduate Student 140804–, UU  
Bo Nordin, PhD, Researcher/Senior Lecturer, (part time) UU  
Lena Nordström, Administration  
Fredrik Nysjö, Research Engineer, UU  
Johan Nysjö, Graduate Student, UU  
Ingela Nyström, Professor, Director, (part time) UU  
Pontus Olsson, Graduate Student, UU  
Alexandra Pacureanu, PhD, Post Doc –140131, UU  
Petter Ranefall, PhD, Bioinformatician, UU  
Sajith Sadanandan Kecheril, Graduate Student, UU  
Kalyan Ram, Graduate Student, UU  
Stefan Seipel, Professor, (part time) UU and University of Gävle  
Bettina Selig, Graduate Student, SLU  
Ida-Maria Sintorn, Docent, Assistant Professor, SLU –140131; Associate Senior Lecturer, UU –140201  
Natasa Sladoje, Researcher 140901–, UU  
Robin Strand, Docent, Researcher, UU  
Lennart Svensson, Graduate Student –141231, SLU  
Erik Wernersson, Graduate Student –141231, SLU  
Fredrik Wahlberg, Graduate Student, UU  
Tomas Wilkinson, Graduate Student, UU  
Carolina Wählby, Docent, Senior Lecturer –140331, Professor 140401–, (part time) UU

The letters after the name indicate the employer for each person:

UU — Uppsala University

SLU — Swedish University of Agricultural Sciences

The e-mail address of the staff is `Firstname.Lastname@it.uu.se`

## **Docent degrees from CBA**

1. Lennart Thurfjell, 1999, UU
2. Ingela Nyström, 2002, UU
3. Lucia Ballerini, 2006, UU
4. Stina Svensson, 2007, SLU
5. Tomas Brandtberg, 2008, UU
6. Hans Frimmel, 2008, UU
7. Carolina Wählby, 2009, UU
8. Anders Hast, 2010, UU
9. Pasha Razifar, 2010, UU
10. Cris Luengo, 2011, SLU
11. Robin Strand, 2012, UU
12. Ida-Maria Sintorn, 2012, UU

## **CBA staff appointed Excellent Teachers**

1. Anders Hast 2014, UU

### 3 Undergraduate education

CBA is a popular place to for Master theses students. This year a record number of 18 theses were completed with someone from CBA as either supervisor or reviewer. Most of the theses were initiated from outside CBA, either from industry or from other university departments. CBA is also involved in undergraduate courses. We organize courses in image analysis and visualization (3.1.1-4) and participate in various other courses.

#### 3.1 UU courses

##### 1. Computer Assisted Image Analysis I, 5hp

**Anders Brun**, Azadeh Fakhrzadeh, Kristina Lidayova, Cris Luengo, Robin Strand

*Period:* 140120–0316

##### 2. Computer Assisted Image Analysis I, 5hp

**Ida-Maria Sintorn**, Kristina Lidayova, Cris Luengo, Robin Strand, Tomas Wilkinson

*Period:* 141027–1218

##### 3. Computer Graphics, 10hp

**Anders Hast**, Johan Nysjö, Pontus Olsson

*Period:* 140324–0527

##### 4. Scientific Visualization, 5hp

Anders Hast, Johan Nysjö, **Stefan Seipel**

*Period:* 140904–1024

##### 5. Scientific Computing III, 5hp

Elisabeth Linnér

*Period:* 140122–0318

##### 6. Bioimaging and Cell Analysis, 7.5hp

Ida-Maria Sintorn, Robin Strand, Carolina Wählby

*Period:* 140903–0929

#### 3.2 Master theses

##### 1. An applied model for implementation of innovative IT-solutions for telehealth into the healthcare system

*Student:* Hannah Lundström, Tomas Berglund and Sara Lycke

*Supervisor:* Per Matsson, Cenvigo AB, Uppsala, Anders Hast

*Reviewer:* Tomas Nyberg, Dept. of Engineering Sciences, and Göran Lindström, Dept. of Engineering Sciences

*Publisher:* UPTEC F 14019

*Abstract:* Today, new technologies are introduced to the market every day, and constantly changing our way of living. Especially in the healthcare sector, the change process is approaching a point where doctors can benefit from the use of, for example, connected portable reading devices instead of paper-based medical record systems. The information and communication technology is promoting the evolution of a new pathway of care delivery, a paradigm shift that alters the fundamental relationship between a doctor and its patient. The concept is defined as telehealth and formulates the provision of care at a distance and provides the possibility to treat patients in their home environment instead of at the hospital.

This master's thesis has been performed on the request of Cenvigo AB, a company active in the implementation of new IT-solutions into the healthcare and eldercare. Cenvigo AB are the owners of the Parkinson's Digital Assessment (PANDA) application. The application has been developed through research at Dalarna University and Uppsala University Hospital. This project will initiate the launch of PANDA and also create a model for implementation of innovative IT-solutions into the healthcare systems.

The model is founded in a theoretical framework and shaped with interviews related to the implementation of technology with a focus on telehealth applications. Interviews have been performed with healthcare

professionals, technology developers and users to acquire a complete picture and opinions regarding the introduction of innovation in healthcare today. From the acquired information, a model is formulated as a stepwise and chronological linear process where identified key activities are included to promote a successful implementation process. The model is connected to the practice through the implementation of PANDA. In the process of implementing PANDA into the Swedish healthcare system, a collaboration with the innovation centre at Uppsala University Hospital as a healthcare organization stakeholder, has been initiated.

The model consists of five phases; Assessment, Dissemination, Adoption, Implementation and Continuation. The phases are seen as transitional steps in the innovation process, critical barriers to overcome towards a successful implementation in a mainstream routine setting. Each phase includes a number of activities and to achieve progression in each phase, these activities must be performed in order to advance to the next phase. In the case of PANDA, the process of progression has passed assessment and are currently involved in activities related to the dissemination phase.

The purpose of the model is to be used both for existing and future applications in the segment of medicine technology sector. The structure of the model is designed to promote a co-design or a common value principle of development and practice regarding an innovation. By connecting actors from both technology and healthcare in close relationships the actual needs of healthcare professionals could more effectively be identified and developed into a solution, a result from the amplification of a two-way engagement. The outmost aim is to serve as a catalysing factor, complementing the implementation models of healthcare in Sweden today.

Through this study, a need for facilitating the implementation process of new technology into the healthcare systems has been identified. This model offers the necessary input that many technology companies lack. The recommendation to Cenvigo AB is to continue to develop the model during the last step in the process of launching PANDA, and parallel use this model as a business model mainly for technology start-ups and larger foreign companies that have not yet established pathways into the Swedish healthcare system.

## **2. Adobe Flash Professional for iOS Game Development : A Feasible and Viable Alternative to Xcode?**

*Student:* Leila Svantrö

*Supervisor:* Christopher Okhravi, Dept. of Informatics and Media, Faculty of Social Sciences, UU

*Reviewer:* Anders Hast and Olle Gällmo, Dept. of IT, UU

*Publisher:* UPTEC IT, 14 028

*Abstract:* The smartphone operating system iOS is the second highest ranked after Android. The apps in App Store and Google Play combined consist of 70-80 % games, which are the primary entertainment applications. Many developers are learning game development or refreshing their skills to profit on this trend. The problem statements are: is it viable and feasible to use Adobe Flash Professional (AFP) for the iOS game development compared to Xcode and could AFP be used exclusively for iOS game development? Information on both IDEs has been analyzed. Furthermore, implementations and code comparisons have been made. The results and analysis shows differences regarding expenses while possibilities for developing the same kind of games essentially are equivalent. The conclusions are that AFP is a viable IDE for iOS game development in the aspect of possibilities. It is not feasible on a long-term basis when considering the expenses however it could be feasible on a short-term basis depending on the developer's requirements of extension and Mac OS for App Store publishing. AFP is not able to be used exclusively for the iOS game development if publishing to the App Store is a requirement however it is if publishing is restricted to single devices.

## **3. 3D rendering and interaction in an augmented reality mobile system**

*Student:* Gabriel Tholsgård

*Supervisor:* Aman Hamdan, BMW Group, Shanghai, China

*Reviewer:* Anders Hast and Olle Gällmo, Dept. of IT, UU

*Publisher:* UPTEC IT, 14 007

*Abstract:* Augmented Reality(AR) is a concept that is getting more and more popular, and the number of applications using it is increasing. AR applications include several concepts such as image recognition and camera calibration, together known as tracking, and it also uses 2D and 3D graphics rendering. The most important and difficult part of AR applications is the tracking, where an object not only should be recognized in many different conditions, but it should also be determined how the object is viewed upon. This report describes how the task given by BMW Group in Shanghai was solved, which was to create an iPhone prototype AR application, that should be able to recognize objects inside of a car and be able to

interact with them through the mobile phone. The report explains the implemented solution to this problem, what different recognition methods were tested and the different ways of creating the 3D graphics overlay that was evaluated. The AR application resulted in a functional AR application capable of recognizing the determined objects, draw their corresponding 3D representations and interact with them. However, the application was not complete as camera calibration was not used and a connection between the mobile phone and the car was never established.

#### 4. Realtime Virtual 3D Image of Kidney Using Pre-Operative CT Image for Geometry and Realtime US-Image for Tracking

*Student:* Sebastian Ärleryd

*Supervisor:* Massimiliano Collarieti-Tosti, KTH, Stockholm

*Reviewer:* Anders Hast and Anders Nyberg, Dept. of T, UU

*Publisher:* UPTEC F 14042

*Abstract:* In this thesis a method is presented to provide a 3D visualization of the human kidney and surrounding tissue during kidney surgery. The method takes advantage of the high detail of 3D X-Ray Computed Tomography (CT) and the high time resolution of Ultrasonography (US). By extracting the geometry from a single preoperative CT scan and animating the kidney by tracking its position in real time US images, a 3D visualization of the surgical volume can be created. The first part of the project consisted of building an imaging phantom as a simplified model of the human body around the kidney. It consists of three parts: the shell part representing surrounding tissue, the kidney part representing the kidney soft tissue and a kidney stone part embedded in the kidney part. The shell and soft tissue kidney parts were cast with a mixture of the synthetic polymer Polyvinyl Alcohol (PVA) and water. The kidney stone part was cast with epoxy glue. All three parts were designed to look like human tissue in CT and US images. The method is a pipeline of stages that starts with acquiring the CT image as a 3D matrix of intensity values. This matrix is then segmented, resulting in separate polygonal 3D models for the three phantom parts. A scan of the model is then performed using US, producing a sequence of US images. A computer program extracts easily recognizable image feature points from the images in the sequence. Knowing the spatial position and orientation of a new US image in which these features can be found again allows the position of the kidney to be calculated. The presented method is realized as a proof of concept implementation of the pipeline. The implementation displays an interactive visualization where the kidney is positioned according to a user-selected US image scanned for image features. Using the proof of concept implementation as a guide, the accuracy of the proposed method is estimated to be bounded by the acquired image data. For high resolution CT and US images, the accuracy can be in the order of a few millimeters.

#### 5. Detection and Quantification of Small Changes in MRI Volumes

*Student:* Mariana Bustamante

*Supervisor:* Robin Strand

*Reviewer:* Anders Brun and Christoff Ivan, Dept. of IT

*Publisher:* IT, 14 013

*Abstract:* The focus of this research is to attempt to solve the problem of comparing two MRI brain volumes of the same subject taken at different times, and detect the location and size of the differences between them, especially when such differences are too small to be perceived with the naked eye.

The research focuses on a combination of registration and morphometry techniques in order to create two different possible solutions: A voxel-based method and a tensor-based method. The first method uses Affine or B-Spline registration combined with voxel-by-voxel subtraction of the volumes; the second method uses Demons registration and analysis of the Jacobian determinants at each point of the deformation field obtained. The methods are implemented as modules for 3D Slicer, a software for medical image analysis and visualization.

Both methods are tested on two types of experiments: Artificial experiments, in which made-up differences of distinct sizes are added to volumes of healthy subjects; and real experiments, in which MRIs of real patients are compared.

The results obtained from the voxel-based method are very useful, since it was able to detect with almost complete accuracy all of the artificial differences and expected real differences during the experiments.

The tensor-based method's results are not as accurate in location or size of the detected differences, and it usually includes more areas of differences where there seems to be none; even though it behaves adequately when the differences are large.

Most of the results obtained are useful for the diagnostic of patients with non-severe trauma to the head; especially when using the voxel-based method. However, the results from both methods are just a suggestion of the size and location of injuries; and as a consequence, the procedure requires the presence of a medical practitioner.

## 6. A Method for Detecting Resident Space Objects and Orbit Determination Based on Star Trackers and Image Analysis

*Student:* Karl Bengtsson Bernander

*Supervisor:* Daniel Skaborn, ÅAC Microtec, Uppsala

*Reviewer:* Cris Luengo and Tomas Nyberg, Dept. of IT

*Publisher:* UPTEC F 14050

*Abstract:* Satellites commonly use onboard digital cameras, called star trackers. A star tracker determines the satellite's attitude, i.e. its orientation in space, by comparing star positions with databases of star patterns. In this thesis, I investigate the possibility of extending the functionality of star trackers to also detect the presence of resident space objects (RSO) orbiting the earth. RSO consist of both active satellites and orbital debris, such as inactive satellites, spent rocket stages and particles of different sizes.

I implement and compare nine detection algorithms based on image analysis. The input is two hundred synthetic images, consisting of a portion of the night sky with added random Gaussian and banding noise. RSO, visible as faint lines in random positions, are added to half of the images. The algorithms are evaluated with respect to sensitivity (the true positive rate) and specificity (the true negative rate). Also, a difficulty metric encompassing execution times and computational complexity is used.

The Laplacian of Gaussian algorithm outperforms the rest, with a sensitivity of 0.99, a specificity of 1 and a low difficulty. It is further tested to determine how its performance changes when varying parameters such as line length and noise strength. For high sensitivity, there is a lower limit in how faint the line can appear.

Finally, I show that it is possible to use the extracted information to roughly estimate the orbit of the RSO. This can be accomplished using the Gaussian angles-only method. Three angular measurements of the RSO positions are needed, in addition to the times and the positions of the observer satellite. A computer architecture capable of image processing is needed for an onboard implementation of the method.

## 7. A Study of Digital In-Line Holographic Microscopy for Malaria Detection

*Student:* Carl Christian Kirchmann, Elin Lundin and Jakob Andrén

*Supervisor:* Cris Luengo

*Reviewer:* Martin Sjödin, Dept. of Engineering Sciences

*Publisher:* UPTEC TVE 14 054

*Abstract:* The main purpose of the project was to create an initial lab set-up for a digital in-line holographic microscope and a reconstruction algorithm. Different parameters including: light source, pin-hole size and distances pinhole-object and object-camera had to be optimized. The lab set-up is to be developed further by a master student at the University of Nairobi and then be used for malaria detection in blood samples. To acquire good enough resolution for malaria detection it has been found necessary to purchase a gray scale camera with smaller pixel size. Two different approaches, in this report called the on-sensor approach and the object-magnification approach, were investigated. A reconstruction algorithm and a phase recovery algorithm was implemented as well as a super resolution algorithm to improve resolution of the holograms. The on-sensor approach proved easier and cheaper to use with approximately the same results as the object-magnification method. Necessary further research and development of experimental set-up was thoroughly discussed.

## 8. Moving Object Detection based on Background Modeling

*Student:* Yuanqing Luo

*Supervisor:* Changqing Yin, Tongji University, Shanghai, China

*Reviewer:* Cris Luengo and Christoff Ivan, Dept. of IT

*Publisher:* UPTEC IT 14 046

*Abstract:* Aim at the moving objects detection, after studying several categories of background modeling methods, we design an improved Vibe algorithm based on image segmentation algorithm. Vibe algorithm builds background model via storing a sample set for each pixel. In order to detect moving objects, it uses several techniques such as fast initialization, random update and classification based on distance between pixel value and its sample set. In our improved algorithm, firstly we use histograms of multiple layers to

extract moving objects in block-level in pre-process stage. Secondly we segment the blocks of moving objects via image segmentation algorithm. Then the algorithm constructs region-level information for the moving objects, designs the classification principles for regions and the modification mechanism among neighboring regions. In addition, to solve the problem that the original Vibe algorithm can easily introduce the ghost region into the background model, the improved algorithm designs and implements the fast ghost elimination algorithm. Compared with the tradition pixel-level background modeling methods, the improved method has better robustness and reliability against the factors like background disturbance, noise and existence of moving objects in the initial stage. Specifically, our algorithm improves the precision rate from 83.17% in the original Vibe algorithm to 95.35%, and recall rate from 81.48% to 90.25%.

Considering the affection of shadow to moving objects detection, this paper designs a shadow elimination algorithm based on Red Green and Illumination (RGI) color feature, which can be converted from RGB color space, and dynamic match threshold. The results of experiments demonstrate that the algorithm can effectively reduce the influence of shadow on the moving objects detection.

At last this paper makes a conclusion for the work of this thesis and discusses the future work.

## 9. Pixel-based video coding

*Student:* Johannes Olsson Sandgren

*Supervisor:* Jonatan Samuelsson, Ericsson AB.

*Reviewer:* Cris Luengo and Lars-Åke Nordén, Dept. of IT

*Publisher:* UPTEC IT 14 003

*Abstract:* This paper studies the possibilities of extending the pixel-based compression algorithm LOCO-I, used by the lossless and near lossless image compression standard JPEG-LS, introduced by the Joint Photographic Experts Group (JPEG) in 1999, to video sequences and very low bit-rates. Bitrates below 1 bit per pixel are achieved through skipping signaling when the prediction of a pixels sufficiently good. The pixels to be skipped are implicitly detected by the decoder, minimizing the overhead. Different methods of quantization are tested, and the possibility of using vector quantization is investigated, by matching pixel sequences against a dynamically generated vector tree. Several different prediction schemes are evaluated, both linear and non-linear, with both static and adaptive weights. Maintaining the low computational complexity of LOCO-I has been a priority. The results are compared to different HEVC implementations with regards to compression speed and ratio.

## 10. Usability Analysis of SmartPaint

*Student:* Nadia Röning

*Supervisor:* Filip Malmberg

*Reviewer:* Mats Lind and Olle Gällmo, Dept. of IT, UU

*Publisher:* UPTEC IT 14 051

*Abstract:* Image segmentation is the process of identifying and separating relevant objects and structures in an image. The purpose of segmentation is to simplify and/or change the representation of an image into something that is easier to analyze. SmartPaint is a software for semi-automatic segmentation of medical volume images, developed by Filip Malmberg. This thesis investigates whether SmartPaint is useful on several levels, such as usability, functionality and instructional effectiveness. The developer's ambition is that SmartPaint should be accessible to users without a background in computer science. Hence a formative usability study (Cooperative evaluation) was conducted, involving testing and interviewing participants. Given the result from the study and feedback from the participants, design proposals are given. Furthermore, ideas on how to expand the functionality, the instructional effectiveness and the learnability of SmartPaint are given.

## 11. An interactive interface for multiple-resolution analysis of large images

*Student:* Nguyen-Anh-Thu Tran

*Supervisor:* Petter Ranefall

*Reviewer:* Carolina Wählby and Olle Gällmo, Dept. of IT, UU

*Publisher:* UPTEC IT 14 034

*Abstract:* Digital image analysis has contributed greatly to medical sciences. Modern microscope slide scanning systems are capable of producing large images which can be more than one giga-pixel. It is useful for researchers to be able to view these images at multiple resolutions. For instance, to implement image-based sequencing of messenger ribonucleic acid (mRNA), high resolution images are required in detailed analysis while those at low resolution offer better overall visualization. Taking that as the motivation, a

map-viewer-like user interface with zooming and panning options has been developed to support detailed analysis in high resolution and at the same time be able to get a full overview in lower resolution. This thesis describes the context in which the interface is used as well as its design process.

## 12. Methods for automatic analysis of glucose uptake in adipose tissue using quantitative PET/MRI data

*Student:* Jonathan Andersson

*Supervisor:* Joel Kullberg, Dept. of ROS, Faculty of Medicine, UU

*Reviewer:* Robin Strand and Tomas Nyberg, Dept. of IT

*Publisher:* UPTEC F 14044

*Abstract:* Brown adipose tissue (BAT) is the main tissue involved in non-shivering heat production. A greater understanding of BAT could possibly lead to new ways of prevention and treatment of obesity and type 2 diabetes. The increasing prevalence of these conditions and the problems they cause society and individuals make the study of the subject important.

An ongoing study performed at the Turku University Hospital uses images acquired using PET/MRI with <sup>18</sup>F-FDG as the tracer. Scans are performed on sedentary and athlete subjects during normal room temperature and during cold stimulation. Sedentary subjects then undergo scanning during cold stimulation again after a six weeks long exercise training intervention. This degree project used images from this study.

The objective of this degree project was to examine methods to automatically and objectively quantify parameters relevant for activation of BAT in combined PET/MRI data. A secondary goal was to create images showing glucose uptake changes in subjects from images taken at different times.

Parameters were quantified in adipose tissue directly without registration (image matching), and for neck scans also after registration. Results for the first three subjects who have completed the study are presented. Larger registration errors were encountered near moving organs and in regions with less information.

The creation of images showing changes in glucose uptake seem to be working well for the neck scans, and somewhat well for other sub-volumes. These images can be useful for identification of BAT. Examples of these images are shown in the report.

*Comment:* In cooperation with Turku University Hospital

## 13. Cell Tracking in Microscopy Images Using a Rao-Blackwellized Particle Filter

*Student:* Sofia Lindmark

*Supervisor:* Thomas Schön, Dept. of IT

*Reviewer:* Carolina Wählby and Tomas Nyberg, Dept. of IT

*Publisher:* UPTEC F 14048

*Abstract:* Analysing migrating cells in microscopy time-lapse images has already helped the understanding of many biological processes and may be of importance in the development of new medical treatments. Today's biological experiments tend to produce a huge amount of dynamic image data and tracking the individual cells by hand has become a bottleneck for the further analysis work. A number of cell tracking methods have therefore been developed over the past decades, but still many of the techniques have a limited performance.

The aim of this Master Project is to develop a particle filter algorithm that automatically detects and tracks a large number of individual cells in an image sequence. The solution is based on a Rao-Blackwellized particle filter for multiple object tracking. The report also covers a review of existing automatic cell tracking techniques, a review of well-known filter techniques for single target tracking and how these techniques have been developed to handle multiple target tracking. The designed algorithm has been tested on real microscopy image data of neutrophils with 400 to 500 cells in each frame. The designed algorithm works well in areas of the images where no cells touch and can in these situations also correct for some segmentation mistakes. In areas where cells touch, the algorithm works well if the segmentation is correct, but often makes mistakes when it is not. A target effectiveness of 77 percent and a track purity of 80 percent are then achieved.

## 4 Graduate education

We give a number of PhD courses each year, both for our own students and for PhD students in subjects that use image analysis as a tool and need to know more about it. This year Cris Luengo gave a new course on Scientific Data Presentation. The available places were filled within an hour and we expect to give this popular course soon again. Carlina Wählby gave several courses to researchers in biomedicine, Ida-Maria Sintorn gave a course focussed on microscopy applications in Umeå and Robin Strand gave our long-running course in Application Oriented Image Analysis once again.

There were seven PhD defences this year.

### 4.1 Graduate courses

#### 1. Research methodology for information technology, 4hp

*Examiner:* Gunilla Borgefors

*Lecturer(s):* Gunilla Borgefors, Ulrika Haak

*Period:* 140424–0630

*Venue:* The course was given at CBA

*Description:* The goal is to give general and useful knowledge about how to become a good and published researcher in information technology and/or various applications thereof. The first part consists of five traditional lectures on general themes. The second part is a series of seminars held by the participants, describing a relevant scientific conference or journal and making an oral and a written report.

*Comment:* The written reports are collected in CBA internal Report No. 53.

#### 2. Scientific Data Presentation, 2hp

Gunilla Borgefors, **Cris Luengo**

*Period:* 141008–1105

*Venue:* The course was given at CBA

*Description:* The goal of the course is to give PhD students the ability to effectively present the data resulting from their experiments. The course covered different forms of graphs and tables for one and two-dimensional sampled data, categorical data, discrete values, etc.; certain aspects of human perception relevant to displaying data, including colour perception; the need to highlight the story in the data, refraining from displaying the non-essential things (without, of course, misrepresenting the data); and how to use drawing tools such as Illustrator or Inkscape to edit figures generated by Excel, MATLAB, or any other graphing tool.

*Comment:* Funded by FUN, TekNat

#### 3. Live Cell Imaging, 3hp

**Ida-Maria Sintorn**

*Venue:* The course was held at KI in Huddinge.

*Period:* 141013–1013

#### 4. Basic Image Analysis: Focused on Microscopy Applications, 3hp

Cris Luengo, **Ida-Maria Sintorn**, Carolina Wählby

*Period:* 140917–1009

*Venue:* The course was held at KI in Huddinge.

*Description:* This postgraduate course in Basic Image Analysis was organized administered by the Regenerative Medicine Doctoral Program for PhD students at Karolinska Institutet and KTH.

*Comment:* PhD level course: 9 lectures, 2 computer exercises (Fiji, CellProfiler), 1 week project on own data

#### 5. Classical & Modern Papers

PhD students at CBA, **Cris Luengo**

*Period:* During the whole year

*Venue:* The course was given at CBA

*Description:* Presentations and discussions of classical or modern papers in image processing.

**6. Scientific Visualization Workshop, 1hp**

**Anders Hast**, Johan Nysjö, Pontus Olsson

*Period:* 141127–1128

*Venue:* The workshop was given at CBA

*Description:* A workshop for PhDs and other researchers arranged by SNIC-UPPMAX and SeSE.

## 4.2 Dissertations

1. Date: 141020

### **Automated Tissue Image Analysis Using Pattern Recognition**

*Student:* Jimmy Azar

*Supervisor:* Anders Hast

*Assistant Supervisor:* Ewert Bengtsson and Martin Simonsson

*Opponent:* Marco Loog, Pattern Recognition & Bioinformatics Group, Delft University of Technology, The Netherlands

*Committee:* Gunilla Borgefors, Thomas Schön, Mats Gustafsson, Department of Information Technology, Uppsala University; Arne Östman, Department of Oncology-Pathology, Karolinska Institutet; Fritz Albregtsen, Department of Informatics, University of Oslo

*Publisher:* Acta Universitatis Upsaliensis, ISBN: 978-91-554-9028-7

*Abstract:* Automated tissue image analysis aims to develop algorithms for a variety of histological applications. This has important implications in the diagnostic grading of cancer such as in breast and prostate tissue, as well as in the quantification of prognostic and predictive biomarkers that may help assess the risk of recurrence and the responsiveness of tumors to endocrine therapy. In this thesis, we use pattern recognition and image analysis techniques to solve several problems relating to histopathology and immunohistochemistry applications. In particular, we present a new method for the detection and localization of tissue microarray cores in an automated manner and compare it against conventional approaches. We also present an unsupervised method for color decomposition based on modeling the image formation process while taking into account acquisition noise. The method is unsupervised and is able to overcome the limitation of specifying absorption spectra for the stains that require separation. This is done by estimating reference colors through fitting a Gaussian mixture model trained using expectation-maximization. Another important factor in histopathology is the choice of stain, though it often goes unnoticed. Stain color combinations determine the extent of overlap between chromaticity clusters in color space, and this intrinsic overlap sets a main limitation on the performance of classification methods, regardless of their nature or complexity. In this thesis, we present a framework for optimizing the selection of histological stains in a manner that is aligned with the final objective of automation, rather than visual analysis. Immunohistochemistry can facilitate the quantification of biomarkers such as estrogen, progesterone, and the human epidermal growth factor 2 receptors, in addition to Ki-67 proteins that are associated with cell growth and proliferation. As an application, we propose a method for the identification of paired antibodies based on correlating probability maps of immunostaining patterns across adjacent tissue sections. Finally, we present a new feature descriptor for characterizing glandular structure and tissue architecture, which form an important component of Gleason and tubule-based Elston grading. The method is based on defining shape-preserving, neighborhood annuli around lumen regions and gathering quantitative and spatial data concerning the various tissue-types.

2. Date: 20140411

### **Image Analysis Methods and Tools for Digital Histopathology Applications Relevant to Breast Cancer Diagnosis**

*Student:* Andreas Kårsnäs

*Supervisor:* Robin Strand

*Assistant Supervisor:* Ewert Bengtsson and Carolina Wählby

*Opponent:* Anant Madabhushi, Case Western Reserve University, OH, US

*Committee:* Johan Lundin, Institute for Molecular Medicine Finland, Helsinki, Finland; Arne Östman, Karolinska Institute, Stockholm; Andrew Mehnert, Chalmers Univ. of Technology; Irene Yu-Hua Gu, Chalmers Univ. of Technology; Anders Hast

*Publisher:* Acta Universitatis Upsaliensis, ISBN: 978-91-554-8889-5

*Abstract:* In 2012, more than 1.6 million new cases of breast cancer were diagnosed and about half a million women died of breast cancer. The incidence has increased in the developing world. The mortality, however, has decreased. This is thought to partly be the result of advances in diagnosis and treatment. Studying tissue samples from biopsies through a microscope is an important part of diagnosing breast cancer. Recent techniques include camera-equipped microscopes and whole slide scanning systems that allow for digital high-throughput scanning of tissue samples. The introduction of digital pathology has simplified parts of the analysis, but manual interpretation of tissue slides is still labor intensive and costly, and involves the risk for human errors and inconsistency. Digital image analysis has been proposed as an alternative approach

that can assist the pathologist in making an accurate diagnosis by providing additional automatic, fast and reproducible analyses. This thesis addresses the automation of conventional analyses of tissue, stained for biomarkers specific for the diagnosis of breast cancer, with the purpose of complementing the role of the pathologist. In order to quantify biomarker expression, extraction and classification of sub-cellular structures are needed. This thesis presents a method that allows for robust and fast segmentation of cell nuclei meeting the need for methods that are accurate despite large biological variations and variations in staining. The method is inspired by sparse coding and is based on dictionaries of local image patches. It is implemented in a tool for quantifying biomarker expression of various sub-cellular structures in whole slide images. Also presented are two methods for classifying the sub-cellular localization of staining patterns, in an attempt to automate the validation of antibody specificity, an important task within the process of antibody generation. In addition, this thesis explores methods for evaluation of multimodal data. Algorithms for registering consecutive tissue sections stained for different biomarkers are evaluated, both in terms of registration accuracy and deformation of local structures. A novel region-growing segmentation method for multimodal data is also presented. In conclusion, this thesis presents computerized image analysis methods and tools of potential value for digital pathology applications.

3. Date:

Automatic Virus Identification using TEM – Image Segmentation and Texture Analysis

*Student:* Gustaf Kylberg

*Supervisor:* Ida-Maria Sintorn

*Assistant Supervisor:* Gunilla Borgefors

*Opponent:* Walter Kropatsch, Vienna University of Technology

*Committee:* Stina Svensson, Ray Search Labs, Stockholm; Magnus Borga, Linköping University; Robin Strand; Abdenour Hadid, Oulu University, Finland; Kjell Hultenby, Karolinska Institute, Stockholm

*Publisher:* Acta Universitatis Upsaliensis, ISBN: 978-91-554-8873-4

*Abstract:* Viruses and their morphology have been detected and studied with electron microscopy (EM) since the end of the 1930s. The technique has been vital for the discovery of new viruses and in establishing the virus taxonomy. Today, electron microscopy is an important technique in clinical diagnostics. It both serves as a routine diagnostic technique as well as an essential tool for detecting infectious agents in new and unusual disease outbreaks.

The technique does not depend on virus specific targets and can therefore detect any virus present in the sample. New or reemerging viruses can be detected in EM images while being unrecognizable by molecular methods.

One problem with diagnostic EM is its high dependency on experts performing the analysis. Another problematic circumstance is that the EM facilities capable of handling the most dangerous pathogens are few, and decreasing in number.

This thesis addresses these shortcomings with diagnostic EM by proposing image analysis methods mimicking the actions of an expert operating the microscope. The methods cover strategies for automatic image acquisition, segmentation of possible virus particles, as well as methods for extracting characteristic properties from the particles enabling virus identification.

One discriminative property of viruses is their surface morphology or texture in the EM images. Describing texture in digital images is an important part of this thesis. Viruses show up in an arbitrary orientation in the TEM images, making rotation invariant texture description important. Rotation invariance and noise robustness are evaluated for several texture descriptors in the thesis. Three new texture datasets are introduced to facilitate these evaluations. Invariant features and generalization performance in texture recognition are also addressed in a more general context.

The work presented in this thesis has been part of the project Panvirshield, aiming for an automatic diagnostic system for viral pathogens using EM. The work is also part of the miniTEM project where a new desktop low-voltage electron microscope is developed with the aspiration to become an easy to use system reaching high levels of automation for clinical tissue sections, viruses and other nano-sized particles.

4. Date: 20141205

**Characterisation of wood-fibre-based materials using image analysis**

*Student:* Erik Wernersson

*Supervisor:* Gunilla Borgefors

*Assistant Supervisor:* Cris Luengo and Anders Brun

*Opponent:* Michal Kozubek, Masaryk University, Brno, Czech Republic

*Committee:* Gunnar Sparr, Lund Institute of Technology /Lund University; Björn Kruse Linköping University, Örjan Smedby Linköping University

*Publisher:* Acta Universitatis agriculturae Sueciae, ISBN: 978-91-576-8146-1

*Abstract:* Wood fibres are the main constituent of paper and are also used to alter properties of plastics in wood-fibre-based composite materials. The manufacturing of these materials involves numerous parameters that determine the quality of the products. The link between the manufacturing parameters and the final products can often be found in properties of the microstructure, which calls for advanced characterisation methods of the materials. Computerised image analysis is the discipline of using computers to automatically extract information from digital images. Computerised image analysis can be used to create automated methods suitable for the analysis of large data volumes. Inherently these methods give reproducible results and are not biased by individual analysts. In this thesis, three-dimensional X-ray computed tomography (CT) at micrometre resolution is used to image paper and composites. Image analysis methods are developed to characterise properties of individual fibres, properties of fibre-fibre bonds, and properties of the whole fibre networks based on these CT images. The main contributions of this thesis is the development of new automated image-analysis methods for characterisation of wood-fibre-based materials. This include the areas of fibre-fibre contacts and the free-fibre lengths. A method for reduction of phase contrast in mixed mode CT images is presented. This method retrieves absorption from images with both absorption and phase contrast. Curvature calculations in volumetric images are discussed and a new method is proposed that is suitable for three-dimensional images of materials with wood fibres, where the surfaces of the objects are close together.

5. *Date:*

**Image Analysis and Interactive Visualization Techniques for Electron Microscopy Tomograms**

*Student:* Lennart Svensson

*Supervisor:* Ida-Maria Sintorn

*Assistant Supervisor:* Ingela Nyström, Gunilla Borgefors

*Opponent:* Willy Wriggers, Associate Professor, Weill Cornell Medical College & Researcher, D.E. Shaw Research New York, US

*Committee:* Hans Hebert, Karolinska Institutet, Stockholm; Natasa Sladoje, University of Novi Sad, Serbia; Stefan Seipel, CBA

*Publisher:* Acta Universitatis agriculturae Sueciae, ISBN: 978-91-576-8136-2

*Abstract:* Images are an important data source in modern science and engineering. A continued challenge is to perform measurements on and extract useful information from the image data, i.e., to perform image analysis. Additionally, the image analysis results need to be visualized for best comprehension and to enable correct assessments. In this thesis, research is presented about digital image analysis and three-dimensional (3-D) visualization techniques for use with transmission electron microscopy (TEM) image data and in particular electron tomography, which provides 3-D reconstructions of the nano-structures. The electron tomograms are difficult to interpret because of, e.g., low signal-to-noise ratio, artefacts that stem from sample preparation and insufficient reconstruction information. Analysis is often performed by visual inspection or by registration, i.e., fitting, of molecular models to the image data. Setting up a visualization can however be tedious, and there may be large intra- and inter-user variation in how visualization parameters are set. Therefore, one topic studied in this thesis concerns automatic setup of the transfer function used in direct volume rendering of these tomograms. Results indicate that histogram and gradient based measures are useful in producing automatic and coherent visualizations. Furthermore, research has been conducted concerning registration of templates built using molecular models. Explorative visualization techniques are presented that can provide means of visualizing and navigating model parameter spaces. This gives a new type of visualization feedback to the biologist interpreting the TEM data. The introduced probabilistic template has an improved coverage of the molecular flexibility, by incorporating several conformations into a static model. Evaluation by cross-validation shows that the probabilistic template gives a higher correlation response than using a Protein Databank (PDB) devised model. The software ProViz (for Protein Visualization) is also introduced, where selected developed techniques have been incorporated and are demonstrated in practice.

6. *Date:* 140523

**Distance Functions and Their Use in Adaptive Mathematical Morphology**

*Student:* Vladimir Curic

*Supervisor:* Gunilla Borgefors

*Assistant Supervisor:* Cris Luengo

*Opponent:* Hugues Talbot, University Paris-Est - ESIEE, France

*Committee:* Christer Kiselman, UU; Gabriella Sanniti di Baja, Istituto di Cibernetica, Napoli, Italy; Alexander Medveded, UU; Reiner Lenz, Linköping University; Anders Heiden, Lund University

*Publisher:* Acta Universitatis Upsaliensis, ISBN: 978-91-554-8923-6

*Abstract:* One of the main problems in image analysis is a comparison of different shapes in images. It is often desirable to determine the extent to which one shape differs from another. This is usually a difficult task because shapes vary in size, length, contrast, texture, orientation, etc. Shapes can be described using sets of points, crisp or fuzzy. Hence, distance functions between sets have been used for comparing different shapes.

Mathematical morphology is a non-linear theory related to the shape or morphology of features in the image, and morphological operators are defined by the interaction between an image and a small set called a structuring element. Although morphological operators have been extensively used to differentiate shapes by their size, it is not an easy task to differentiate shapes with respect to other features such as contrast or orientation. One approach for differentiation on these type of features is to use data-dependent structuring elements.

In this thesis, we investigate the usefulness of various distance functions for: (i) shape registration and recognition; and (ii) construction of adaptive structuring elements and functions.

We examine existing distance functions between sets, and propose a new one, called the Complement weighted sum of minimal distances, where the contribution of each point to the distance function is determined by the position of the point within the set. The usefulness of the new distance function is shown for different image registration and shape recognition problems. Furthermore, we extend the new distance function to fuzzy sets and show its applicability to classification of fuzzy objects.

We propose two different types of adaptive structuring elements from the salience map of the edge strength: (i) the shape of a structuring element is predefined, and its size is determined from the salience map; (ii) the shape and size of a structuring element are dependent on the salience map. Using this salience map, we also define adaptive structuring functions. We also present the applicability of adaptive mathematical morphology to image regularization. The connection between adaptive mathematical morphology and Lasry-Lions regularization of non-smooth functions provides an elegant tool for image regularization.

#### 7. Date:

*Student:* Patrik Malm

*Supervisor:*

*Assistant Supervisor:*

*Opponent:*

*Committee:*

*Publisher:* Acta Universitatis Upsaliensis, ISBN:

*Abstract:*

## 5 Research

Our research activities are conducted in a large number of projects, both very application oriented and theoretical, both large and small, both long-running and short. Our largest application field is biomedicine, with many projects developing methods for analysing microscopic images of molecules, viruses, cells, and tissue. In addition we also have much going on in analysis and visualization of 3D medical images. In the latter case we develop haptic tools for interactive exploration of such images. We are also active in the analysis of wood and wood fibre based materials. In addition to these areas especially mentioned in our charter we are involved in other applications, the biggest of which is analysis of old, handwritten texts. There are also projects for the urban and rural environments – and for tracking bees. In our application projects we have a partner with a set of images and a problem getting information from them, a problem interesting enough to generate new analysis methods. We also develop new, general theory for image analysis and visualization, especially in digital geometry and mathematical morphology and usually in volume images, but not as much as we would like to. The reason is that it is much easier to get grants for applications of image analysis than for image analysis itself.

In Section 5.6 we have collected all partners, national and international, with which we had active co-operation in 2013. They can all also be found somewhere else in this report.

### 5.1 Forestry related applications

#### 1. Diffraction Artifact Reduction in $\mu$ CT Imaging

Erik Wernersson, Cris Luengo, Anders Brun, Gunilla Borgefors

*Partners:* Jan Van den Bulcke, Dept. of Forest and Water Management, Ghent University, Belgium; Matthieu Boone, Dept. of Physics and Astronomy, Ghent University, Belgium

*Funding:* S-faculty, SLU

*Period:* 1009 – 1412

*Abstract:* When imaging wood based materials, diffraction causes artefacts especially around sharp edges. While sometimes useful, and the only measurable properties of the imaged objects, they might as well be a nuisance which hinders proper analysis of the absorption coefficient. In this project, different ways to reduce such artefacts are investigated, especially in already reconstructed images. Compare to previous approaches, this is much faster and does not require that the original projection images are stored.

This year we presented a paper at SSBA that showed how to tune the parameters of the method that we published in the Journal of the Optical Society of America A (2013).

#### 2. Image Analysis of the Internal Structure of Paper and Wood Fibre Based Composite Materials in 3D images

Erik Wernersson, Anders Brun, Cris Luengo, Gunilla Borgefors

*Partners:* Gary Chinga, Norwegian Pulp and Fibre Research Institute, Trondheim, Norway; Catherine Östlund, Innventia, Stockholm; Thomas Joffre, Dept. of Engineering Sciences, Applied Mechanics, UU; Arttu Miettinen, Dept. of Physics, University of Jyväskylä (UJ), Finland; Joakim Lindblad, University of Novi Sad, Serbia; Svetlana Borodulina, Department of Solid Mechanics and BiMaC Innovation Center, KTH

*Funding:* S-faculty, SLU; WoodWisdom-Net

*Period:* 0406–1412

*Abstract:* The internal structure of paper is important because many of its properties correspond directly to the properties of single fibres and their interaction in the fibre network. How single fibres in paper bond and how this affects paper quality is not fully understood, since most structure analysis of paper has been performed in cross-sectional, two-dimensional (2D) images whereas paper is a complex, three-dimensional (3D) structure. Another application for wood fibres that has recently gained interest is wood polymer composite materials. The properties of these materials do not only depend on the structure of the fibre network, but also on the interaction between the fibres and the polymer matrix surrounding the fibres.

Advances in imaging technology have made it possible to acquire 3D images of paper and wood polymer composite materials. In this project, image analysis methods for characterising the 3D material structure in such images are developed. The detailed knowledge of the material structure attainable with these methods is useful for improving material properties and for developing new materials.

The project objective is to achieve a complete segmentation of individual fibres and pores in volume images of the material. Given such a segmentation, any desired measurement of the internal structure is available. A sample segmentation result is shown in Figure 2. Measurements on individual fibres and the structural arrangement of fibres can then be related to macroscopic material properties.

In this project, different volume images of paper and composite materials are available: one volume created from a series of 2D scanning electron microscopy (SEM) images at StoraEnso, Falun; and X-ray microtomography volume images of paper and composite samples imaged at the European Synchrotron Radiation Facility (ESRF) in Grenoble, France, at the Paul Scherrer Institut (PSI) in Villigen, Switzerland and also from tabletop scanners at University of Jyväskylä, Finland, at Applied Mechanics, Uppsala University, and at Innventia, Stockholm.

This year we published papers in Nordic Pulp & Paper Research Journal 29(3):468-475, Cellulose 21(6):3941-3950, and Mechanics of Materials 75:125-136.

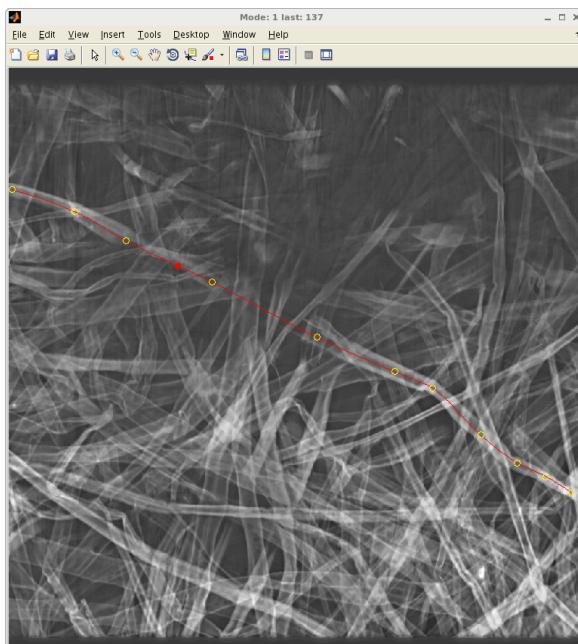


Figure 2: pending

### **3. Ring Width and Density Profiling with Helical CT**

Erik Wernersson, Cris Luengo, Anders Brun, Gunilla Borgefors

*Partners:* Jan Van den Bulcke, Dept. of Forest and Water Management, Ghent University, Belgium

*Funding:* S-faculty, SLU

*Period:* 1201 – 1412

*Abstract:* Dendrochronology relies on accurate measurements of annual ring widths. The most common method is to use a flatbed scanner to acquire high resolution images of polished wood surfaces. In this project we investigate potential gains using a helical X-ray device which produces volume images. Direct advantages include non destructive and simplified sample preparation procedures as well as compensation for the orientation of the inner structure which can not be seen with ordinary flatbed scans. It is also possible to find density profiles using the same images.

One article was published in *Dendrochronologia* 32(1):39-46.

### **4. Light scattering in paper**

Erik Wernersson, Cris Luengo

*Partners:* Tomas Linder and Torbjörn Löfqvist, Luleå University of Technology, Luleå

*Funding:* S-faculty, SLU

*Period:* 1212 – 1412

*Abstract:* Fibre orientation is an important structural property in paper and other fibrous materials. In this study we explore the relation between light scattering and in-plane fibre orientation in paper sheets. Light diffusion from a focused light source is simulated using a Monte Carlo technique where parameters describing the paper micro-structure were determined from 3D x-ray computed tomography images. Measurements and simulations on both spatially resolved reflectance and transmittance light scattering patterns show an elliptical shape where the main axis is aligned towards the fibre orientation.

Good qualitative agreement was found at low intensities and the results indicate that fibre orientation in thin fibre-based materials can be determined using spatially resolved reflectance or transmittance. Published in *Optics Express* 22(14):16829-16840, 2014.

## 5.2 Analysis of microscopic biomedical images

### 5. Identification of Highly Pathogenic Viruses in Transmission Electron Microscopy Images

Gustaf Kylberg, Ida-Maria Sintorn, Ewert Bengtsson, Gunilla Borgefors

*Partner:* Vironova AB; Delong Instruments, Brno, Czech Republic; Ali Mirazimi, Kjell-Olof Höglund, Centre for Microbiological Preparedness; Swedish Institute for Infectious Disease Control (SMI)

*Funding:* 2008–2011 Swedish Civil Contingencies Agency (MSB); Swedish Defense Materiel Administration (FMV); Swedish Agency for Innovative Systems (VINNOVA). 2011–2013 Eurostar project E!6143

*Period:* 0801–

*Abstract:* This project aims at automating the virus identification process in high resolution TEM images. This, in combination with Project 6 to create a rapid, objective, and user independent virus diagnostic system. The identification task consists of method development for segmenting virus particles with different shapes and sizes and extracting descriptive features of both shape and texture to enable the classification into virus species. Texture features such as variants of Local Binary Patterns and Regional Moments (filter banks constructed from orthogonal moments), are being evaluated on virus textures as well as other texture datasets to get a deeper understanding of the discriminant power of the features under different conditions. A paper comparing, combining and evaluating the discriminating power of local texture descriptors for virus classification was presented at the International Conference on Pattern Recognition (ICPR) in Stockholm in August and Gustaf Kylberg defended his PhD thesis closely linked to this project in March.

### 6. The miniTEM Project - Development of a Desk-top TEM with Automated Image Acquisition

Gustaf Kylberg, Ida-Maria Sintorn, Ewert Bengtsson, Gunilla Borgefors

*Partner:* Vironova AB; Delong Instruments, Brno, Czech Republic

*Funding:* Eurostar project E!6143

*Period:* 1107–1310

*Abstract:* Transmission electron microscopy (TEM) is an important clinical diagnostic and material analysis tool. Transmission electron microscopes are expensive, complex, sensitive and bulky machines, often housed in specially built rooms to avoid vibrations affecting the imaging process. They are to a very large extent manually operated, meaning that an expert in electron microscopy and preferably also in the application at hand needs to perform the analysis at the microscope, an often very time consuming task.

This project aimed at developing the MiniTEM, a desk-top low voltage TEM designed for imaging biological samples, with a high degree of automation regarding instrument alignment, image acquisition and analysis. The goal was a small, cheap, robust, and easy to use system that requires no more training than any simple lab equipment, and can be hosted in any office or lab (even mobile).

Automating the image acquisition process is key for reducing the manual input and making the imaging and analysis more objective. Within the project different strategies for automating the image acquisition were developed and investigated. The first was acquisition of images at random positions on the grid. The second was to search for a specific structure/object and only acquire (store) the images containing the structure/object of interest. The third was similar to the second approach but embedded in a multi-scale approach with the goal to make the acquisition more efficient.

The MiniTEM was launched and displayed at the International Microscopy Congress in Prague in September. One instrument was at the conference site and a second piece, physically in Stockholm, was operated remotely from Prague. Abstracts and posters about the project, the developed image analysis methods, and actual instrument, have been presented at various international and

national conferences and meetings throughout the year. Gustaf Kylberg successfully defended his PhD thesis early 2014, which was closely linked to this project. The MiniTEM, its GUI and two example images showing a mixture of typical clinical application areas are shown in Figure 3.

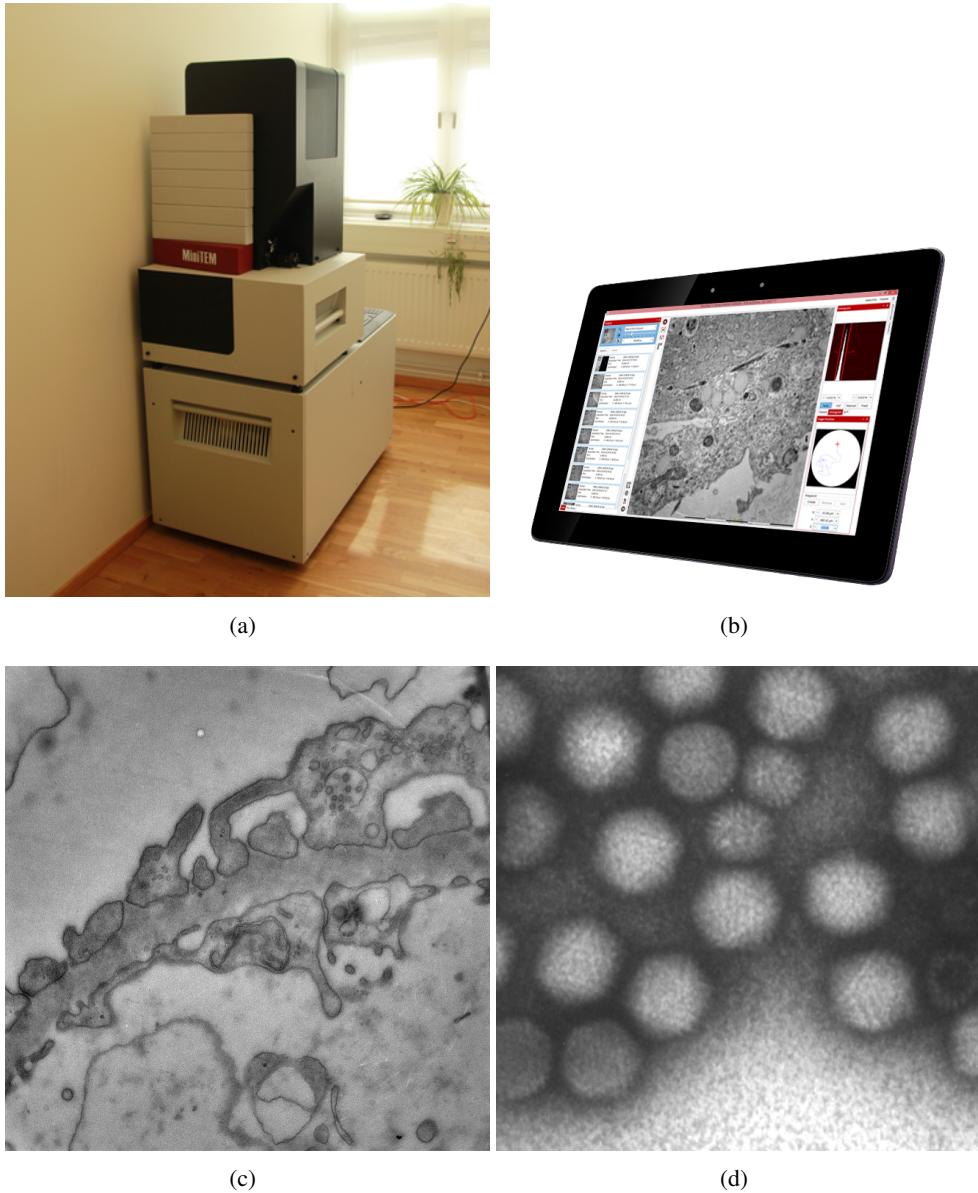


Figure 3: The MiniTEM instruments, its GUI and images of a filtering membrane in a kidney section and a mixture of Adeno and Rota viruses.

## 7. Detection and Localization of Fluorescent Signals in STORM Data Using Compressed Sensing

Omer Ishaq, Alexandra Pacureanu, Carolina Wählby

*Partners:* Johan Elf, Gustaf Ullman, Fredrik Persson, Dept. of Cell & Molecular Biology, UU

*Funding:* SciLifeLab Uppsala, eSSENCE, VR junior researcher grant to CW

*Period:* 1211-

*Abstract:* Stochastic optical reconstruction microscopy (STORM) is a super-resolution microscopy image acquisition technique for single-molecule localization. Like other stochastic super-resolution microscopy techniques it incorporates a trade-off between spatial- and temporal-resolution. Recently, a compressed-sensing (CS) based variant of STORM, called FasterSTORM, has been de-

veloped which substantially increases the temporal sampling of a stack of STORM image frames. This improvement is realized by increasing the density of activated fluorophores in each frame, followed by a subsequent CS-based retrieval of single-molecule positions even with overlapping fluorescent signals. However, the CS-based retrieval/decoding step is time consuming and can take as much as three hours for each image frame. We have accelerated the FasterSTORM method through parallel processing on multi-core processors. Additionally, we have tested and tried a number of  $L_1$ -solvers for CS-based recovery of molecule positions. A paper comparing convex and greedy solvers and evaluating the sensitivity of the FasterSTORM to estimation bias of the point spread function (PSF) was submitted to a conference. We are in the process of comparing the performance of the Faster STORM against a wavelet-based approach to localize fluorescent signals in time-lapse images of bacterial cells.

## 8. *In Situ* Sequencing of mRNA

Carolina Wählby, Alexandra Pacureanu, Petter Ranefall

*Partners:* Mats Nilsson, Rongqin Ke, Marco Mignardi, Thomas Hauling, Xiaoyan Qian, SciLifeLab Stockholm/Stockholm University

*Funding:* SciLifeLab Uppsala; TN-faculty, UU

*Period:* 1109–

*Abstract:* Profiling of gene expression is prerequisite for understanding the function of cells, organs and organisms, in health and disease. The sequencing techniques currently in use rely on homogenization of the samples. Therefore, the obtained information represents either the average expression profile of the tissue sample or expression profiles of isolated single cells. Our collaborators have developed a new molecular method, enabling *in situ* sequencing of mRNA, so that protein expression can be observed directly in cultured cells or tissue samples. We have developed image analysis tools for automated analysis of sequencing data, mapping, and visualization of gene expression patterns. In 2013 we presented the work as part of a Special Session on Advances in Computer-Aided Histopathology at the IEEE International Symposium on Biomedical Imaging (ISBI), Beijing 2014. The project was also presented at the 1st annual conference for the Society of Biomolecular Imaging and Informatics SBI2, at the JB Martin Conference Center at Harvard Medical School, Boston, MA, USA, where Carolina Wählby was honored with the 'SBI2 President's innovation award' for her presentation on 'Combining image-based *in situ* RNA screening with quantitative analysis of cell and tissue morphology'.

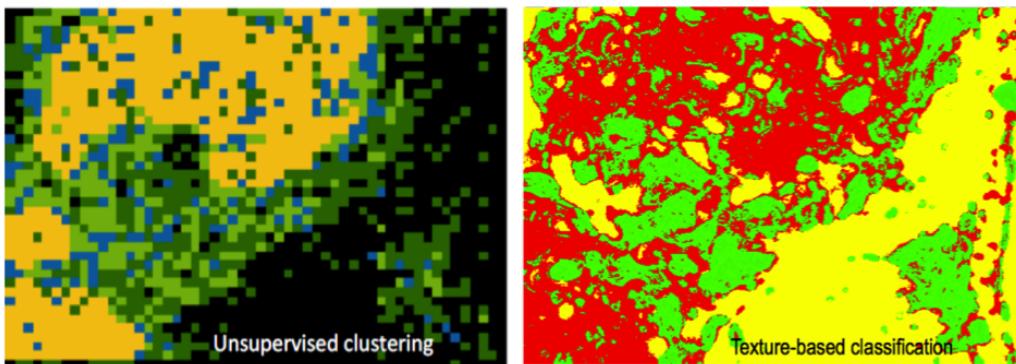


Figure 4: Coupling gene expression to cell and tissue morphology. The gene expression map was divided into patches of  $100 \times 100$  pixels, and patches were clustered by k-means clustering (100 random seeds). The resulting spatial patterns (left) correlate with independent texture-based classification of an H&E staining of the same tissue sample.

## 9. Evaluation of the Effect of Compaction Oligonucleotides on the Strength and Integrity of

## **Florescent Signals**

Omer Ishaq, Petter Ranefall, Carolina Wählby

*Partners:* Carl-Magnus Claesson, Linda Andersson, Ola Söderberg, Dept. of Immunology, Genetics and Pathology

*Funding:* SciLife Lab Uppsala

*Period:* 1310–

*Abstract:* Rolling circle amplification (RCA) performs nucleic acid replication for rapid synthesis of multiple concatenated copies of circular DNA. These molecules can be visually observed through the use of fluorescent markers. Moreover, the introduction of a compaction oligonucleotide during RCA results in brighter and more compact signals. The project aims to evaluate the effect of compaction oligonucleotides on the strength and integrity of fluorescent signals. A manuscript has been submitted.

## **10. Skeleton-Based Vascular Segmentation at Interactive Speed**

Kristína Lidayová, Hans Frimmel, Ewert Bengtsson

*Partner:* Örjan Smedby, Chunliang Wang, Center for Medical Image Science and Visualization (CMIV), Linköping University

*Funding:* VR grant to Örjan Smedby

*Period:* 1207–

*Abstract:* Precise segmentation of vascular structures is crucial for studying the effect of stenoses on arterial blood flow. The goal of this project is to develop and evaluate vascular segmentation, which will be fast enough to permit interactive clinical use. The first part is the extraction of the centerline tree (skeleton) from the gray-scale CT image. Later this skeleton is used as a seed region. The method should offer sub-voxel accuracy.

During 2013 we improved the software for fast vessel centerline tree extraction. The method has been tested on several CT data and the results look promising. Generally main vessel centerlines are detected, but an improvement needs to be done in order to remove some false positive centerlines.

In year 2014 we improved the software to its final stage. It works on the original Computed Tomography Angiography (CTA) image as the input and produces a node-link representation of the vascular structures for the lower limbs. The method (Figure. 5) works in two passes: first pass extracts the skeleton of large arteries, and second pass focus on extracting small arteries. Each pass contains three major steps: (1) sets proper intensity ranges for different anatomy structures based on Gaussian curve fitting to the image histogram; (2) apply different filters to detect voxels that are part of arteries, where filters are designed based on intensity and size analysis of ellipse shape on 2-D planes; (3) connect nodes to obtain a centerline tree for the entire vasculature. The method has been tested on 25 CTA scans of the lower limbs (Figure. 6) and achieved an average of 96% overlap rate with ground truth. The average computational time is 121 sec/scan.

A paper summarizing this work was written and was sent to a Special issue of Pattern Recognition Letters on skeletonization and its applications. At the current stage the paper is under major revision. The work was presented at SSBA conference and Medicinteknikdagarna.

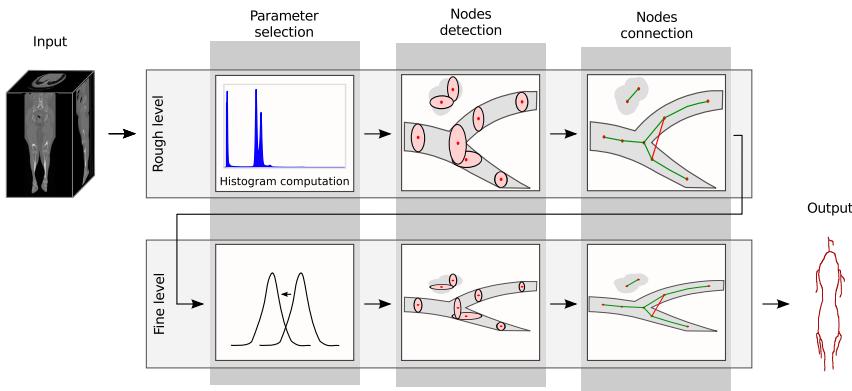


Figure 5: Flow chart of the proposed method

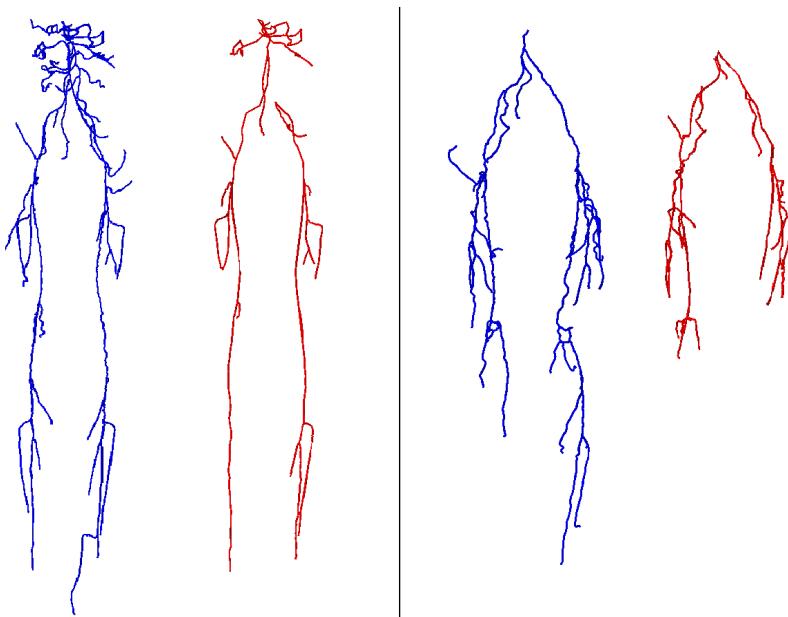


Figure 6: Ground truth skeleton in blue colour and resulting skeleton in red colour are shown for two cases from a clinical routine. The case on the right side contains an occluded segment in the femoral artery and severe stenoses.

## 11. SciLifeLab Cancer Stem Cell Program

Damian Matuszewski, Carolina Wählby, Ida-Maria Sintorn

*Partners:* Sven Nelander, Karin Forsberg-Nilsson, Irina Alafuzoff, Ulf Landegren, Anna Segerman, Tobias Sjöblom, Lene Urborn and Bengt Westermark, Department of Immunology, Genetics and Pathology and SciLifeLab, UU, Bo Lundgren, the Karolinska Institute and SciLifeLab, Stockholm, Rebecka Jörnsten, Chalmers, Gothenburg, and Göran Hesselager, UU Hospital, Uppsala

*Funding:* AstraZeneca-Science for Life Laboratory Joint Research Program

*Period:* 1303–

*Abstract:* The SciLifeLab Cancer Stem Cell Program is a cross-platform initiative to characterize cancer stem cells (CSCs). Previously, the development of drugs targeting the CSC population in solid tumors has been curbed by the lack of valid cell model systems, and the complex genetic heterogeneity across tumors, factors that make it hard to assess new targets or predict drug responses in the individual patient. To solve these problems, our aim is to develop a biobank of highly char-

acterized CSC cultures as a valid model of cancer heterogeneity. We will combine mathematical and experimental approaches, including image-based high-throughput cell screening, to define the spectrum of therapeutically relevant regulatory differences between patients. This will help elucidate mechanisms of action and enable accurate targeting of disease subgroups. During 2013-2014, patient data was collected, and a number of primary cell lines were established. Cultured cells were exposed to a different treatments and doses (more than 2500 different treatments per cell line), and imaged by fluorescence as well as bright-field microscopy, and current focus is on extracting meaningful morphological descriptors from the image data. Developed tools are also applied in a cell cycle analysis project realized together with Jordi Carreras Puigvert, the Karolinska Institute and SciLifeLab, Stockholm.

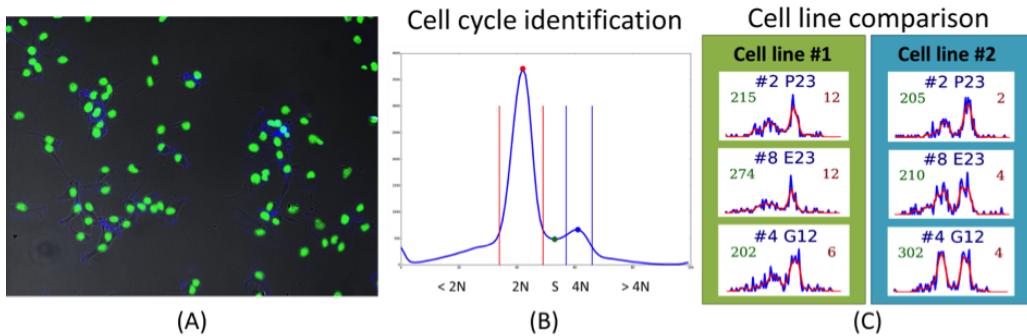


Figure 7: (A) Sample cancer stem cells image. Figures (B) and (C) present histograms of one of the automatically extracted features – DNA content per cell. (B) The different phases of the cell cycle can be identified based on the DNA content in negative control cells, by assuming that cells spend the majority of their time with either two (2N phase) or four (4N phase) copies of the DNA. Cells from different cell lines respond in a slightly different way to the same drug treatments, and (C) shows DNA histograms for treatments that arrest part of the cell population in the 4N phase.

## 12. Endothelial Cell Segmentation of the Cornea of Human Eyes

Bettina Selig, Cris Luengo

*Partners:* Bernd Rieger, Quantitative Imaging Group, Delft University of Technology, Netherlands; Koen Vermeer, The Rotterdam Eye Hospital, The Netherlands

*Funding:* S-faculty, SLU

*Period:* 1103–

*Abstract:* The corneal endothelium plays a key role in maintaining the transparency of the cornea. Because the cells in the endothelium do not regenerate, the cell density decreases with age; this reduces its ability to maintain the processes needed to keep the cornea transparent. Thus, being able to measure this density in patients is very important. The endothelium can be imaged by specular microscopy or by confocal scanners, and measurements can be obtained manually, automatically with manual corrections, or fully automatically with current software (e.g., Nidek's NAVIS). Unfortunately, the results of the automatic methods are often useless, especially at low cell densities. Together with the Rotterdam Eye Hospital, we have developed a fully automatic method to segment individual cells in the corneal endothelium. The result of the method can be used to determine the cell density, but also other parameters of interest, like pleomorphism (cell shape) and polymegathism (cell size variation). Our segmentation method produces a segmentation that matches a manual segmentation reasonably well, for a wide range of cell densities and image qualities. These results have been submitted for publication during 2014.

## 13. CerviScan

Ewert Bengtsson, Patrik Malm, Bo Nordin

*Partners:* Rajesh Kumar, Centre for Development of Advanced Computing (CDAC), Thiruvananthapuram, Kerala, India; K. Sujathan, Regional Cancer Centre, Thiruvananthapuram, Kerala, India; Andrew Mehnert, Chalmers

*Funding:* Swedish Governmental Agency for Innovation Systems (VINNOVA); Swedish Research Council; SIDA

*Period:* 0801–

*Abstract:* Cervical cancer is a disease that annually kills over a quarter of a million women worldwide. This number could be substantially reduced if women were regularly screened for signs of cancer precursors using the well-established Pap-test. If detected early, these precursors can be treated with a very high rate of success. A problem with the Pap-test is that it requires highly trained cytotechnologists to perform the time consuming visual analysis of the specimen. For over 50 years attempts to automate this process have been made but still no cost effective systems are available.

The CerviScan project is an initiative from the Indian government, managed by the research institute CDAC in cooperation with the Regional Cancer Centre (RCC) in Kerala and CBA in Sweden, aimed at creating a low cost, automated screening system. The system will reduce the number of cytotechnologists needed for population screening by identifying and removing specimen that are clearly normal. A prototype system has been created and used to screen over 1000 specimen. Initial classification results are promising but screening times are still about 10 times longer than what is realistic in a real screening setting. Plans for the next phase of the project, focusing on dedicated hardware, are awaiting the result of a funding application in India.

A subproject on developing improved ways of describing the nuclear chromatin patterns based on new image analysis methods has been spun off and is described as project XX ([Advanced methods for reliable and cost efficient image processing in life sciences](#))

The project has resulted in several recent publications and a PhD thesis: "Image Analysis in Support of Computer-Assisted Cervical Cancer Screening" which was defended February 7, 2014 by Patrik Malm.

#### **14. Automated Tissue Image Analysis using Pattern Recognition**

Jimmy Azar, Anders Hast, Ewert Bengtsson

*Funding:* TN-faculty, UU

*Period:* 1001–1410

*Abstract:* The research was initially part of a VR supported project for grading of prostate cancer. The final part of the research which took place during 2013-2014 extended this to more general ways of describing the architecture of histological tissues.

Immunohistochemistry can facilitate the quantification of biomarkers such as estrogen, progesterone, and the human epidermal growth factor 2 receptors, in addition to Ki-67 proteins that are associated with cell growth and proliferation. We developed a method for the identification of paired antibodies based on correlating probability maps of immunostaining patterns across adjacent tissue sections. Samples from the Human Protein Atlas project were used to test the method.

We also developed a new feature descriptor for characterizing glandular structure and tissue architecture, which form an important component of Gleason and tubule-based Elston grading. The method is based on defining shape-preserving, neighborhood annuli around lumen regions.

These two studies were accepted as journal papers. They also became part of the PhD thesis by Jimmy Azar, with the same title as the project, defended on October 10 2014.

#### **15. Segmentation and Tracking of E.coli Bacteria in Bright-Field Microscopy Images**

Sajith Kecheril Sadanandan, Carolina Wählby

*Partners:* Johan Elf and David Fange and Alexis Boucharin, Dept. of Cell & Molecular Biology, UU

*Funding:* SciLifeLab Uppsala, eSSENCE, VR junior researcher grant to CW

*Period:* 1210–

*Abstract:* Live cell experiments pave way to understand the complex biological functions of living organisms. Most live cell experiments require monitoring of cells under different conditions over several generations. The biological experiments display wide variations even when performed under similar conditions, and therefore need to include large population studied over several generations to provide statistically verifiable conclusions. Time-lapse images of such experiments usually generate large quantities of data, which become extremely difficult for human observers to evaluate. Thus, automated systems are helpful to analysis of such data and provide valuable inference from the experiment. In this work we segment and track E. coli bacteria cells over time. We developed a novel segmentation method, which is fast and robust in delineating bacterial cells in phase contrast microscopy images. The preliminary results (Figure 8) were presented as poster at the international Bioimage Informatics 2014 conference in Leuven, Belgium.

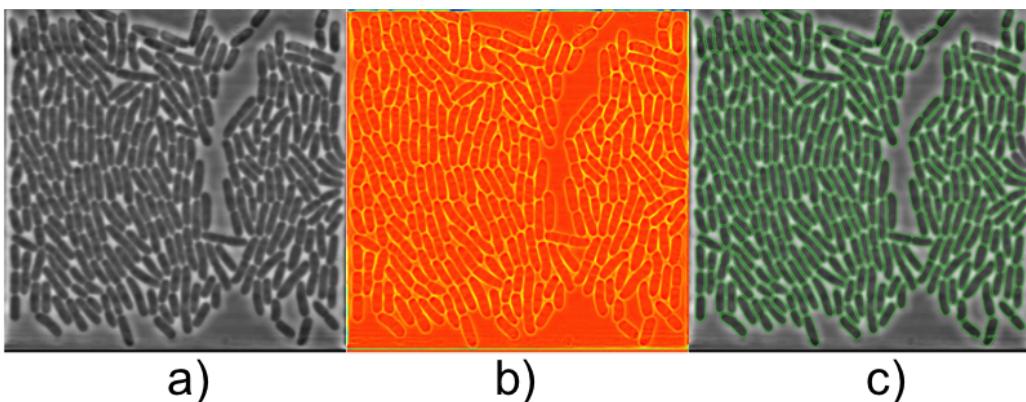


Figure 8: a) Input phase contrast image of E. coli bacteria, b) contrast enhanced image, c) segmentation result overlaid on the input image.

## 16. Modelling Diffusion on Cell Surfaces

Ida-Maria Sintorn, Robin Strand

*Partners:* Ingela Parmryd, Dept. of Medical Cell Biology, UU; Jeremy Adler, Dept. Of Immunology, Genetics and Pathology, UU

*Funding:* TN-faculty, UU; S-faculty, SLU; VINNIMER programme, Swedish Governmental Agency for Innovation Systems

*Period:* 1101–

*Abstract:* A cell surface is a highly irregular and rough. The surface topography is however usually ignored in current models of the plasma membrane, which are based on 2D observations of diffusion that really occurs in 3D. In this project we model diffusion on non-flat surfaces to explain biological processes occurring on the cellsurface.

## 17. Analysis of Male Reproductive Tract Morphology in Reproductive Toxicology

Azadeh Fakhrzadeh, Cris Luengo, Gunilla Borgefors

*Partners:* Ellinor Spörndly-Nees, Lena Holm, Dept. of Anatomy, Physiology and Biochemistry, SLU

*Funding:* SLU (KoN)

*Period:* 1009–

*Abstract:* Reproductive toxicology is the study of chemicals and their effects on the reproductive system of humans and animals. In reproductive toxicology, there is a strong need to detect structural differences in organs that often have both a complex microscopic structure and function. This problem is further complicated because standard techniques are based on the examination of two-dimensional sections of a three-dimensional structure. The aim of this project is to develop methods to objectively describe microscopic structures of male reproductive organs and to test these in reproductive toxicology research. The project is comparative and includes studies of organs from rooster and mink. We are developing automatic and interactive methods to analyze the relevant structures in the histology images of testis. We have constructed a semi-automatic method to delineate the epithelium cell layer in testicular tissue. The cell nuclei are detected using the fast radial symmetry filter. A graph is constructed on top of the epithelial cells (Fig. 9). Graph-cut optimization method is used to cut the links between cells of different tubules. Generating sperms in seminiferous tubules is a cyclic process, during which various generations of germ cells in epithelial layer undergo a series of developmental steps. This cycle can be subdivided into 12 different stages. We are currently developing a texture-based classification method to determine each tubule's stage.

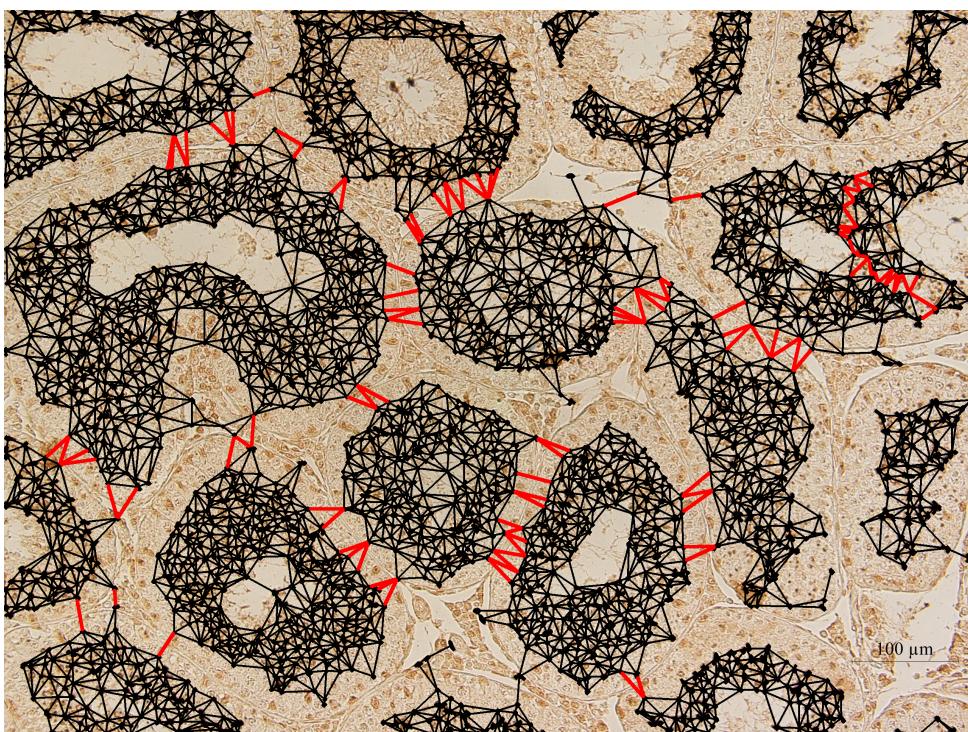


Figure 9: A graph constructed on top of Gata-4 marked germ cells.

## 18. Automated Classification of Immunostaining Patterns in Breast Tissue from the Human Protein Atlas

Andreas Kårsnäs, Martin Simonsson, Carolina Wählby, Robin Strand

*Partners:* Caroline Kampf, The Human Protein Atlas (HPA); Virginie Uhlmann, Imaging Platform, Broad Institute of Harvard and MIT, Cambridge, Massachusetts MA, USA; S. Issac Niwas, P. Palanisamy, Dept. of ECE, National Institute of Technology (NIT), Tiruchirappalli, India

*Funding:* SciLifeLab Uppsala

*Period:* 1201-1303

**Abstract:** The Human Protein Atlas (HPA) is an effort to map the location of all human proteins (<http://www.proteinatlas.org/>) and contains a large number of histological images of sections from human tissue. Methods for quantification of staining patterns in histopathology have many applications, ranging from antibody quality control to tumor grading. In this project we have tested a new method based on complex wavelets textural features as well as an approach inspired by WNDCHARM (Weighted Neighbor Distances using a Compound Hierarchy of Algorithms Representing Morphology) for classifying nuclear versus cytoplasmic staining. During 2013, a paper was published in Journal of Pathology Informatics.

## 19. Combating Breast Cancer by Digital Pathology

Andreas Kårsnäs, Robin Strand, Carolina Wählby, Ewert Bengtsson

*Partners:* Visiopharm, Hørsholm, Denmark; Clinical Pathology Division, Vejle hospital, Vejle, Denmark

*Funding:* NordForsk Private Public Partnership PhD Programme and Visiopharm

*Period:* 0909–

**Abstract:** The results of analyses of tissue biopsies by pathologists are crucial for breast cancer patients. In particular, the precision of a patient's prognosis, and the ability to predict the consequences of various treatment opportunities before actually exposing the cancer patient, depend on the detection and quantification of biomarkers in tissue sections by microscopy. Experience from the last decade has revealed that manual detection and quantification of biomarkers by microscopy of tissue biopsies is highly dependent on the competencies and stamina of the individual pathologist. The aim of the present PhD project is to develop software-based algorithms that can facilitate the workflow and ensure objective and more precise results of the quantitative microscopy procedures in breast cancer.

During 2012, we worked on a project for verifying antibodies by comparing staining patterns in immune-stained histological images. The project was made in collaboration with the Human Protein Atlas project. We made a comparison of different methods for classifying staining patterns in histology. This work was presented at MICCAI'12 in Nice. We also presented the *vectorial minimum barrier distance*, a new method for computing gray-weighted distance transforms while incorporating vectorial data, at ICPR'12 in Tsukuba, Japan.

Early 2013, we started a new project aimed at developing a new method for registering histological images of consecutive sections with different staining. The project resulted in an article about multimodal registration using locally rigid transforms. The article is currently under review. In 2013, we also finished a journal article presenting a histopathological tool for sub-cellular quantification. The article was accepted early 2014 for publication in the journal *Computer methods in Biomechanics and Biomedical Engineering: Imaging & Visualization*.

## 20. Automatic, Quantitative Malignancy Grading of Prostate Cancer using Image Analysis

Ingrid Carlbom, Christophe Avenel

*Partners:* Christer Busch and Anna Tolf, Department of Immunology, Genetics and Pathology, University Hospital

*Funding:* The Swedish Research Council, Hillevi Fries Research Fund

*Period:* 1001–

**Abstract:** Gleason grading is the most widely used system for determining the severity of prostate cancer. The Gleason grade is determined visually under a microscope from prostate tissue that is most often stained with Hematoxylin-Eosin (H&E).

*Stain for blind color decomposition* In an earlier study we demonstrated that H&E is not ideal for machine learning applications, but that other stains, such as Sirius-hematoxylin (Sir-Htx), may perform better. This year we demonstrated the advantages of this stain over H&E for blind color

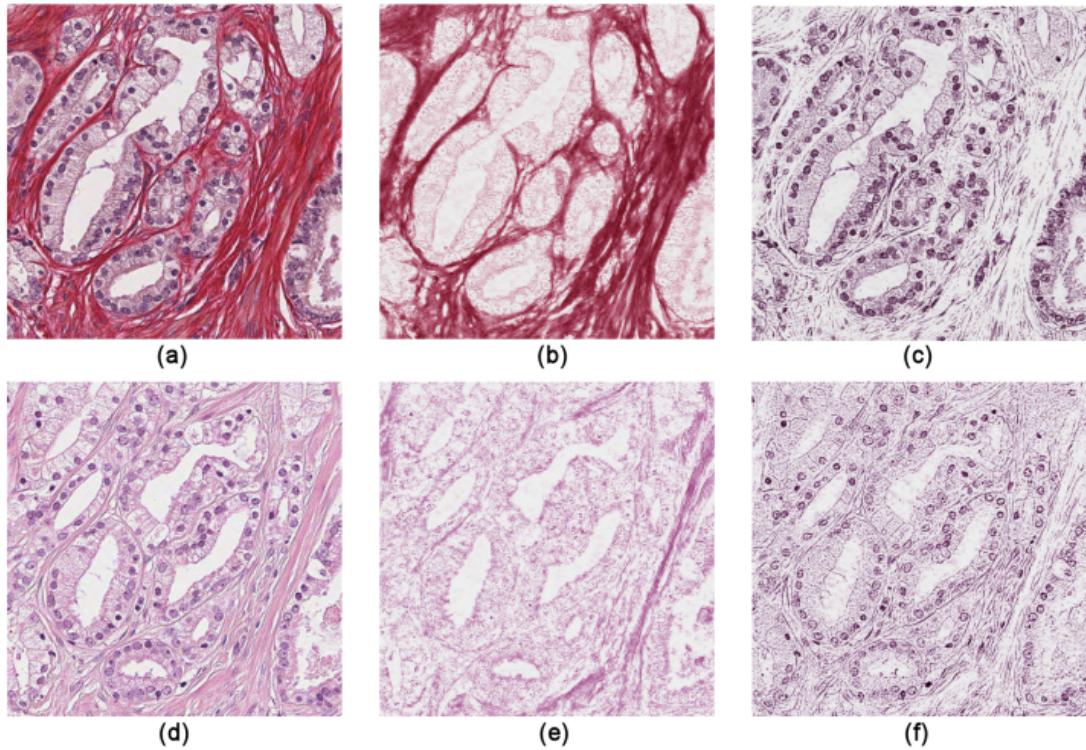


Figure 10: Results of color decomposition: (a) original tissue image stained with Sir-Htx, (b) stroma density map, and (c) epithelial density map; (d) original tissue image stained with H&E, (e) stroma density map, and (f) nuclei density map.

decomposition (Fig. 10). When compared to ground truth defined by an experienced pathologist, the relative root-mean-square errors of the color decomposition mixing matrices for Sir-Htx are better than those for H&E by a factor of two, and the Pearson correlation coefficients of the density maps resulting from the decomposition of Sir-Htx-stained tissue gives a 99% correlation with the ground truth. Qualitative examples of the density maps confirm the quantitative findings and illustrate that the density maps will allow accurate segmentation of morphological features that determine the Gleason grade.

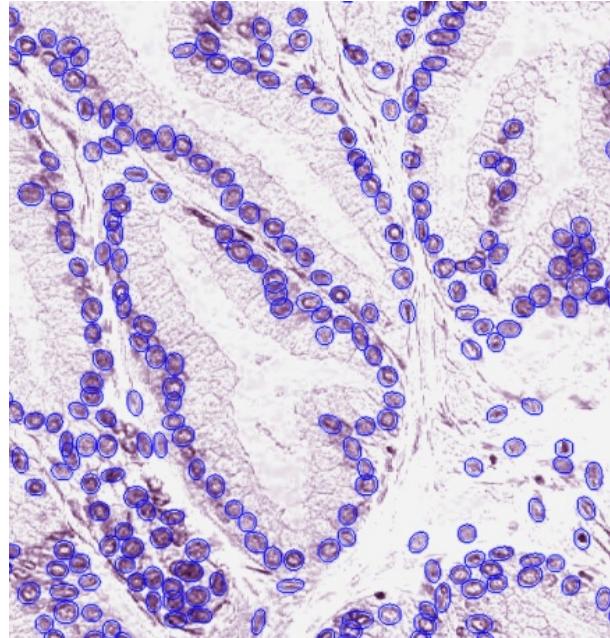


Figure 11: Epithelial nuclei identified by the marked point process.

*Identification of epithelial nuclei* From the epithelial density map, resulting from the blind color decomposition of Sir-Htx-stained prostate tissue, we used a marked point process to segment the epithelial nuclei (Fig. 11). This enables us to extract nuclei as individual, joint, or overlapping objects generally without discarding overlapping parts and therefore without major loss in segmentation precision. The algorithm, which was originally developed for breast cancer tissue nuclei identification, uses simulated annealing combined with a "birth and death" process to find the best match with the density map, and was adapted to prostate tissue by pre-and-post processing methods.

*Database of images from whole mount sections* We have created two online tools in order to build a database of graded images. The image selection tool is based on OpenSeaDragon (an open-source, web-based viewer for zoomable images) and facilitates the selection of small images from whole mount sections. With this tool we are building an image database where each image has a dominant pattern that represents for example one Gleason grade, benign tissue, stroma, or artifacts such as a tear in the tissue. The grading tool allows multiple pathologists to grade and comment on the previously selected images, without seeing each other grades, and is a basis for a consensus-graded database for developing and testing automatic Gleason grading algorithms (Fig. 12).

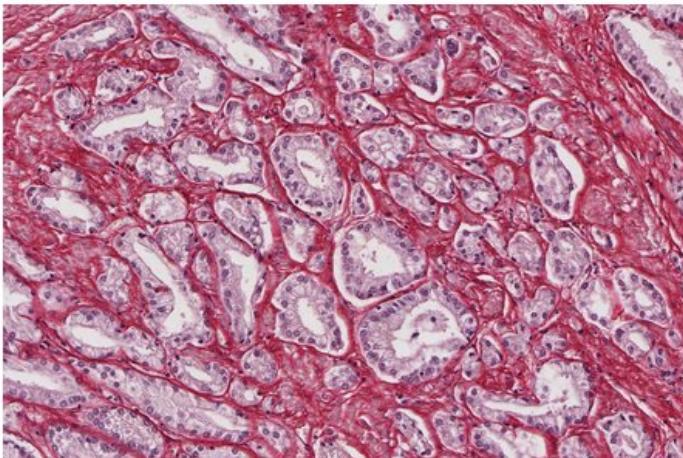
Images		Values	
		CB2-008	Score
		Ingrid	2 + 4
		Christer	2 + 3
		Anna	3 + 5
		Consensus grade	+

Figure 12: Example of a sub-section of a whole-mount tissue section with three individual scores.

## 21. Automated Quantification of Zebrafish Tail Deformation for High-throughput Drug Screening

Omer Ishaq, Alexandra Pacureanu, Carolina Wählby

*Partners:* Joseph Negri, Mark-Anthony Bray, Randall T. Peterson, Broad Institute of Harvard and MIT

*Funding:* SciLifeLab Uppsala

*Period:* 1203–1304

*Abstract:* Zebrafish (*Danio rerio*) is an important model organism in biomedical research due to its ease of handling and translucent body and consequently many human disease models have been established in the Zebrafish. Zebrafish embryos undergo spinal deformation upon exposure to chemical agents, such as Camptothecin (Cpt), that inhibit DNA repair. We are developing automated image-based quantification of spine deformation enabling whole-organism based assays for use in early-phase drug discovery campaigns. Our automated method for accurate high-throughput measurement of tail deformations in multi-fish micro-plate wells generates refined medial representations of partial tail-segments. Subsequently, these disjoint segments are analyzed and fused to generate complete Zebrafish tails (Fig. 13). Based on these estimated tail curvatures we reach a classification accuracy of 91% on individual animals as compared to known control treatment. This accuracy is increased to 95% when combining scores for fish in the same well. A paper describing the methods and results was published and presented at the International Symposium for Biomedical Imaging (ISBI) in April 2013.

## 22. Quantification of Zebrafish Lipid Droplets

Petter Ranefall, Carolina Wählby

*Partners:* Marcel den Hoed, Manoj Bandaru, Erik Ingelsson, Department of Medical Sciences and SciLifeLab, UU

*Funding:* SciLifeLab Uppsala

*Period:* 1308–

*Abstract:* The aim of this project is to identify novel targets for the therapeutic intervention of coronary artery disease. This is done by following-up results from genome-wide association studies in epidemiological studies using a zebrafish model system. Using image analysis we try to identify and characterize causal genes within loci that have so far been identified as associated

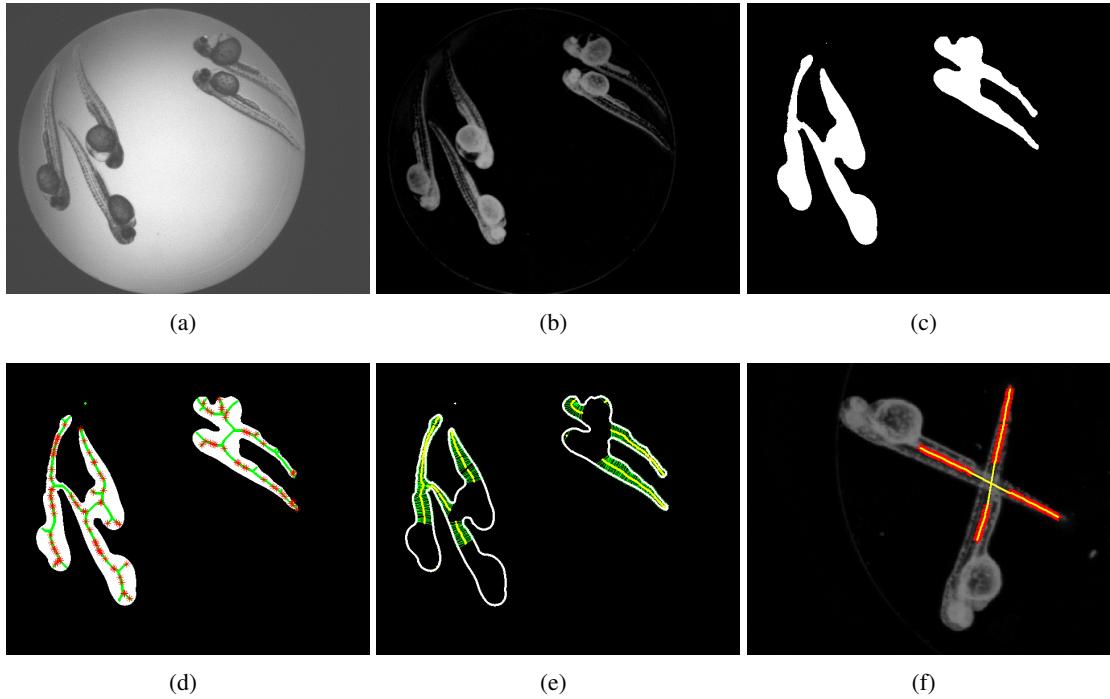


Figure 13: Steps for curvature extraction: (a) An input image; (b) After illumination correction; (c) Binary image after smoothing and thresholding; (d) Computed medial axes (highlighted in green) and seed-points (highlighted in red); (e) Refined medial axes (highlighted in yellow); (f) Medial axis fusion: the red lines represent tail-segments fused together to yield the complete tails (shown in yellow).

with coronary heart disease by (high-throughput) screening of atherogenic processes in wildtype and mutant zebrafish, both before and after feeding on a control diet or a diet high in cholesterol. Using confocal microscopy we can image fat accumulation in the zebrafish (Fig. 14).

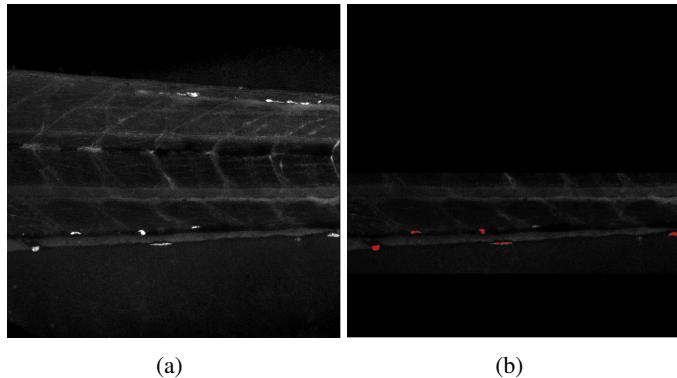


Figure 14: The image to the left is a maximum projection of the zebrafish image volume, and the image to the right shows the detected stationary lipids in red.

### 23. Optical Projection Tomography

Alexandra Pacureanu, Omer Ishaq, Carolina Wählby

*Partners:* Amin Allalou, Izolde AB, Uppsala; Johan Ledin, Evolutionary Biology Centre, Zebrafish platform, SciLifeLab Uppsala; Jos Buijs, Ridgeview Uppsala, Carlos Pardo, Mehmet F. Yanik, Research Laboratory of Electronics, Massachusetts Institute of Technology, Cambridge,

USA

*Funding:* SciLifeLab Uppsala; TN-faculty, UU

*Period:* 1009–

*Abstract:* Isotropic 3D imaging of biological specimens is instrumental for further breakthroughs in life sciences. Many biological specimens with high relevance for basic research, disease studies and drug discovery, such as model organisms or 3D cell cultures, are semi-transparent to visible light. This lead to the advent of the technique dubbed optical projection tomography (OPT). The 3D internal structure is revealed by the attenuation variations of the light traversing the specimen. In OPT transverse slices of the specimen are reconstructed from a set of angular projections and stacked together into a volumetric image. This method enables *in vivo* imaging of relatively large samples with high spatial resolution. A high-throughput platform for cellular resolution, *in vivo* OPT of zebrafish has been developed at MIT, Cambridge, USA. With this system we have shown that OPT of zebrafish embryos can provide 3D information enabling high-throughput screening of subtle phenotypic changes in relation to drug treatment, as published in *Nature Communications* in February 2013. However, OPT imaging systems in general are still quite sophisticated and costly. We are therefore developing a system for optical 3D isotropic imaging at microscopic scale, based on readily accessible hardware. The total price of the setup is kept under 1000 euros and the components can be easily obtained around the world. We have assembled the image acquisition system, acquired, and reconstructed images of zebrafish embryos (Fig. 15) and of 3D cell cultures (Fig. 16). We are complementing the simple hardware with open source computational tools, embedding algorithms for image alignment, correction and reconstruction. Our goal is to enable every life sciences research laboratory to have access to valuable 3D information on biological specimens. In 2013, besides working on improving imaging of zebrafish embryos, we attempted to image 3D cell cultures with our system, in collaboration with Jos Buijs (Ridgeview). A human ovarian carcinoma cell line has been used to grow 3D cell cultures in borosilicate thin tubes. We also tested growing the cells in agar gels and performing a 'biopsy' to extract the cells and transfer them into borosilicate tubes for imaging. We presented a poster at IEEE International Symposium on Biomedical Imaging (ISBI), San Francisco, USA and a journal manuscript is under preparation.

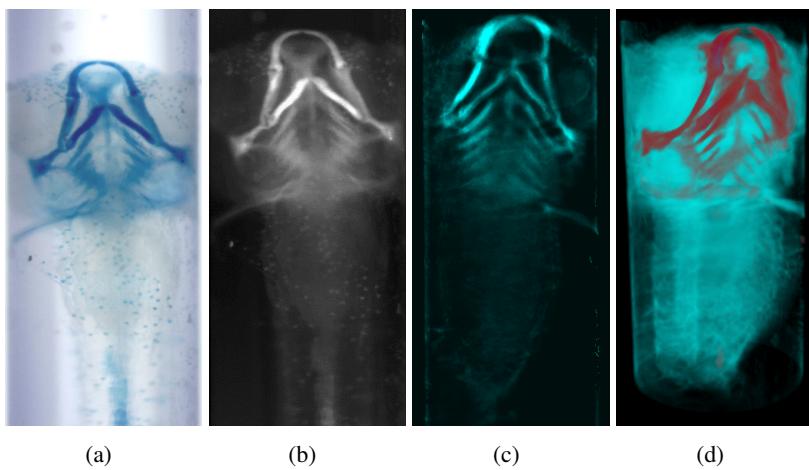


Figure 15: (a) Recorded projection of a zebrafish embryo. (b) The projection after flat field correction. (c) Reconstructed frontal slice. (d) Volume rendering of the reconstructed image.

#### 24. Image-based Approaches for Drug Tablet Quality Assessment

Ida-Maria Sintorn, Carolina Wählby

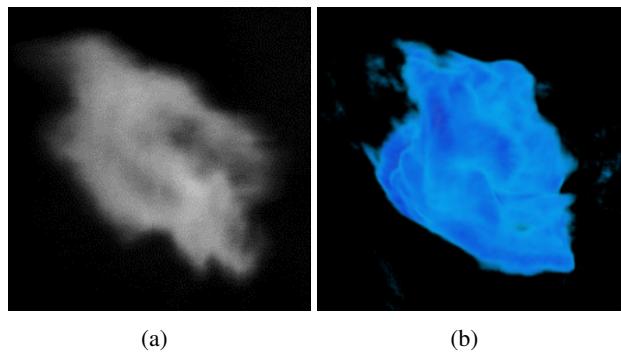


Figure 16: (a) Projection of a 3D cell culture. (b) Volume rendering of the reconstructed image.

*Partners:* Mark Nicholas, Mats Josefson, AstraZeneca, Mölndal, Sweden

*Funding:* Pre-study grant from AIMDay Image, UU Innovation

*Period:* 1204–1302

*Abstract:* It is known qualitatively that microstructural differences in solid dosage forms (e.g. tablets and inhalation powders) affect the performance of the medication. The microstructural differences are differences in the spatial distribution of active and inactive compounds. The aim of this project is to characterize these microstructural differences in order to determine whether imaging techniques such as CLSM (confocal laser scanning microscopy), wide-field fluorescence microscopy, and TOF-SIMS (Time-Of-Flight Secondary Ion Mass Spectroscopy) can reveal quantifiable differences in structure. The problem was addressed using a combination of local intensity features and texture measurements (including granulometry, Zernike moments, and Haralick features), and measurements were correlated with tablet characteristics/treatments. Due to a relatively limited dataset, it was difficult to find statistically significant differences. The data was presented to AstraZeneca researchers in January 2013.

## 25. Tools for Analysis and Visualization of Giga-Pixel Sized Slide-Scanner Images.

Petter Ranefall, Alexandra Pacureanu, Carolina Wählby

*Partners:* Mats Nilsson, Thomas Hauling, Marco Mignardi, Jessica Svedlund, Elin Lundin, Department of Biochemistry and Biophysics and SciLifeLab, Stockholm University.

*Funding:* SciLifeLab

*Period:* 1308–

*Abstract:* The aim is to create a tool for full resolution image analysis of large images, e.g. slide scanner data, with the possibility of visual examination and interaction at multiple resolutions. The tool is built on a free and open-source framework for visual examination at multiple resolutions with the option to toggle results on or off, such as segmentation masks, classification results, and tissue morphology measurements, using a map view with seamless zooming and panning capabilities, allowing for fast navigation between a full-tissue view and high-resolution sub-cellular observations (Fig. 17). The aim is to also have an interface that enables visual/manual selection of regions of interest, target discovery, and understanding of novel spatial relationships within the tissue environment.

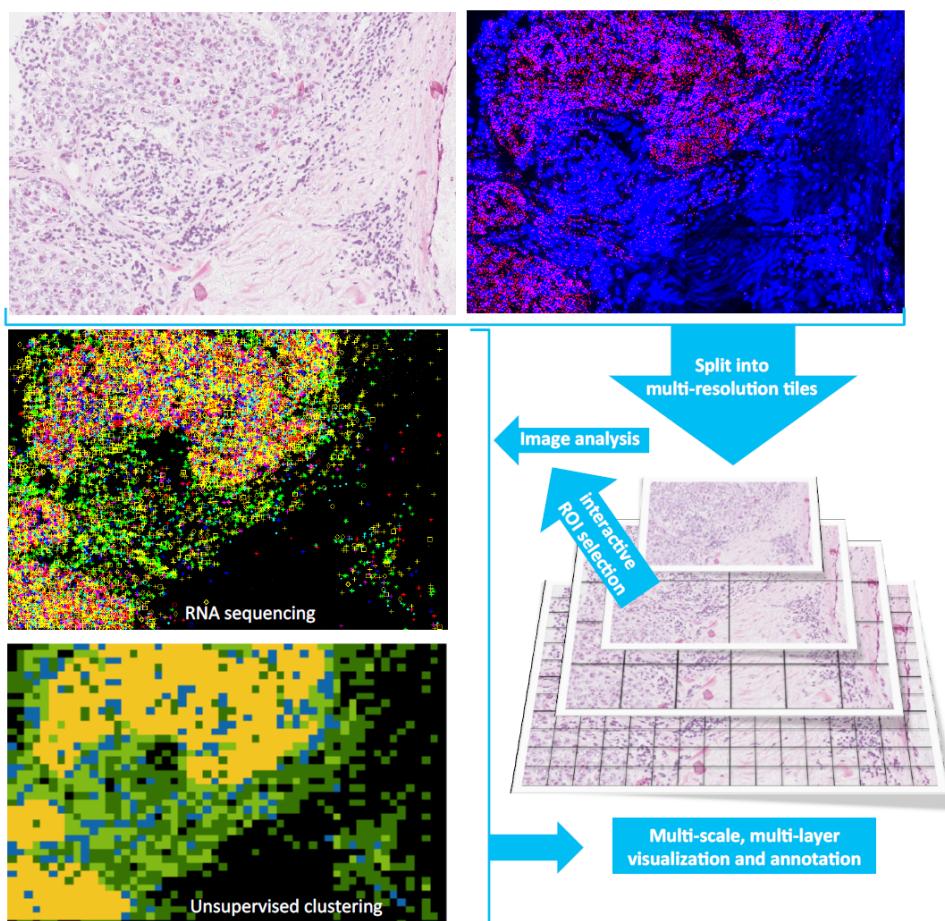


Figure 17: A description of the workflow.

## 5.3 3D analysis and visualization

### 26. Haptics and its Applications to Medicine

Ingrid Carlstrom, Stefan Seipel, Pontus Olsson, Fredrik Nysjö

*Partner:* Stefan Johansson (Division of Microsystems Technology, UU and Teknovest AB); Jan-Michaël Hirsch, Dept. of Surgical Sciences, Oral & Maxillofacial Surgery, UU and Consultant at Dept. of Plastic- and Maxillofacial Surgery, UU Hospital; Andreas Thor, Dept. of Surgical Sciences, Oral & Maxillofacial Surgery, UU Hospital; Andres Rodriguez Lorenzo, Department of Surgical Sciences, Plastic Surgery, UU Hospital; PiezoMotors AB, SenseGraphics AB.

*Funding:* Dept. of Surgical Sciences, Oral & Maxillofacial Surgery, University Hospital

*Period:* 1301–

#### Abstract:

*Two Degrees-of-Freedom Haptic Gripper with Ultrasonic Piezoelectric Motors* Piezoelectric motors have a high force/mass ratio, which makes them a promising alternative to electromagnetic motors for actuation of haptic interfaces. We have previously developed and evaluated a haptic gripper actuated by a quasi-static piezoelectric motor, operating within the audible range. The evaluation highlighted two main areas for improvement: faster and quieter actuation. During the last year we have designed a new admittance-type haptic gripper (see Figure 18) with two degrees-of-freedom (DOF), actuated by ultrasonic piezoelectric motors with higher maximum speed and silent operation compared to quasi-static motors. The gripper provides one DOF for the thumb and one DOF for the remaining fingers. All DOFs are direct-drive, involving no mechanical gearing, to minimize backlash and friction. Two custom-made strain-gauge load cells, mounted on the motor axes, measure forces applied by the user.

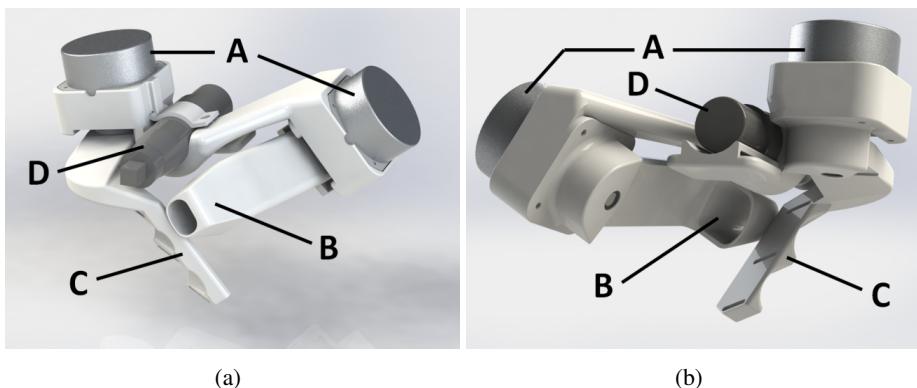


Figure 18: CAD model of haptic gripper seen from the front (left) and back (right). The ultrasonic piezoelectric motors (A) actuate one DOF for the thumb (B) and one DOF for the remaining fingers (C). The connector (D) may be used to attach the gripper to a commercial six DOF haptic arm, for a total of eight DOF.

*SplineGrip - An Eight Degrees-of-Freedom Flexible Haptic Sculpting Tool* SplineGrip is a flexible haptic sculpting tool that senses the articulation of the hand in two degrees-of-freedom (DOF) that we presented as a SIGGRAPH'13 poster. The tool is mounted on a commercial haptic device that tracks hand pose (position and orientation in six DOF) while simultaneously providing three DOF haptic feedback to the hand. The eight DOF input is mapped to the pose and shape of a virtual representation of a sculpting tool (Figure 19), offering versatile interaction with a virtual model.

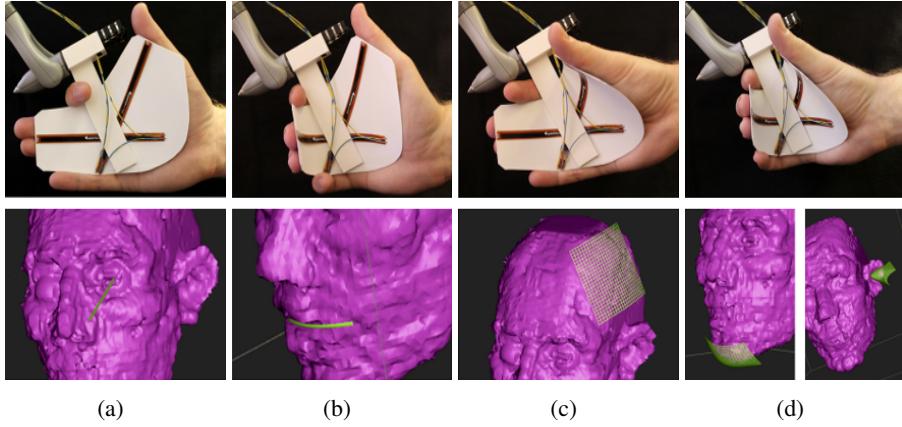


Figure 19: Example of possible mapping between physical and virtual tool: (a) all fingers straight - the virtual sculpting tool becomes a line segment; (b) middle and ring fingers bent - the curvature of the tool changes; (c) thumb bent - the width of the tool changes; (d) both sensors bent - simultaneous control of curvature and width.

**Custom Mandibular Implants** Congenital mandibular bone defects or defects due to tumor resection or trauma often result in substantial functional and aesthetic problems. The use of titanium scaffold implants that may hold bone substitutes for patients that do not require soft tissue transfer has the potential to reduce morbidity, costs, and rehabilitation time.

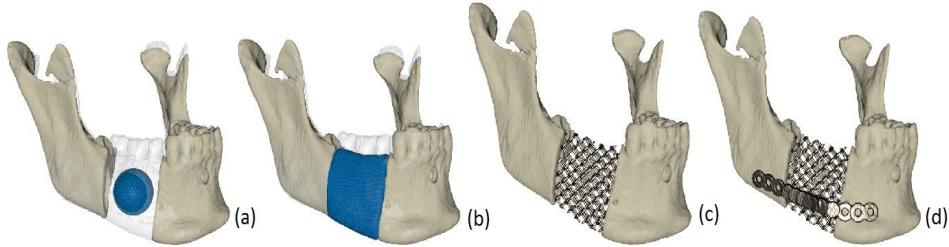


Figure 20: Design steps: (a) initialization of the deformable model (blue). Its growth is constrained by a bounding surface (transparent) and the defect surfaces; (b) model growing; (c) fine-tuning and generation of scaffold structure; (d) plate design.

We developed a semi-automatic method based on deformable models and haptics that allows the design and virtual testing of a scaffold implant before production. Using pre-segmented CT-data, a surgeon begins with virtual bone resection, using an interactive cutting tool, to give the defect region good load bearing contact surfaces. Next he/she positions the initial deformable model, which may be a simple sphere, in the defect region and places the bounding surface around the defect (Figure 20a). The system calculates external forces for the deformable model that expand it towards the defect contact surfaces and the bounding surface until it fills the defect (Figure 20b). The shape may be adjusted interactively. The surgeon may also refine the implant with the cutting tool and reposition it inside the defect relying on haptic feedback to perfect its fit. The system generates the scaffold structures of the implant (Figure 20c), and the surgeon may add fixation plates to the structure (Figure 20d).

## 27. ProViz – Interactive Visualization of 3D Protein Images

Lennart Svensson, Ida-Maria Sintorn, Ingela Nyström, Fredrik Nysjö, Johan Nysjö, Anders Brun, Gunilla Borgefors

*Partners:* Dept. of Cell and Molecular Biology, Karolinska Institute; SenseGraphics AB

*Funding:* The Visualization Program by Knowledge Foundation; Vaardal Foundation; Foundation for Strategic Research; VINNOVA; Invest in Sweden Agency

*Period:* 0807–

*Abstract:* Electron tomography is the only microscopy technique that allows 3-D imaging of biological samples at nano-meter resolution. It thus enables studies of both the dynamics of proteins and individual macromolecular structures in tissue. However, the electron tomography images have a low signal-to-noise ratio, which makes image analysis methods an important tool in interpreting the images. The ProViz project aims at developing visualization and analysis methods in this area.

In general, the project focus 2013 has been on increasing the accessibility of the previously developed methods, by continuing to work on a user-friendly software containing the most important ProViz results. Figure 21 shows how this software can display an electron tomogram, synthetic in this case, and a 3-D fitness landscape showing the matching results for a protein template.

Project highlights during 2013 include a two months research collaboration stay at the Okinawa Institute of Science and Technology, OIST, in Japan and the publishing of a paper at the Iberian Conference on Pattern Recognition and Image Analysis, IbPRIA. During the stay at OIST the software developed in the ProViz project was presented and discussed in depth, with adjustments to the software and improvements to an upcoming manuscript as the result. The research stay was made possible primarily through a JSPS, Japan Society for the Promotion of Science, fellowship. The presented paper concerned a new way of creating registration templates for finding biological structures in electron tomograms.

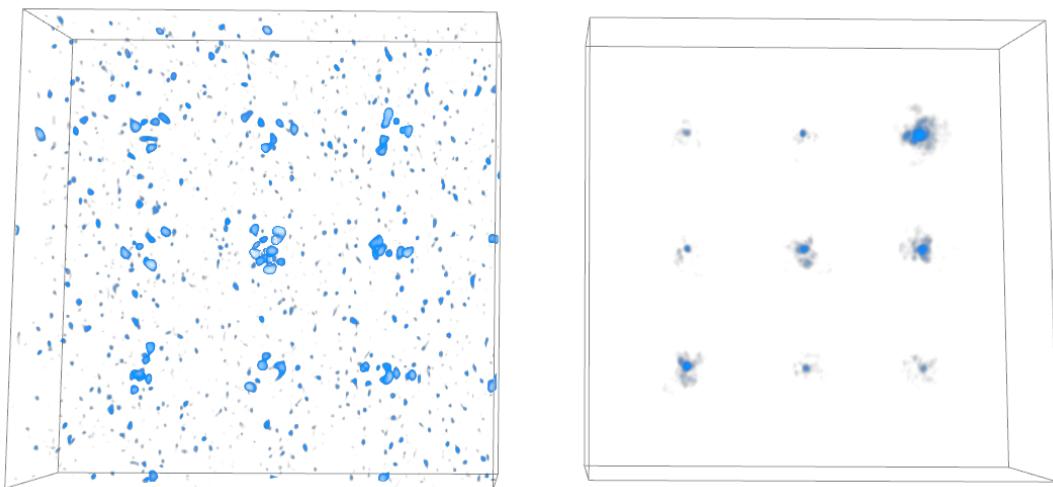


Figure 21: For searching an electron tomography image (left) with a molecular template, a standard, but powerful, method is to use a correlation search with a static template. With the ProViz software a 3-D fitness landscape (right), showing the correlation result at different points, can easily be calculated. The electron tomography image to the left is in this case synthetic for evaluation purposes.

## 28. Analysis and Processing of Three-Dimensional Magnetic Resonance Images on Optimal Lattices

Elisabeth Linnér, Robin Strand

*Funding:* TN-faculty, UU

*Period:* 1005–

*Abstract:* Three-dimensional images are widely used in, for example, health care. With optimal sampling lattices, the amount of data can be reduced by 30% without affecting the image quality. In this project, methods for image acquisition, analysis and visualization using optimal sampling lattices are studied and developed, with special focus on magnetic resonance imaging. The intention is that this project will lead to faster and better processing of images with less demands on data storage capacity.

During 2013, the focus has been on distance transforms. A paper describing a graph-based implementation of the anti-aliased Euclidean distance transform was submitted for publication.

## 29. Registration of Medical Volume Images

Robin Strand, Filip Malmberg

*Partner:* Joel Kullberg, Håkan Ahlström, Dept. of Radiology, Oncology and Radiation Science, UU

*Funding:* Faculty of Medicine, UU

*Period:* 1208–

*Abstract:* In this project, we mainly process magnetic resonance tomography (MR) images. MR images are very useful in clinical use and in medical research, e.g., for analyzing the composition of the human body. At the division of Radiology, UU, a huge amount of MR data, including whole body MR images is acquired for research on the connection between the composition of the human body and disease.

To compare volume images voxel by voxel, we develop image registration methods. For example, large scale analysis is enabled by image registration methods that utilizes, for example, segmented tissue (see, e.g., Project 30) and anatomical landmarks. Another example is interactive image registration where a user can fine-tune the segmentation result by a user interface, see Figure 22.

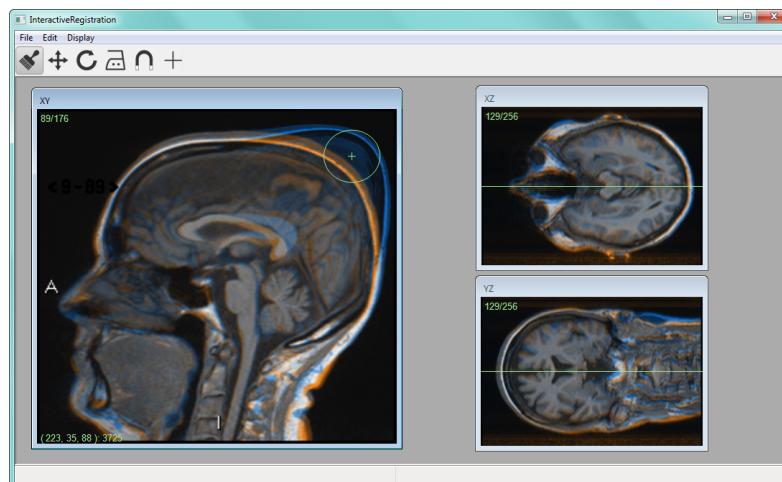


Figure 22: A screen-shot of the user interface of our software for interactive deformable registration. The target image and the transformed source image are displayed using a colored overlay in three orthogonal views. The user can deform the source image by clicking and dragging in any of the views, as shown in the screen-shot.

### 30. Interactive Segmentation and Analysis of Medical Images

Filip Malmberg, Robin Strand, Ingela Nyström, Ewert Bengtsson

*Partners:* Joel Kullberg, Håkan Ahlström, Dept. of Radiology, Oncology and Radiation Science, UU

*Funding:* TN-faculty, UU

*Period:* 1106–

*Abstract:* Three-dimensional imaging technique such as computed tomography (CT) and magnetic resonance imaging (MRI) are now routinely used in medicine. This has lead to an ever increasing flow of high-resolution, high-dimensional, image data that needs to be qualitatively and quantitatively analyzed. Typically, this analysis requires accurate segmentation of the image.

At CBA, we have been developing powerful new methods for interactive image segmentation (see Project 35). In this project, We seek to employ these methods for segmentation of medical images, in collaboration with the Dept. of Radiology, Oncology and Radiation Science at the UU Hospital. In 2013 a software for interactive segmentation, called *Smartpaint*, was made publicly available (Fig. 23). The software can be downloaded from <http://www.cb.uu.se/~filip/SmartPaint/>.

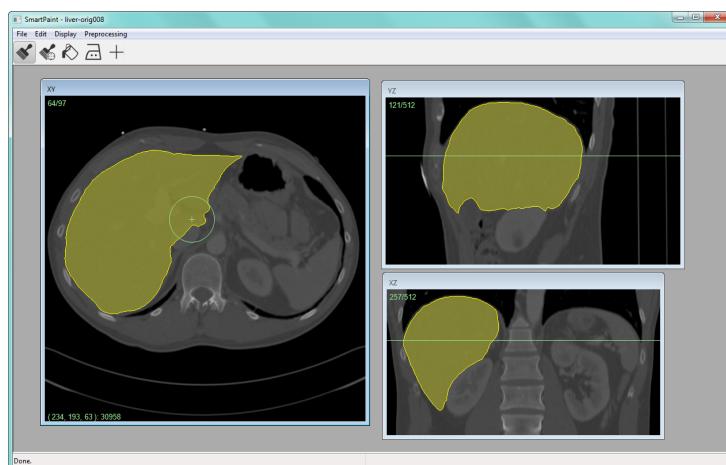


Figure 23: Screenshot from the *Smartpaint* software for interactive segmentation of volume images, developed at CBA. A radiologist segments the prostate in a MR image by interactively “painting” the segmentation using a brush tool.

### 31. Orbit Segmentation for Cranio-Maxillofacial Surgery Planning

Filip Malmberg, Ewert Bengtsson, Ingela Nyström, Johan Nysjö

*Partners:* Jan Michael Hirsch, Andreas Thor, Johanna Nilsson, Dept. of Surgical Sciences, UU Hospital; Roman Khonsari, Pitie Salpêtrière Hospital, Paris, France; Jonathan Britto, Great Ormond Street Hospital, London, United Kingdom

*Funding:* TN-faculty, UU; NovaMedTech

*Period:* 0912–

*Abstract:* A central problem in cranio-maxillofacial (CMF) surgery is to restore the normal anatomy of the skeleton after defects, i.e., malformations, tumors and trauma to the face. This is particularly difficult when a fracture causes vital anatomical structures such as the bone segments to be displaced significantly from their proper position, when bone segments are missing, or when a bone segment is located in such a position that any attempt to restore it into its original position poses considerable risk for causing further damage to vital anatomical structures such as the eye or the central nervous system. There is ample evidence that careful pre-operative planning can

significantly improve the precision and predictability and reduce morbidity of the craniofacial reconstruction. In addition, time in the operating room can be reduced. An important component in surgery planning is to be able to accurately measure the extent of certain anatomical structures. Of particular interest in CMF surgery are the shape and volume of the orbits (eye sockets) comparing the left side with the right side. These properties can be measured in CT images of the skull, but this requires accurate segmentation of the orbits. Today, segmentation is usually performed by manual tracing of the orbit in a large number of slices of the CT image. This task is very time-consuming, and sensitive to operator errors. Semi-automatic segmentation methods could reduce the required operator time significantly. In this project, we are developing a prototype of a semi-automatic system for segmenting the orbit in CT images. The segmentation system is based on WISH, a software package for interactive visualization and segmentation that has been developed at CBA since 2003. WISH has been released under an open-source license and is available for download at <http://www.cb.uu.se/research/haptics>.

In 2011, a paper about the orbit segmentation system was presented at the International Visual Information Conference (IVIC) in Malaysia. We also started investigating other applications for the system, e.g., volumetric measurements of the airway space in cone beam CT images and volumetric measurements of the maxillary sinuses in CT images.

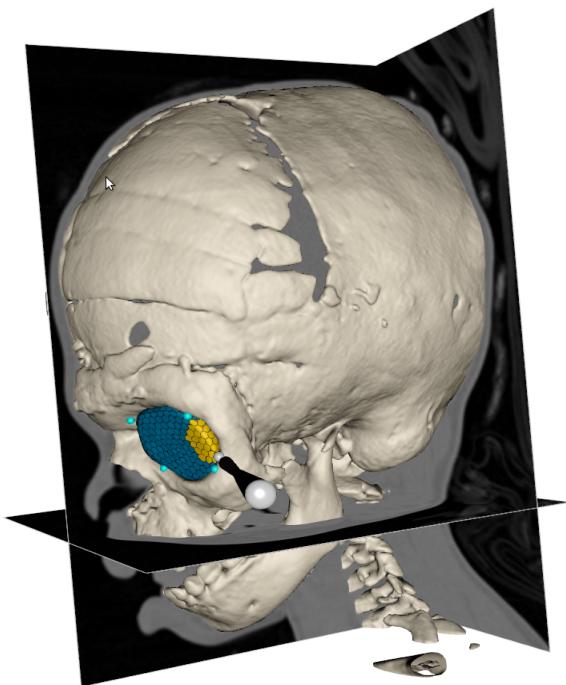


Figure 24: Haptic-aided semi-automatic segmentation of the left orbit (eye-socket) in a post-operative CT scan of a patient suffering from Crouzon syndrom, a congenital disorder that makes the orbits smaller and more shallow than normal.

During 2013, we have been collaborating with people from the Craniofacial Centre at Great Ormond Street Hospital, London, United Kingdom, in a project that aims to analyse the size and shape of the orbits in pre- and post-operative CT images of patients with congenital disorders. The semi-automatic segmentation system has been used to segment the orbits in these datasets (Fig. 24), and we have developed automatic tools for performing size and shape analysis of the segmented orbits (Fig. 25). Several abstracts about the ongoing work has been presented at medical conferences. Next, we plan to summarize the collected data and extend the abstracts to journal publications. In addition, we have performed two smaller orbit segmentation studies together with

people from the UU hospital, resulting in one presented abstract at Tandläkarnas Riksstämma. In collaboration with Roman Khonsari at Pitie Salpetriere Hospital, Paris, France, we also published a paper on shape and volume measurements on intentionally deformed skulls in American Journal of Physical Anthropology.

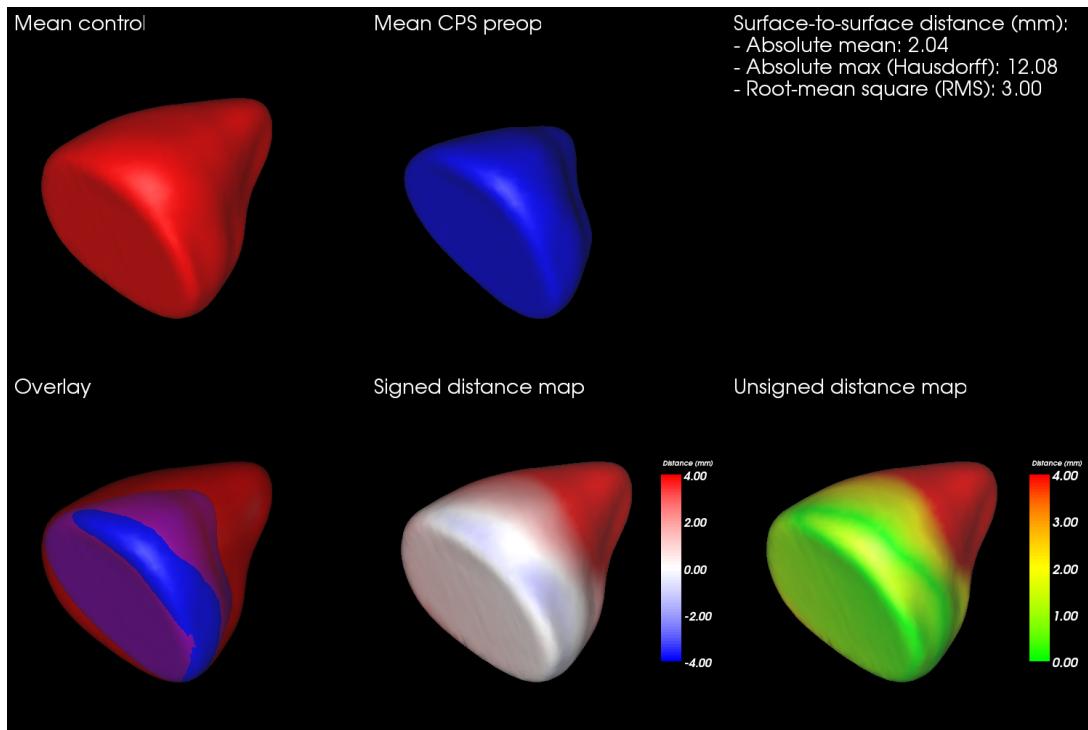


Figure 25: Registration-based comparison of automatically constructed mean size and shape models of the orbit. In this case, a mean control model of normal orbits is compared against a mean model of pre-operative orbits from patients suffering from congenital disorder called Crouzon-Pfeiffer syndrome (CPS). The semi-transparent surface overlays and color-coded distance maps shows that CPS orbits tend to be smaller and more shallow than normal orbits.

### 32. Precise 3D Angle Measurements in CT Wrist Images

Filip Malmberg, Johan Nysjö, Ingela Nyström, Ida-Maria Sintorn

*Partners:* Albert Christersson, Dept. of Orthopedics, UU Hospital

*Funding:* TN-faculty, UU

*Period:* 1111–

*Abstract:* To be able to decide the correct treatment of a fracture, for example, whether a fracture needs to be operated on or not, orthopedic surgeons need to assess the details about the fracture. One of the most important factors is the fracture displacement, particularly the angulation of the fracture. When a fracture is located close to a joint, for example, in the wrist, which is the most common location for fractures in the human being, the angulation of the joint line in relation to the long axis of the long bone needs to be measured (Fig. 26a). Since the surface of the joint line in the wrist is highly irregular, and since it is difficult to take X-rays of the wrist in exactly the same projections from time to time, conventional X-ray is not an optimal method for this purpose. In most clinical cases, conventional 2D angle measurements in X-ray images are satisfactory for making correct decisions about treatment, but when comparing two different methods of treatment, for instance, two different operation techniques, the accuracy and precision of the angle measurements need to be higher.

In this project, we are developing a system for performing precise angle measurements in 3D computed tomography (CT) images of the wrist (Fig. 26b). Our proposed system is semi-automatic; the user is required to guide the system by indicating the approximate position and orientation of various parts of the radius bone. This information is subsequently used as input to an automatic algorithm that makes precise angle measurements. A RANSAC-based method for estimating the long axis of the radius bone was presented at the International Conference on Computer Vision and Graphics (ICCVG' 2012). During 2013, we developed a registration-based method for measuring the orientation of the joint surface of the radius. This method was combined with the previously developed axis estimation method and presented at ICIAP 2013. Currently, we are performing a more extensive case study (involving 40 CT scan sequences of fractures wrists) to further evaluate the performance of the 3D angle measurement method and compare it with the conventional 2D X-ray measurement method.

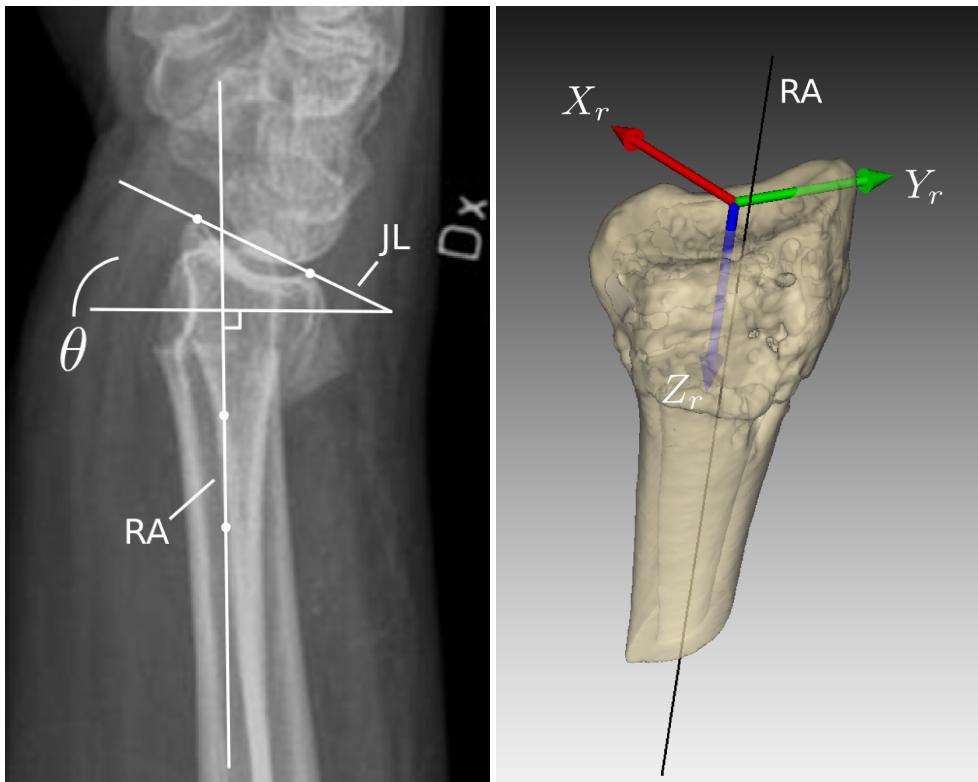


Figure 26: (a) The dorsal angle,  $\theta$ , measured in 2D on a lateral X-ray image of the radius bone in the wrist.  $\theta$  is defined as the angle between the joint line JL and a line that is orthogonal to the long axis RA of the radius. (b) A 3D rendering of the radius bone and the reference axes we identify to measure the dorsal angle in 3D.

### 33. Efficient Algorithms for Computer Graphics

Ewert Bengtsson, Anders Hast

*Partner:* Tony Barrera, Uppsala

*Funding:* TN-faculty, UU

*Period:* 9911–

*Abstract:* Computer graphics is increasingly being used to create realistic images of 3D objects for applications in entertainment, (animated films, games), commerce (showing 3D images of products on the web), industrial design and medicine. For the images to look realistic high quality

shading and surface texture and topology rendering is necessary. A proper understanding of the mathematics behind the algorithms can make a big difference in rendering quality as well as speed. We have in this project over the years re-examined several of the established algorithms and found new mathematical ways of simplifying the expressions and increasing the implementation speeds without sacrificing image quality. We have also invented a number of completely new algorithms. The project is carried out in close collaboration with Tony Barrera, an autodidact mathematician. It has been running since 1999 and resulted in more than 25 international publications and a PhD thesis.

During 2013 a poster was accepted for the ACM Computing Frontiers conference entitled: "An Algorithm for Parallel Calculation of Trigonometric and Exponential Functions".

#### 34. **Ubiquitous Visualization in the Built Environment**

Stefan Seipel, Fei Liu

*Funding:* University of Gävle; TN-faculty, UU

*Period:* 110801–

*Abstract:* This research project in ubiquitous visualization deals with mobile visualization of spatial data in indoor and outdoor environments. Several key problems for robust mobile visualization are addressed such as spatial tracking and calibration, image based 2D and 3D registration and efficient graphical representations in mobile user interfaces. During 2013 we have devised a facade region detection method by analyzing image profiles for repetitive patterns in street view images. These profiles are generated by scanning the hue channel of images along lines constructed with edge line segments and vanishing points. The work has been compiled into a paper titled "Detection of Facade Regions in Street View Images from Split-and-Merge of Perspective Patches" and submitted to the International Conference on Computing and Computer Vision 2014. Meanwhile, we have also been exploring various image features to describe the detected facade regions in order to identify which building is presented in a specific image.

## 5.4 Theory: discrete geometry, mathematical morphology and volume processing

### 35. Improved Methods for Interactive Graph-Based Segmentation

Filip Malmborg, Robin Strand, Ingela Nyström, Ewert Bengtsson

*Funding:* TN-faculty, UU

*Period:* 0901–

*Abstract:* Image segmentation, the process of identifying and separating relevant objects and structures in an image, is a fundamental problem in image analysis. Accurate segmentation of objects of interest is often required before further processing and analysis can be performed. Despite years of active research, fully automatic segmentation of arbitrary images remains an unsolved problem.

*Interactive* segmentation methods use human expert knowledge as additional input, thereby making the segmentation problem more tractable. A successful semi-automatic method minimizes the required user interaction time, while maintaining tight user control to guarantee the correctness of the result. The input from the user is typically given in one of two forms:

*Boundary constraints* The user is asked to provide pieces of the desired segmentation boundary.

*Regional constraints* The user is asked to provide a partial labeling of the image elements (e.g., marking a small number of image elements as “object” or “background”).

Interactive segmentation is often phrased as an optimization problem, i.e., a solution is sought that optimizes some criterion on segmentation “goodness” while satisfying the constraints provided by the user. In this project, we develop new methods for interactive segmentation, using a combinatorial approach. In 2013, results from this project were presented at the International Symposium on Mathematical Morphology (ISMM) in Uppsala.

### 36. The Stochastic Watershed

Bettina Selig, Cris Luengo, Ida-Maria Sintorn, Filip Malmborg

*Funding:* S-faculty, SLU

*Period:* 1102–

*Abstract:* The stochastic watershed is a method recently presented that builds on the classical seeded watershed algorithm. It creates a probability density function for edges in the image by repeated applications of the seeded watershed with random seeds. We have found that adding noise to the input image before every application of the seeded watershed greatly improves the properties of the output. These results were published this year in Pattern Recognition Letters. This year we have developed an efficient algorithm that computes the result one would obtain after an infinite number of repetitions of the seeded watershed, and have been working towards a method to combine this algorithm with the improvements presented in our previous paper.

### 37. Adaptive Mathematical Morphology

Vladimir Ćurić, Cris Luengo, Gunilla Borgefors

*Partner:* Jesús Angulo, Centre for Mathematical Morphology, Ecole des Mines de Paris - MINES ParisTech, Fontainebleau, France; Anders Landström, Matthew Thurley, Luleå University of Technology, Luleå; Sébastien Lefèvre, University of South Brittany, Vannes, France; Santiago Velasco-Forero, National University of Singapore, Republic of Singapore.

*Funding:* Graduate School in Mathematics and Computing (FMB)

*Period:* 1101–

*Abstract:* The construction of adaptive structuring elements that adjust their shape and size to the local structures in the image has recently been a popular topic in mathematical morphology. Despite that several methods for the construction of spatially adaptive structuring elements have been proposed, it is still an open problem, both from a theoretical and implementation point of view.

We have proposed salience adaptive structuring elements that modify their shape and size according to the saliency of the edges in the image. We have examined topological properties of salience adaptive structuring elements and investigated their applicability to image filtering. This work has been published in IEEE Journal of Selected Topics in Signal Processing. We have also proposed structuring elements with predefined shape and adaptive size based on similar type of the salience map as it was used for the construction of the salience adaptive structuring elements. Furthermore, we extended this work to salience-based parabolic structuring functions, which was presented at the International Symposium on Mathematical Morphology (ISMM'2013). More recently, we perform a comparative study of a few most important methods for constructing adaptive structuring elements as well theoretical advances how to properly define respective morphological operators. This work is currently under review.

We intend to further investigate theoretical properties of adaptive morphological operators as well as apply such operators to the task of image regularization. An extension of adaptive morphological operators towards multi-valued images and their definitions for sparse image representations are of interest in future studies.

### 38. Digital Distance Functions and Distance Transforms

*Robin Strand, Gunilla Borgefors*

*Partner:* Benedek Nagy, Dept. of Computer Science, Faculty of Informatics, University of Debrecen, Hungary; Nicols Normand, IRCCyN, University of Nantes, France

*Funding:* TN-faculty, UU; S-faculty, SLU

*Period:* 9309–

*Abstract:* The distance between any two grid points in a grid is defined by a distance function. In this project, weighted distances have been considered for many years. A generalization of the weighted distances is obtained by using both weights and a *neighborhood sequence* to define the distance function. The neighborhood sequence allows the size of the neighborhood to vary along the paths.

In 2013, papers on

- the link between digital distance functions and integer sequences, through Beatty sequences and the Lambek-Moser inverse,
- weight sequence distance functions, where weighted neighborhood sequences of infinite length are allowed, and
- efficient computation of digital distance transforms,

have been published in Computer Vision and Image Understanding and proceedings of DGCI and ISMM.

### 39. The Minimum Barrier Distance

*Robin Strand, Filip Malmberg*

*Partner:* Punam K. Saha, Dept. of Electrical and Computer Engineering and the Dept. of Radiology, University of Iowa, IA, USA; Krzysztof C. Ciesielski, Dept. of Mathematics, West Virginia University, Morgantown, WV, USA; Dept. of Radiology, MIPG, University of Pennsylvania, PA, USA

*Funding:* TN-faculty, UU

*Period:* 1103–

*Abstract:* In this project, we introduce a distance function on a fuzzy subset that gives the minimum barrier that has to be passed to go from one point to another. Theoretical properties as well as efficient computational solutions for minimum barrier distance have been developed. An initial

application of minimum barrier distance in image segmentation is presented. The experiments show that the minimum barrier distance is robust to noise and blur, and also seed point position, since it captures the total change in membership values across an interface instead of gradient as a measure of slope that is sensitive to noise and blur.

A paper on the theoretical foundation of the minimum barrier distance was published in Computer Vision and Image Understanding. Our work in this project during 2013 has been focused on finding efficient, and exact, algorithms for computing the minimum barrier distance.

#### 40. Set Distances and their Application in Image Analysis

Vladimir Ćurić, Gunilla Borgefors

*Partner:* Joakim Lindblad, Nataša Sladoje, Faculty of Technical Sciences, University of Novi Sad, Serbia

*Funding:* Graduate School in Mathematics and Computing (FMB)

*Period:* 0908–

*Abstract:* Methods for measuring distances between sets, which is a measure of how similar the sets are, can be useful for solving various image analysis related problems, such as registration, image retrieval and segmentation evaluation. Depending on how the distance measure is defined, it exhibits different properties, such as metricity, monotonicity, continuity, sensitivity to noise, complexity and speed of computation. It is therefore of interest to study and further develop different set distance measures, to be able to select appropriate distances for the different applications. In this project, we evaluate existing and develop new set distances which are useful in image registration related problems. We have proposed a new set distance between crisp sets of points and evaluated its usefulness for rigid body registration of binary images as well as its applicability for the real task of multi-modal 2D-3D registration of 2D histological sections of bone implant with corresponding 3D synchrotron radiation micro computed tomography (SR $\mu$ CT) bone implant volumes. In addition, it has been shown that this set distance has good performances when applicable to the task of recognition of handwritten characters. This work has been accepted for publication to Pattern Analysis and Applications.

We extended our study to fuzzy objects and proposed four novel point-to-set distances defined for fuzzy or gray-level image data, two based on integration of alpha cuts and two based on the fuzzy distance transform. We further used these point-to-set distances to define distances between fuzzy sets. Theoretical study and performance evaluation of the proposed distances confirm their excellent behaviour in template matching and object classification. New distance measures enable to include and consider both spatial and intensity information, which makes them applicable to texture matching problems as well. The results of this study have been published in IEEE Transactions on Image Processing.

#### 41. Direct Curvature Calculation of Surfaces in 3D Volumes

Erik Wernersson, Cris Luengo, Anders Brun, Gunilla Borgefors

*Funding:* S-faculty, SLU

*Period:* 1009 –

*Abstract:* Curvature is known to be a useful local descriptor of 2D surfaces, embedded in 3D space. Not only for parametric surfaces but also estimated from objects in digital images with applications ranging from visualisation to segmentation.

Within this project, we have studied curvature calculated from the structure tensor, in contrast to the most common methods which derive curvature directly from image differentials. This opens up for new kind of processing, and especially averaging, which we hope will be of interest for the analysis of wood fibres in  $\mu$ CT images of paper and composite materials.

## 5.5 Other projects

### 42. Optical Character Recognition of Handwritten Texts

Anders Brun, Ewert Bengtsson, Fredrik Wahlberg, Tomas Wilkinson, Kalyan Ram

*Partners:* Lasse Mårtensson, Dept. of Scandinavian Languages, UU; Mats Dahllöf, Dept. of Linguistics and Philology, UU

*Funding:* Faculty of Languages and Humanities, UU

*Period:* 1008–

*Abstract:* Optical character recognition (OCR) is still, after nearly 100 years of research, an active area of research. Currently one of the frontiers is the recognition of handwritten text (HTR), in particular from historical documents, see Figure 27. This year, two PhD students were recruited. Bojana Simsic was hired to do part-time work on marketing. The project participated in the book fair Bokmässan in Gothenburg and was featured several times in articles and on national TV. In late 2013, the project started to collaborate with The Swedish Museum of Natural History, to help out with digitization of herbarium sheets.

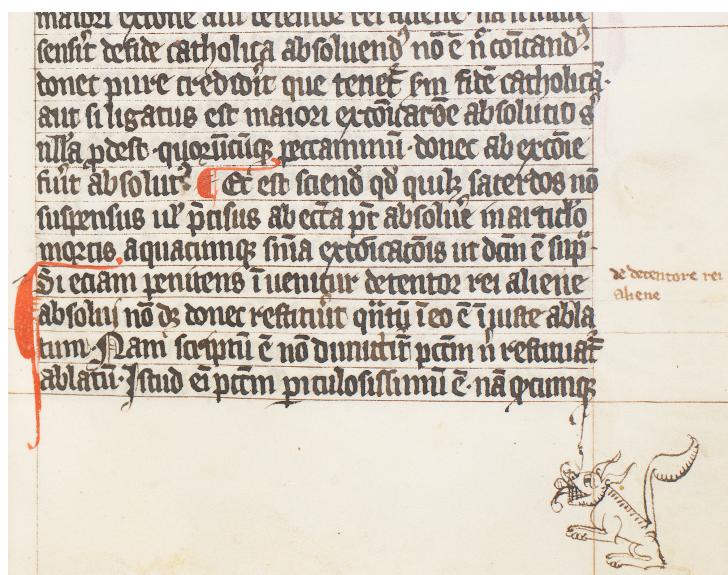


Figure 27: Detail of spread 198 from "Summula de ministris et sacramentis ecclesiasticis" written by Laurentius of Vaksala in the 14th century.

### 43. GeoMemories

Anders Hast

*Partners:* Andrea Marchetti, Salvatore Minutoli, Alessandro Prosperi, Alessandro Lugari, Maurizio Tesconi, Beatrice Rapisarda, Matteo Abrate, Clara Bacci, Davide Gazzé, Sergio Bianchi, Istituto di Informatica e Telematica (IIT), Pisa, Italy

*Abstract:* The GeoMemories project is aimed at making publicly available, through web access, heritage preserved in the archives of Aerofototeca Nazionale in Rome, which contains photographs covering the Italian territory from the end of 1800 till modern days. The web application is based on google earth but oriented towards the management of the temporal variable, so that geospatial changes can be monitored over time. The historical aerial photos need to be digitized, illumination corrected, orthorectified, georeferenced and finally stitched together. Anders Hast spent one year (2011) at IIT, CNR in Pisa Italy as an ERCIM fellow working with image processing and computer vision aspects in the project. Since returning to UU in January he is a research associate at IIT, CNR and continues working with the project.

During 2013 three papers were published, whereof two journal papers and one conference paper. One of the journal papers describes the GeoMemories application and the image pipeline being used, and was accepted in a Special Issue "Geospatial Monitoring and Modelling of Environmental Change" of the ISPRS International Journal of Geo-Information. The title is "Geomemories - A Platform for Visualizing Historical, Environmental and Geospatial Changes of the Italian Landscape". The Figure 28 is taken from that paper and shows how the application can be used to monitor environmental changes. About 400 meters of the shore line outside Pisa has disappeared since 1943, and even more since 1765 (cadastral map).



Figure 28: This blended photo makes it possible to study how the costal shore line outside Pisa has changed and moved in time and space. Images from four different sources are blended together in the GeoMemories application to show the environmental changes. The images are a cadastral map that was published 1765, officially issued by Pietro Leopoldo the Grand Duke of Tuscany, a RAF photo from 1943, an aerial photo from 1962 and a recent Google Earth photo.

#### 44. Image Analysis for Landscape Analysis

Anders Brun

*Partners:* Bo Malmberg, Michael Nielsen, Dept. of Human Geography, Stockholm University;  
Anders Wästfelt, Dept. of Economics, SLU

*Funding:* UU/SU

*Period:* 0901–

*Abstract:* This project is a collaboration with researchers at SU and SLU. It aims to derive information about the landscape (rural and city) from satellite images. The project focuses on using texture analysis of images rather than only pixelwise spectral analysis to segment the image into different meaningful regions. One journal manuscript has been submitted during 2013 and we have started a collaboration with the GLEAN project and the department of Political Science at Stockholm University.

#### **45. Dual-domain Visual Exploration of Urban Solar Potential**

Stefan Seipel

*Partners:* Joakim Widén, David Lingfors, Solid State Physics, Dept. of Engineering Sciences, UU

*Funding:* University of Gävle; TN-faculty, UU

*Period:* 1211–

*Abstract:* This project aims to improve the planning and design of solar electricity installations in the urban environment. One major objective of these studies is to enable a highly detailed temporal and spatial analysis of the expected solar yield, which becomes increasingly important for optimal load balance in electric power networks. In our research we develop a 3D simulation model that integrates geographical data and detailed 3D urban models with temporal solar irradiance and climate data. According to our model the predicted solar yield becomes a multi-dimensional function of several design-specific parameters that are interactively explored by a human expert. This project is an interdisciplinary initiative that involves researchers from Energy Systems and from Computer Science at UU and the University of Gävle. During the first year, a demonstrator system for the interactive exploration of the design parameter space has been developed. Our method and the demonstrator system have been published in two international conferences in 2013. Forthcoming research in this project will concern the refinement and validation of computational models, as well new methods for interactive visual exploration.

#### **46. Automatically Determining Road Condition with a Camera**

Cris Luengo

*Partners:* Pertti Kuusisto and Jonas Hallenberg, the Swedish Transport Administration (Trafikverket), Borlänge.

*Funding:* The Swedish Transport Administration

*Period:* 1303–1307

*Abstract:* We performed a pre-study on the possibilities to automatically determine road conditions (dry, wet, icy, snow-covered, etc.) using only images obtained from the network of road monitoring cameras that the Swedish Transport Administration has set up throughout the country. Currently, these images are sent to a central location where personnel examines them. Automating this task is desirable for several reasons, including more frequent updates of road condition that would be possible if the images do not have to be sent to a central location. The pre-study included a literature review and an interview with a Swedish researcher working in the field.

#### **47. Tracking Honey Bees and Their Interactions**

Cris Luengo

*Partners:* Olle Terenius, Ingemar Fries, Joachim Rodrigues de Miranda, Eva Forsgren, Barbara Locke, Dept. of Ecology, SLU; Fredrik Liljeros, Dept. of Sociology, Stockholm University

*Funding:* Åke Wiberg foundation; and S-faculty, SLU

*Period:* 1003–

*Abstract:* In this project, we are creating a system in which we can observe a portion of a bee hive (containing about one thousand individuals, each tagged with a unique identifier on its back) over days or weeks. Bees will be free to enter and exit the hive, and the environment will be set up to be as natural as possible for the bees. The purpose is to observe the natural behaviour of the bees, and record the type and duration of interaction between individuals. In 2013, Iulian Florea finished his MSc thesis within this project, developing and testing real-time algorithms to process video, including background removal, tracking and detection (Fig. 29). He also established a good video compression protocol to be used in future experiments.

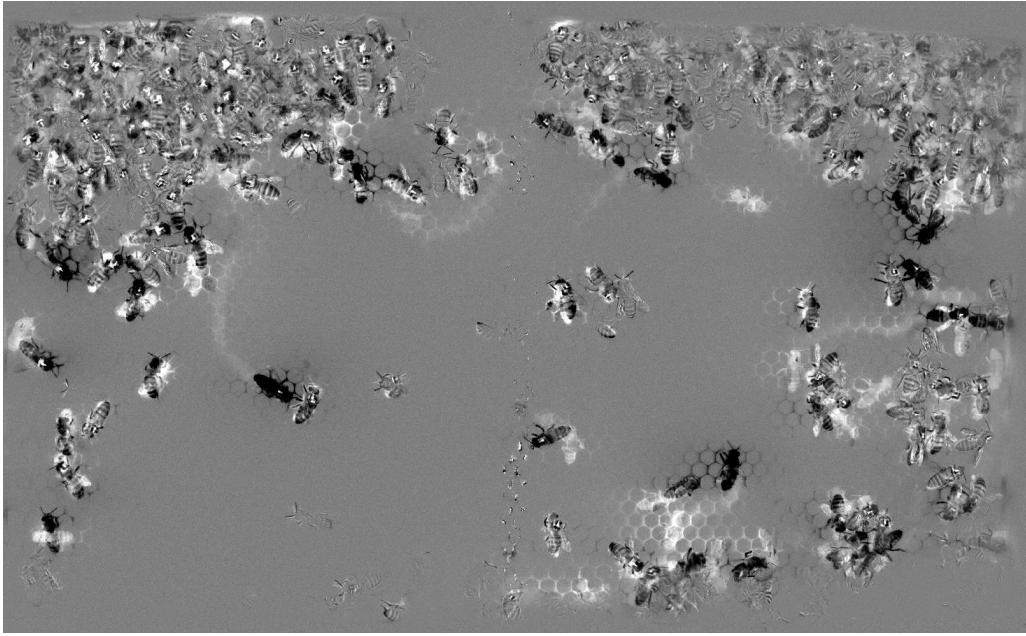


Figure 29: The result of a method for background subtraction, where only moving individuals are still visible.

#### 48. Fish Type Recognition in Underwater Videos for Sustainable Fishing

Vladimir Ćurić, Ida-Maria Sintorn

*Partners:* Arne Fjälling, SLU Aqua, Stockholm

*Funding:* Graduate School in Mathematics and Computing

*Abstract:* This project investigates whether it is possible to construct a system, which can determine the fish type using the underwater camera mounted in the tube at the end of the fishing trap (Fig. 30). The result of the image analysis will signal to the ramp at the end of the tube to either catch the fish or return the fish to the sea. Wild salmon are caught, bred, and planted back in the sea. To distinguish between wild and farmed salmon, each farmed salmon is marked by cutting off the adipose fin on the back of the salmon. Sustainable fishing is performed in a way that the farmed salmon should be caught, while the wild ones should be released back into the sea. The goal of the project is also to separate salmon from sea trout using texture and morphometric measurements.

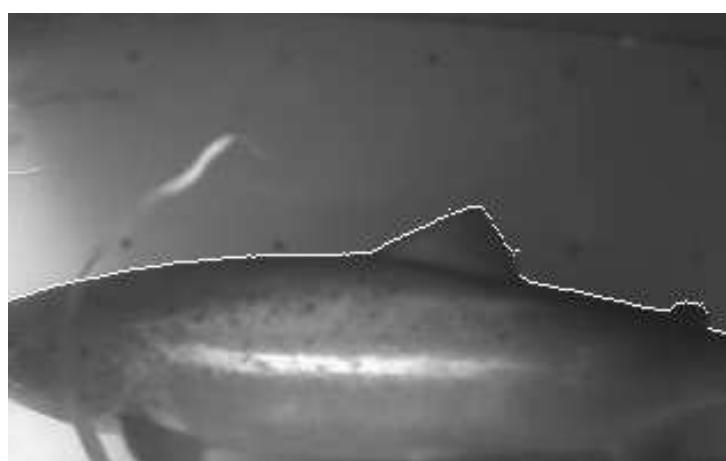


Figure 30: Detecting adipose fin in salmon and sea trout.

## 49. DIPimage and DIPlib

Cris Luengo

*Partners:* Bernd Rieger, Lucas van Vliet, Quantitative Imaging Group, Delft University of Technology, The Netherlands; Michael van Ginkel, Unilever Research and Development, Colworth House, Bedford, UK

*Funding:* S-faculty, SLU

*Period:* 0807–

*Abstract:* DIPimage is a MATLAB toolbox for scientific image analysis, useful for both teaching and research (<http://www.diplib.org>). It has been in active development since 1999, when it was created at Delft University of Technology. In 2008, when Cris Luengo moved to Uppsala, CBA was added to the project as a main development site. DIPlib, created in 1995, is a C library containing many hundreds of image analysis routines. DIPlib is the core of the DIPimage toolbox, and both projects are developed in parallel. Because DIPlib provides efficient algorithms, MATLAB is useful for image analysis beyond the prototyping stage. Together, MATLAB and DIPimage form a powerful tool for working with scalar and vector images in any number of dimensions. Version 2.5 was released in 2013, and improved the speed of image skew and rotation operations, the Fourier transform, and the reading of time series from disk; it also added some minor features and fixing some bugs. We also implemented the option to do arithmetic operations without changing the data type of the image, useful when working with very large images. This last change will appear in the next release.

## 50. UPPMAX Cluster Computing

Martin Simonsson, Carolina Wählby

*Partners:* Hans Karlsson, Elias Rudberg, Ola Spjuth, UPPMAX

*Funding:* SciLife Lab Uppsala; eSSENCE; Dept. of IT, UU

*Period:* 1110–

*Abstract:* Life science applications generate a huge amount of image data that has to be stored and analysed in an efficient way. This project is focused on providing easy access to high-performance computers and large-scale storage. In collaboration with Uppsala Multidisciplinary Center for Advanced Computational Science (UPPMAX) image analysis software are being installed and maintained on the cluster. Database solutions with easy web access to image data are also being developed and maintained. This project has also provided workshops and seminars to help life science researchers to get started and use the resources. In the end of 2013 we initiated our first large-scale image analysis project using the computer cluster working with 900 000 images from drug screening project.

## **5.6 Cooperation partners**

### **International**

Dept. of Forest and Water Management, Ghent University, Belgium  
Dept. of Physics and Astronomy, Ghent University, Belgium  
Dept. Genie Electrique et Electronique, Institut National Polytechnique, Ivory Coast  
Delong Instruments, Brno, Czech Republic  
Clinical Pathology Division, Vejle hospital, Vejle, Denmark  
Risø National Laboratory, Technical University of Denmark  
Visiopharm, Hørsholm, Denmark  
Dept. of Physics, University of Jyväskylä (UJ), Finland  
IRCCyN, University of Nantes, France  
University of South Brittany, Vannes, France  
Pitie Salpetriere Hospital, France  
Centre for Mathematical Morphology, Ecole des Mines de Paris - MINES ParisTech, Fontainebleau, France  
Dept. of Computer Science, University of Debrecen, Hungary  
Centre for Development of Advanced Computing, Thiruvananthapuram, India  
Regional Cancer Centre, Thiruvananthapuram, India  
Dept. of ECE, National Institute of Technology (NIT), Tiruchirappalli, India  
Istituto di Informatica e Telematica (IIT), Pisa, Italy  
Eye Hospital Rotterdam, The Netherlands  
Quantitative Imaging Group, Delft University of Technology, The Netherlands  
Norwegian Pulp and Paper Research Institute, Trondheim, Norway  
SINTEF Materials and Chemistry, Norway  
Faculty of Technical Sciences, University of Novi Sad, Serbia  
National University of Singapore, Republic of Singapore  
Unilever Research and Development, Colworth House, Bedford, UK  
Great Ormond Street Hospital, UK  
Broad Institute of Harvard and MIT, USA  
Dept. of Electrical and Computer Engineering, University of Iowa, IA, USA  
Dept. of Radiology, University of Pennsylvania, PA, USA  
Dept. of Mathematics, West Virginia University, Morgantown, WV, USA  
Research Laboratory of Electronics, Massachusetts Institute of Technology, Cambridge, USA

### **National**

Dept. of Cell and Molecular Biology, Karolinska Institute, Stockholm  
Dept. of Engineering Sciences, Applied Mechanics, UU  
Dept. of Engineering Sciences, Solid State Physics, UU  
Dept. of Genetics and Pathology, UU  
Dept. of Immunology, Genetics and Pathology, UU  
Dept. of Linguistics and Philology, UU

Dept. of Medical Cell Biology, UU  
Dept. of Cell and Molecular Biology, UU  
Dept. of Plastic- and Maxillofacial Surgery, UU Hospital  
Dept. of Orthopedics, UU Hospital  
Dept. of Neuroscience, Neurosurgery, UU Hospital  
Dept. of Radiology, Oncology and Radiation Science, UU  
Dept. of Scandinavian Languages, UU  
Dept. of Surgical Sciences, Oral and Maxillofacial Surgery, UU  
Dept. of Surgical Sciences, Plastic Surgery, UU  
SciLifeLab, Stockholm  
SciLifeLab, UU  
Division of Microsystems Technology, UU  
Evolutionary Biology Centre, Zebrafish platform, SciLifeLab Uppsala  
Dept. of Anatomy, Physiology and Biochemistry, SLU  
Dept. of Ecology, SLU  
Dept. of Economics, SLU  
SenseGraphics AB, Kista  
Center for Medical Image Science and Visualization (CMIV), Linköping University  
Dept. of Computer Science, Electrical and Space Engineering, Luleå University of Technology  
Centre for Microbiological Preparedness; Swedish Institute for Infectious Disease Control (SMI), Solna  
Dept. of Human Geography, Stockholm University  
Dept. of Sociology, Stockholm University  
Dept. of Biochemistry and Biophysics and SciLifeLab, Stockholm University.  
Dept. of Solid Mechanics and BiMaC Innovation Center, KTH, Stockholm  
Dept. Medical Biochemistry and Biophysics, Karolinska Institute and SciLifeLab, Stockholm  
Dept. Mathematical Sciences, Chalmers University of Technology, Göteborg  
Biomedical Electromagnetics Research Group, Chalmers University of Technology, Göteborg  
Swedish Transport Administration ("Trafikverket")  
AstraZeneca, Mölndal  
Innventia, Stockholm  
Vironova AB, Stockholm  
Gradientech AB, Uppsala  
Izolde AB, Uppsala  
PiezoMotors AB, Uppsala  
Ridgeview, Uppsala  
Technovest AB  
Tony Barrera, Uppsala  
UPPMAX, UU  
The Human Protein Atlas, Uppsala

## 6 Publications

In 2013 we published 50 internationally reviewed papers, more than any year before in the history of CBA, see Figure 31. There are several reasons for this, but the main one is that after two years without PhD dissertations there will be about eight new CBA doctors in 2014 and PhD students publish most at the end of their studies. Another reason is that we have more researcher than before and are involved in more co-operation projects.

In our research field the quality and impact of many conference proceedings are higher than many of the Journals. As the proceedings also usually are a faster way to publish we often chose that outlet of our results. But of course we also publish in scientific journals, especially when reporting results on medical applications in co-operation with medical researchers, as that field is more journal oriented.

This year we edited the proceedings of the ISMM conference which was published in the prestigious Springer Lecture notes in Computer Science. We published 29 journal articles in journals as different as the theoretical Computer Vision and Image Understanding and prestigious Nature Methods, from Artificial Intelligence Tools to Magnetic Resonance Imaging and Composite Science and Technology. We also published 21 papers in fully reviewed conference proceedings; both at meetings dedicated to the theory of image analysis, such as DGCI, ISMM, and SIGGRAPH, and to more application oriented ones, such as HIP, ISBI, and WHC. We also had many presentations at non-reviewed conferences.

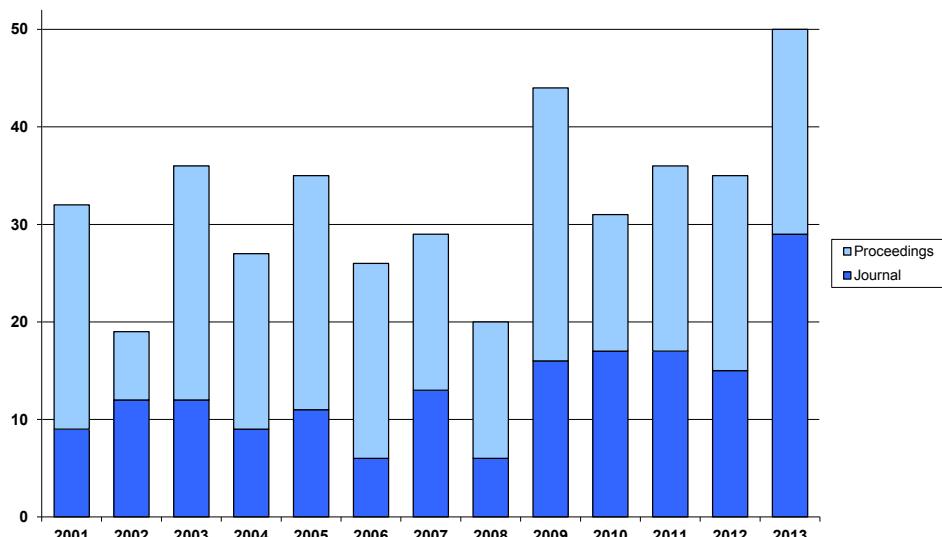


Figure 31: The number of publications from CBA.

### 6.1 Edited conference proceedings

Editors affiliated with CBA are written in bold.

1. **Conference name:** 11th International Symposium on Mathematical Morphology and Its Applications to Signal and Image Processing

*Editors: Cris L. Luengo Hendriks, Gunilla Borgefors, Robin Strand*

*Comment:* The conference was held in Uppsala in May. The proceedings is Lecture Notes in Computer Science, No. 7883, Springer Verlag, 532 pages.

## 6.2 Journal articles

Authors affiliated with CBA are in bold.

### 1. Improving the Stochastic Watershed

**Authors:** Karl B. Bernander, Kenneth Gustavsson, Bettina Selig, Ida-Maria Sintorn, Cris L. Luengo Hendriks

*Journal:* Pattern Recognition Letters, volume 34, number 9, pages 993-1000

*Abstract:* The stochastic watershed is an unsupervised segmentation tool recently proposed by Angulo and Jeulin. By repeated application of the seeded watershed with randomly placed markers, a probability density function for object boundaries is created. In a second step, the algorithm then generates a meaningful segmentation of the image using this probability density function. The method performs best when the image contains regions of similar size, since it tends to break up larger regions and merge smaller ones. We propose two simple modifications that greatly improve the properties of the stochastic watershed: (1) add noise to the input image at every iteration, and (2) distribute the markers using a randomly placed grid. The noise strength is a new parameter to be set, but the output of the algorithm is not very sensitive to this value. In return, the output becomes less sensitive to the two parameters of the standard algorithm. The improved algorithm does not break up larger regions, effectively making the algorithm useful for a larger class of segmentation problems.

### 2. A Fast and Reliable Approach to Cell Nuclei Segmentation in PAP Stained Cervical Smears

**Authors:** Balakrishnan Buju (1), Vilayil Sujathan (2) **Patrik Malm**, Rajesh Kumar (1)

(1) CDAC Thiruvananthapuram, India

(2) Regional Cancer Centre, Thiruvananthapuram, India

*Journal:* CSI Transactions on ICT, Volume 1, number 4, pages 309-315

*Abstract:* Fast and reliable segmentation of cervical cell nuclei is one of the crucial steps of an automated screening system that aims early detection of cervical cancer. In this paper, we propose an edge based approach using customized Laplacian of Gaussian (LoG) filter to segment free lying cell nuclei in bright-field microscope images of Papsmear. The LoG is generally employed as a second order edge detector in image processing. The images may have the challenges of inconsistent staining, overlapping and folded cells. Experimenting proposed method over all types of cervical images including sufficient number of high grade lesions of cervical cancer shows that our method performs well for stain varied images containing focused nuclei.

### 3. Virtual Surgery "Virtuell Kirurgi"

**Author:** Ingrid Carlbom, Mats Karlsson

*Journal:* Tandläkartidningen, number 6, pages 12-15

*Abstract:* Virtual surgery - a dream? Not at all; in just a few years it might be the reality. The surgeon can already today perform a virtual rehearsal of the real surgery. (in Swedish)

### 4. Blind Color Decomposition of Histological Images

**Authors:** Milan Gavrilovic, Jimmy Azar, Joakim Lindblad, Carolina Wählby, Ewert Bengtsson, Christer Busch (1), **Ingrid Carlbom**

(1) Dept. of Immunology, Genetics and Pathology, Uppsala University

*Journal:* IEEE Transactions on Medical Imaging, volume 32, number 6, pages 983-994

*Abstract:* Cancer diagnosis is based on visual examination under a microscope of tissue sections from biopsies. But whereas pathologists rely on tissue stains to identify morphological features, automated tissue recognition using color is fraught with problems that stem from image intensity variations due to variations in tissue preparation, variations in spectral signatures of the stained tissue, spectral overlap and spatial aliasing in acquisition, and noise at image acquisition. We present a blind method for color decomposition of histological images. The method decouples intensity from color information and bases the decomposition only on the tissue absorption characteristics of each stain. By modeling the charge-coupled device sensor noise, we improve the method accuracy. We extend current linear decomposition methods to include stained tissues where one spectral signature cannot be separated from all combinations of the other tissues' spectral signatures. We demonstrate both qualitatively and quantitatively that our method results in more accurate decompositions than methods based on non-negative matrix factorization and independent component analysis. The result is one density map for each stained tissue type that classifies portions of pixels into the correct stained tissue allowing accurate identification of morphological features that may be linked to cancer.

## 5. Canine Body Composition Quantification Using 3 Tesla Fat Water MRI

*Authors:* Aliya Gifford (1), Joel Kullberg (1), Johan Berglund (1), **Filip Malmberg**, Katie C. Coate (2), Phillip E. Williams (2), Alan D. Cherrington(2), Malcolm J. Avison(2), E. Brian Welch (2)

(1) Dept. of Radiology, Uppsala University

(2) Institute of Imaging Science, Vanderbilt University, Nashville, TN, USA

*Journal:* Journal of Magnetic Resonance Imaging

*Abstract:* Purpose: To test the hypothesis that a whole-body fat-water MRI (FWMRI) protocol acquired at 3 Tesla combined with semi-automated image analysis techniques enables precise volume and mass quantification of adipose, lean, and bone tissue depots that agree with static scale mass and scale mass changes in the context of a longitudinal study of large-breed dogs placed on an obesogenic high-fat, high-fructose diet.

Materials and methods: Six healthy adult male dogs were scanned twice, at weeks 0 (baseline) and 4, of the dietary regimen. FWMRI-derived volumes of adipose tissue (total, visceral, and subcutaneous), lean tissue, and cortical bone were quantified using a semi-automated approach. Volumes were converted to masses using published tissue densities.

Results: FWMRI-derived total mass corresponds with scale mass with a concordance correlation coefficient of 0.931 (95% confidence interval = [0.813, 0.975]), and slope and intercept values of 1.12 and -2.23 kg, respectively. Visceral, subcutaneous and total adipose tissue masses increased significantly from weeks 0 to 4, while neither cortical bone nor lean tissue masses changed significantly. This is evidenced by a mean percent change of 70.2% for visceral, 67.0% for subcutaneous, and 67.1% for total adipose tissue.

Conclusion: FWMRI can precisely quantify and map body composition with respect to adipose, lean, and bone tissue depots. The described approach provides a valuable tool to examine the role of distinct tissue depots in an established animal model of human metabolic disease.”

## 6. Optimal RANSAC - Towards a Repeatable Algorithm for Finding the Optimal Set

*Authors:* Anders Hast, Johan Nysjö

*Journal:* Journal of WSCG, volume 21, number 1, pages 21-30

*Abstract:* A novel idea on how to make RANSAC repeatable is presented, which will find the optimal set in nearly every run for certain types of applications. The proposed algorithm can be used for such transformations that can be constructed by more than the minimal points required. We give examples on matching of aerial images using the Direct Linear Transformation, which requires at least four points. Moreover, we give examples on how the algorithm can be used for finding a plane in 3D using three points or more. Due to its random nature, standard RANSAC is not always able to find the optimal set even for moderately contaminated sets and it usually performs badly when the number of inliers is less than 50%. However, our algorithm is capable of finding the optimal set for heavily contaminated sets, even for an inlier ratio under 5%. The proposed algorithm is based on several known methods, which we modify in a unique way and together they produce a result that is quite different from what each method can produce on its own.

## 7. Automated Classification of Immunostaining Patterns in Breast Tissue from the Human Protein Atlas

*Authors:* Swamidoss Issac Niwas (1), **Andreas Kårnsäs** (2), Virginie Uhlmann (3,4), P. Palanisamy (1), Caroline Kampf (4), **Martin Simonsson** (5), **Carolina Wählby** (3,5), **Robin Strand**

(1) Dept. of Electronics and Communication Engineering (ECE), National Institute of Technology (NIT), Tiruchirappalli, India

(2) Visiopharm A/S, Hørsholm, Denmark

(3) Imaging Platform, Broad Institute of Harvard and MIT, Cambridge, Massachusetts MA, USA

(4) Biomedical Imaging Group, École Polytechnique Fédérale de Lausanne (EPFL), Switzerland

(5) Science for Life Laboratory, SciLifeLab, UU

(6) Dept. Immunology, Genetics and Pathology, UU

*Journal:* Journal of Pathology Informatics, volume 4, number 14

*Abstract:* Background: The Human Protein Atlas (HPA) is an effort to map the location of all human proteins (<http://www.proteinatlas.org/>). It contains a large number of histological images of sections from human tissue. Tissue micro arrays (TMA) are imaged by a slide scanning microscope, and each image represents a thin slice of a tissue core with a dark brown antibody specific stain and a blue counter stain. When generating antibodies for protein profiling of the human proteome, an important step in the quality control

is to compare staining patterns of different antibodies directed towards the same protein. This comparison is an ultimate control that the antibody recognizes the right protein. In this paper, we propose and evaluate different approaches for classifying sub-cellular antibody staining patterns in breast tissue samples.

**Materials and Methods:** The proposed methods include the computation of various features including gray level co-occurrence matrix (GLCM) features, complex wavelet co-occurrence matrix (CWCM) features, and weighted neighbor distance using compound hierarchy of algorithms representing morphology (WND-CHARM)-inspired features. The extracted features are used into two different multivariate classifiers (support vector machine (SVM) and linear discriminant analysis (LDA) classifier). Before extracting features, we use color deconvolution to separate different tissue components, such as the brownly stained positive regions and the blue cellular regions, in the immuno-stained TMA images of breast tissue.

**Results:** We present classification results based on combinations of feature measurements. The proposed complex wavelet features and the WND-CHARM features have accuracy similar to that of a human expert.

**Conclusions:** Both human experts and the proposed automated methods have difficulties discriminating between nuclear and cytoplasmic staining patterns. This is to a large extent due to mixed staining of nucleus and cytoplasm. Methods for quantification of staining patterns in histopathology have many applications, ranging from antibody quality control to tumor grading.

## 8. Color deconvolution method for breast tissue core biopsy images cell nuclei detection and analysis using multiresolution techniques

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*Journal:* International Journal of Imaging and Robotics, volume 9, number 1, pages 61-72

**Abstract:** Breast cancer is the second most common cause of cancer induced death in women in the world. Testing for detection of the cancer involves visual microscopic assessment of breast tissue samples such as core needle biopsies. Analysis on this sample by pathologist is crucial for breast cancer patient. In this paper, a color deconvolution method is used to detect nuclei of core needle biopsy images and then it is investigated after decomposition by means of the curvelet transform. The curvelet statistical features are used for breast cancer diagnosis using the Naive Bayes Classifier (NBC) system. The ability of properly trained Naive Bayes Classifiers correctly classify and recognize patterns which is particularly suitable for use in an expert system assisting the diagnosis of cancer tissue samples.

## 9. Analysis of Nuclei Textures of Fine Needle Aspirated Cytology Images for Breast Cancer Diagnosis using Complex Daubechies Wavelets

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*Journal:* Signal Processing, volume 93, number 10, pages 2828-2837

**Abstract:** Breast cancer is the most frequent cause of cancer induced death among women in the world. Diagnosis of this cancer can be done through radiological, surgical, and pathological assessments of breast tissue samples. A common test for detection of this cancer involves visual microscopic inspection of Fine Needle Aspiration Cytology (FNAC) samples of breast tissue. The result of analysis on this sample by a cytopathologist is crucial for the breast cancer patient. For the assessment of malignancy, the chromatin texture patterns of the cell nuclei are essential. Wavelet transforms have been shown to be good tools for extracting information about texture. In this paper, it has been investigated whether complex wavelets can provide better performance than the more common real valued wavelet transform. The features extracted through the wavelets are used as input to a k-nn classifier. The correct classification results are obtained as 93.9% for the complex wavelets and 70.3% for the real wavelets.

## 10. Swelling of Cellulose Fibres in Composite Materials : Constraint Effects of the Surrounding Matrix

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*Journal:* Composites Science And Technology, volume 74, pages 52-59

**Abstract:** Wood fibres have several highly desirable properties as reinforcement in composite materials for structural applications, e.g. high specific stiffness and strength, renewability and low cost. However, one of the main drawbacks is the swelling of these hydrophilic fibres due to moisture uptake. Since the fibres in the composite are generally embedded in a relatively hydrophobic matrix, the surrounding matrix should restrain the swelling of the fibres. The present study investigates this constraint effect and establishes a micromechanical model to predict the swelling of embedded fibres based on experimentally characterised microstructural parameters and hygroelastic properties of the constituents. The predicted swelling is in concert with direct measurement of various wood-pulp fibre composites by means of three-dimensional X-ray microtomographic images.

**11. In Situ Sequencing for RNA Analysis in Preserved Tissue and Cells**

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**Journal:** Nature Methods, volume 10, number 9, pages 857-860

**Abstract:** Tissue gene expression profiling is performed on homogenates or on populations of isolated single cells to resolve molecular states of different cell types. In both approaches, histological context is lost. We have developed an *in situ* sequencing method for parallel targeted analysis of short RNA fragments in morphologically preserved cells and tissue. We demonstrate *in situ* sequencing of point mutations and multiplexed gene expression profiling in human breast cancer tissue sections.

**12. Shape and Volume of Craniofacial Cavities in Intentional Skull Deformations**

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**Journal:** American Journal of Physical Anthropology, volume 151, number 1, pages 110-119

**Abstract:** Intentional cranial deformations (ICD) have been observed worldwide but are especially prevalent in preColombian cultures. The purpose of this study was to assess the consequences of ICD on three cranial cavities (intracranial cavity, orbits, and maxillary sinuses) and on cranial vault thickness, in order to screen for morphological changes due to the external constraints exerted by the deformation device. We acquired CT-scans for 39 deformed and 19 control skulls. We studied the thickness of the skull vault using qualitative and quantitative methods. We computed the volumes of the orbits, of the maxillary sinuses, and of the intracranial cavity using haptic-aided semi-automatic segmentation. We finally defined 3D distances and angles within orbits and maxillary sinuses based on 27 anatomical landmarks and measured these features on the 58 skulls. Our results show specific bone thickness patterns in some types of ICD, with localized thinning in regions subjected to increased pressure and thickening in other regions. Our findings confirm that volumes of the cranial cavities are not affected by ICDs but that the shapes of the orbits and of the maxillary sinuses are modified in circumferential deformations. We conclude that ICDs can modify the shape of the cranial cavities and the thickness of their walls but conserve their volumes. These results provide new insights into the morphological effects associated with ICDs and call for similar investigations in subjects with deformational plagioccephalies and craniostostoses.

### **13. Evaluation of Noise Robustness for Local Binary Pattern Descriptors in Texture Classification**

**Authors:** Gustaf Kylberg, Ida-Maria Sintorn

**Journal:** EURASIP Journal on Image and Video Processing, 2013:17, 20 pages

**Abstract:** Local binary pattern (LBP) operators have become commonly used texture descriptors in recent years. Several new LBP-based descriptors have been proposed, of which some aim at improving robustness to noise. To do this, the thresholding and encoding schemes used in the descriptors are modified. In this article, the robustness to noise for the eight following LBP-based descriptors are evaluated; improved LBP, median binary patterns (MBP), local ternary patterns (LTP), improved LTP (ILTP), local quinary patterns, robust LBP, and fuzzy LBP (FLBP). To put their performance into perspective they are compared to three well-known reference descriptors; the classic LBP, Gabor filter banks (GF), and standard descriptors derived from gray-level co-occurrence matrices. In addition, a roughly five times faster implementation of the FLBP descriptor is presented, and a new descriptor which we call shift LBP is introduced as an even faster approximation to the FLBP. The texture descriptors are compared and evaluated on six texture datasets; Brodatz, KTH-TIPS2b, Kylberg, Mondial Marmi, UIUC, and a Virus texture dataset. After optimizing all parameters for each dataset the descriptors are evaluated under increasing levels of additive Gaussian white noise. The discriminating power of the texture descriptors is assessed using tenfolded cross-validation of a nearest neighbor classifier. The results show that several of the descriptors perform well at low levels of noise while they all suffer, to different degrees, from higher levels of introduced noise. In our tests, ILTP and FLBP show an overall good performance on several datasets. The GF are often very noise robust compared to the LBP-family under moderate to high levels of noise but not necessarily the best descriptor under low levels of added noise. In our tests, MBP is neither a good texture descriptor nor stable to noise.

### **14. Brain Pathology After Mild Traumatic Brain Injury: An Exploratory Study by Repeated Magnetic Resonance Examination**

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**Journal:** Journal of Rehabilitation Medicine, volume 45, number 8, pages 721-728

**Abstract:** Objective: To explore brain pathology after mild traumatic brain injury by repeated magnetic resonance examination.

Design: A prospective follow-up study.

Subjects: Nineteen patients with mild traumatic brain injury presenting with Glasgow Coma Scale (GCS) 14-15.

Methods: The patients were examined on day 2 or 3 and 3-7 months after the injury. The magnetic resonance protocol comprised conventional T1- and T2-weighted sequences including fluid attenuated inversion recovery (FLAIR), two susceptibility-weighted sequences to reveal haemorrhages, and diffusion-weighted sequences. Computer-aided volume comparison was performed. Clinical outcome was assessed by the Rivermead Post-Concussion Symptoms Questionnaire (RPQ), Hospital Anxiety and Depression Scale (HADS) and Glasgow Outcome Scale Extended (GOSE).

Results: At follow-up, 7 patients (37%) reported  $\geq 3$  symptoms in RPQ, 5 reported some anxiety and 1 reported mild depression. Fifteen patients reported upper level of good recovery and 4 patients lower level of good recovery (GOSE 8 and 7, respectively). Magnetic resonance pathology was found in 1 patient at the first examination, but 4 patients (21%) showed volume loss at the second examination, at which 3 of them reported  $< 3$  symptoms and 1  $\geq 3$  symptoms, all exhibiting GOSE scores of 8.

Conclusion: Loss of brain volume, demonstrated by computer-aided magnetic resonance imaging volumetry, may be a feasible marker of brain pathology after mild traumatic brain injury.

### **15. Debris Removal in Pap-smear Images**

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*Journal:* Computer Methods and Programs in Biomedicine, volume 111, number 1, pages 128-138

*Abstract:* Since its introduction in the 1940s the Pap-smear test has helped reduce the incidence of cervical cancer dramatically in countries where regular screening is standard. The automation of this procedure is an open problem that has been ongoing for over fifty years without reaching satisfactory results. Existing systems are discouragingly expensive and yet they are only able to make a correct distinction between normal and abnormal samples in a fraction of cases. Therefore, they are limited to acting as support for the cytotechnicians as they perform their manual screening. The main reason for the current limitations is that the automated systems struggle to overcome the complexity of the cell structures. Samples are covered in artefacts such as blood cells, overlapping and folded cells, and bacteria, that hamper the segmentation processes and generate large number of suspicious objects. The classifiers designed to differentiate between normal cells and pre-cancerous cells produce unpredictable results when classifying artefacts. In this paper, we propose a sequential classification scheme focused on removing unwanted objects, debris, from an initial segmentation result, intended to be run before the actual normal/abnormal classifier. The method has been evaluated using three separate datasets obtained from cervical samples prepared using both the standard Pap-smear approach as well as the more recent liquid based cytology sample preparation technique. We show success in removing more than 99% of the debris without loosing more than around one percent of the epithelial cells detected by the segmentation process.

**16. A New Algorithm for Computing Riemannian Geodesic Distance in Rectangular 2-D and 3-D Grids**

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*Journal:* International Journal on Artificial Intelligence Tools, volume 22, number 6, 25 pages

*Abstract:* We present a novel way to efficiently compute Riemannian geodesic distance over a two- or three-dimensional domain. It is based on a previously presented method for computation of geodesic distances on surface meshes. Our method is adapted for rectangular grids, equipped with a variable anisotropic metric tensor. Processing and visualization of such tensor fields is common in certain applications, for instance structure tensor fields in image analysis and diffusion tensor fields in medical imaging.

The included benchmark study shows that our method provides significantly better results in anisotropic regions in 2-D and 3-D and is faster than current stat-of-the-art solvers in 2-D grids. Additionally, our method is straightforward to code; the test implementation is less than 150 lines of C++ code. The paper is an extension of a previously presented conference paper and includes new sections on 3-D grids in particular.

**17. Intracranial Volume Estimated with Commonly Used Methods Could Introduce Bias in Studies including Brain Volume Measurements**

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*Journal:* NeuroImage, volume 83, pages 355-360

*Abstract:* In brain volumetric studies, intracranial volume (ICV) is often used as an estimate of pre-morbid brain size as well as to compensate for inter-subject variations in head size. However, if the estimated ICV is biased by for example gender or atrophy, it could introduce errors in study results. To evaluate how two commonly used methods for ICV estimation perform, computer assisted reference segmentations were created and evaluated. Segmentations were created for 399 MRI volumes from 75-year-old subjects, with 53 of these subjects having an additional scan and segmentation created at age 80. ICV estimates from Statistical Parametric Mapping (SPM, version 8) and Freesurfer (FS, version 5.1.0) were compared to the reference segmentations, and bias related to skull size (approximated with the segmentation measure), gender or atrophy were tested for. The possible ICV related effect on associations between normalized hippocampal volume and factors gender, education and cognition was evaluated by normalizing hippocampal volume with different ICV measures. Excellent agreement was seen for inter- ( $r=0.999$ ) and intra- ( $r=0.999$ ) op-

erator reference segmentations. Both SPM and FS overestimated ICV. SPM showed bias associated with gender and atrophy while FS showed bias dependent on skull size. All methods showed good correlation between time points in the longitudinal data (reference: 0.998, SPM: 0.962, FS: 0.995). Hippocampal volume showed different associations with cognition and gender depending on which ICV measure was used for hippocampal volume normalization. These results show that the choice of method used for ICV estimation can bias results in studies including brain volume measurements.

**18. Minimal-Delay Distance Transform for Neighborhood-Sequence Distances in 2D and 3D**

*Authors:* Nicolas Normand (1), **Robin Strand**, Pierre Evenou (1), Aurore Arlicot (1)

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*Journal:* Computer Vision and Image Understanding, volume 117, number 4, pages 409-417

*Abstract:* This paper presents a path-based distance, where local displacement costs vary both according to the displacement vector and with the travelled distance. The corresponding distance transform algorithm is similar in its form to classical propagation-based algorithms, but the more variable distance increments are either stored in look-up-tables or computed on-the-fly. These distances and distance transform extend neighborhood-sequence distances, chamfer distances and generalized distances based on Minkowski sums. We introduce algorithms to compute a translated version of a neighborhood sequence distance map both for periodic and aperiodic sequences and a method to derive the centered distance map. A decomposition of the grid neighbors, in  $Z^2$  and  $Z^3$ , allows to significantly decrease the number of displacement vectors needed for the distance transform. Overall, the distance transform can be computed with minimal delay, without the need to wait for the whole input image before beginning to provide the result image

**19. A Haptics-Assisted Crano-Maxillofacial Surgery Planning System for Restoring Skeletal Anatomy in Complex Trauma Cases**

*Authors:* Pontus Olsson, Fredrik Nysjö, Jan-Michaël Hirsch (1), Ingrid B. Carlstrom

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*Journal:* International Journal of Computer Assisted Radiology and Surgery, volume 8, number 6, pages 887-894

*Abstract:* Cranio-maxillofacial (CMF) surgery to restore normal skeletal anatomy in patients with serious trauma to the face can be both complex and time-consuming. But it is generally accepted that careful pre-operative planning leads to a better outcome with a higher degree of function and reduced morbidity in addition to reduced time in the operating room. However, today's surgery planning systems are primitive, relying mostly on the user's ability to plan complex tasks with a two-dimensional graphical interface. A system for planning the restoration of skeletal anatomy in facial trauma patients using a virtual model derived from patient-specific CT data. The system combines stereo visualization with six degrees-of-freedom, high-fidelity haptic feedback that enables analysis, planning, and preoperative testing of alternative solutions for restoring bone fragments to their proper positions. The stereo display provides accurate visual spatial perception, and the haptics system provides intuitive haptic feedback when bone fragments are in contact as well as six degrees-of-freedom attraction forces for precise bone fragment alignment. A senior surgeon without prior experience of the system received 45 min of system training. Following the training session, he completed a virtual reconstruction in 22 min of a complex mandibular fracture with an adequately reduced result. Preliminary testing with one surgeon indicates that our surgery planning system, which combines stereo visualization with sophisticated haptics, has the potential to become a powerful tool for CMF surgery planning. With little training, it allows a surgeon to complete a complex plan in a short amount of time.

**20. Adaptive Filtering for Enhancement of the Osteocyte Cell Network in 3D Microtomography Images**

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*Journal:* IRBM, volume 34, number 1-SI, pages 48-52

*Abstract:* The osteocyte cell network in bone tissue is thought to orchestrate tissue adaptation and remodeling, thus holding responsibility for tissue quality. Previously, this structure has been studied mainly in 2D

and its architecture and functions are not fully elucidated. The assessment of the osteocyte system is prerequisite for deeper understanding of bone remodeling and for advances in management of bone diseases. Our goal is to enable 3D isotropic imaging of bone at cellular level and to develop algorithms for quantitative image analysis of the cell network. We recently demonstrated accurate 3D imaging of this cell structure with synchrotron radiation tomography at submicrometric scale. Due to the limited spatial resolution of the imaging system and the constraints in terms of radiation dose, the images suffer from low signal to noise ratio and the detection of the cell dendrites is challenging. Here we detail a method for enhancement of the osteocyte network in human bone from 3D microtomography images. The approach combines Hessian-based 3D line enhancement and bilateral filtering. Our method enables extraction of the interconnected cells from noisy images, preserving the integrity of the cells and of their slender dendrites. Qualitative and quantitative results are presented.

## 21. High-Throughput Hyperdimensional Vertebrate Phenotyping

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*Journal:* Nature Communications, volume 4, pages 1467

*Abstract:* Most gene mutations and biologically active molecules cause complex responses in animals that cannot be predicted by cell culture models. Yet animal studies remain too slow and their analyses are often limited to only a few readouts. Here we demonstrate high-throughput optical projection tomography with micrometre resolution and hyperdimensional screening of entire vertebrates in tens of seconds using a simple fluidic system. Hundreds of independent morphological features and complex phenotypes are automatically captured in three dimensions with unprecedented speed and detail in semitransparent zebrafish larvae. By clustering quantitative phenotypic signatures, we can detect and classify even subtle alterations in many biological processes simultaneously. We term our approach hyperdimensional *in vivo* phenotyping. To illustrate the power of hyperdimensional *in vivo* phenotyping, we have analysed the effects of several classes of teratogens on cartilage formation using 200 independent morphological measurements, and identified similarities and differences that correlate well with their known mechanisms of actions in mammals

## 22. Bisphenol a Exposure Increases Liver Fat in Juvenile Fructose-Fed Fischer 344 Rats

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*Journal:* Toxicology, volume 303, number 1, pages 125-132

*Abstract:* Background: Prenatal exposure to bisphenol A (BPA) has been shown to induce obesity in rodents. To evaluate if exposure also later in life could induce obesity or liver damage we investigated these hypotheses in an experimental rat model.

METHODS: From five to fifteen weeks of age, female Fischer 344 rats were exposed to BPA via drinking water (0.025, 0.25 or 2.5mgBPA/L) containing 5% fructose. Two control groups were given either water or 5% fructose solution. Individual weight of the rats was determined once a week. At termination magnetic resonance imaging was used to assess adipose tissue amount and distribution, and liver fat content. After sacrifice the left perirenal fat pad and the liver were dissected and weighed. Apolipoprotein A-I in plasma was analyzed by western blot.

Results: No significant effects on body weight or the weight of the dissected fat pad were seen in rats exposed to BPA, and MRI showed no differences in total or visceral adipose tissue volumes between the groups. However, MRI showed that liver fat content was significantly higher in BPA-exposed rats than in fructose controls ( $p=0.04$ ). BPA exposure also increased the apolipoprotein A-I levels in plasma ( $p<0.0001$ ).

Conclusion: We found no evidence that BPA exposure affects fat mass in juvenile fructose-fed rats. How-

ever, the finding that BPA in combination with fructose induced fat infiltration in the liver at dosages close to the current tolerable daily intake (TDI) might be of concern given the widespread use of this compound in our environment.

**23. Quantification of Total and Visceral Adipose Tissue in Fructose-Fed Rats Using Water-Fat Separated Single Echo MRI**

**Authors:** Monika Rönn (1), Monica P. Lind (1), Helen Karlsson (2), Katarina Cvek (3), Johan Berglund (4), **Filip Malmborg**, Jan Örberg (5), Lars Lind (6), Francisco Ortiz-Nieto (4), Joel Kullberg (4)

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**Journal:** Obesity, volume 21, number 9, pages E388-395

**Abstract:** Objective: The aim of this study was to setup a rodent model for modest weight gain and an MRI-based quantification of body composition on a clinical 1.5 T MRI system for studies of obesity and environmental factors and their possible association.

Design and Methods: Twenty-four 4-week-old female Fischer rats were divided into two groups: one exposed group (n=12) and one control group (n 12). The exposed group was given drinking water containing fructose (5% for 7 weeks, then 20% for 3 weeks). The control group was given tap water. Before sacrifice, whole body MRI was performed to determine volumes of total and visceral adipose tissue and lean tissue. MRI was performed using a clinical 1.5 T system and a chemical shift based technique for separation of water and fat signal from a rapid single echo acquisition. Fat signal fraction was used to separate adipose and lean tissue. Visceral adipose tissue volume was quantified using semiautomated segmentation. After sacrifice, a perirenal fat pad and the liver were dissected and weighed. Plasma proteins were analyzed by Western blot.

Results: The weight gain was 5.2% greater in rats exposed to fructose than in controls ( $P=0.042$ ). Total and visceral adipose tissue volumes were 5.2 cm<sup>3</sup>(3) ( $P=0.017$ ) and 3.1 cm<sup>3</sup>(3) ( $P=0.019$ ) greater, respectively, while lean tissue volumes did not differ. The level of triglycerides and apolipoprotein A-I was higher ( $P=0.034$ ,  $P=0.005$ , respectively) in fructose-exposed rats.

**24. Introducing a Novel Analysis Technique for Osseointegrated Dental Implants Retrieved 29 Years Postsurgery**

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**Journal:** Clinical Implant Dentistry and Related Research, volume 15, number 4, pages 538-549

**Abstract:** Purpose: To investigate osseointegration of oral implants, which were retrieved from a patient after 29 years in situ, we use novel three-dimensional analysis methods and visualization techniques that supplement conventional two-dimensional analysis. Materials and Methods: The sample processing involved nondecalcification and embedment in resin. Conventional two-dimensional histomorphometrical methods were conducted. Additionally, the quantification was extended to three-dimensional by using synchrotron radiation micro-computed tomography (SRmCT) technique and two relevant visualization methods for the three-dimensional data were introduced. Results: The three-dimensional results involved three-dimensional quantification and visualization of two implant samples with methods beyond state-of-the-art. Traditional two-dimensional histomorphometrical results revealed a mean bone-implant contact (BIC) of about 50%. In most samples, bone area (BA) was lower inside the treads compared with out-folded mirror images, which were confirmed by the three-dimensional quantification. The BIC along four selected regions showed highest percentages in the bottom/valley region and lowest in the thread-peak region. Qualitative observations revealed ongoing bone remodeling areas in all samples. The apical hole demonstrated high osseointegration. Conclusion: The novel techniques including an animation and an out-folding of BIC and BA enabled a simultaneous visualization of the three-dimensional material obtained from SRmCT data. However, the two-dimensional histological sections were needed for qualitative and quantitative evaluation of osseointegration and, thus, both methods are considered equally important.

## 25. Evaluating 2D and 3D Geovisualisations for Basic Spatial Assessment

*Author:* Stefan Seipel

*Journal:* Behavior and Information Technology, volume 32, number 8, pages 845-858

*Abstract:* This study investigates the use of 2D and 3D presentations of maps for the assessment of distances in a geographical context. Different types of 3D representations have been studied: A weak 3D visualisation that provides static monocular depth cues and a strong 3D visualisation that uses stereoscopic and kinetic depth cues. Two controlled experiments were conducted to test hypotheses regarding subjects' efficiency in visually identifying the shortest distance among a set of market locations in a map. As a general result, we found that participants were able to correctly identify shortest distances when the difference to potential alternatives was sufficiently large, but performance decreased systematically when this difference decreased. Noticeable differences emerged for the investigated visualisation conditions. Participants in this study were equally efficient when using a weak 3D representation and a 2D representation. When the strong 3D visualisation was employed, they reported visual discomfort and tasks solved were significantly less correct. Presentations of intrinsic 2D content (maps) in 3D context did not, in this study, benefit from cues provided by a strong 3D visualisation and are adequately implemented using a weak 3D visualisation.

## 26. The Minimum Barrier Distance

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(4) Dept. Radiology, The University of Iowa, Iowa City, IA, USA

*Journal:* Computer Vision and Image Understanding, volume 117, number 4, pages 429-437

*Abstract:* In this paper we introduce a minimum barrier distance, MBD, defined for the (graphs of) real-valued bounded functions  $f(A)$ , whose domain  $D$  is a compact subsets of the Euclidean space  $R^n$ . The formulation of MBD is presented in the continuous setting, where  $D$  is a simply connected region in  $R^n$ , as well as in the case where  $D$  is a digital scene. The MBD is defined as the minimal value of the barrier strength of a path between the points, which constitutes the length of the smallest interval containing all values of  $f(A)$  along the path. We present several important properties of MBD, including the theorems: on the equivalence between the MBD  $\rho(A)$  and its alternative definition  $\phi(A)$ ; and on the convergence of their digital versions,  $\widehat{\rho(A)}$  and  $\widehat{\phi(A)}$ , to the continuous MBD  $\rho(A) = \phi(A)$  as we increase a precision of sampling. This last result provides an estimation of the discrepancy between the value of  $\widehat{\rho(A)}$  and of its approximation  $\widehat{\phi(A)}$ . An efficient computational solution for the approximation  $\widehat{\phi(A)}$  of  $\widehat{\rho(A)}$  is presented. We experimentally investigate the robustness of MBD to noise and blur, as well as its stability with respect to the change of a position of points within the same object (or its background). These experiments are used to compare MBD with other distance functions: fuzzy distance, geodesic distance, and max-arc distance. A favorable outcome for MBD of this comparison suggests that the proposed minimum barrier distance is potentially useful in different imaging tasks, such as image segmentation.

## 27. 3D Tree-Ring Analysis Using Helical X-Ray Tomography

*Authors:* Jan Van den Bulcke (1), Erik L. G. Wernersson, Manuel Dierick (2), Denis Van Loo (2), Bert Masschaele (2), Loes Brabant (2), Matthieu N. Boone (2), Luc Van Hoorebeke (2), Kristof Haneca(3), Anders Brun, Cris L. Luengo Hendriks, Joris Van Acker (1)

(1) Dept. Forest and Water Management, Laboratory of Wood Technology, UGCT-Ghent University, Belgium

(2) Dept. Physics and Astronomy, UGCT-Ghent University, Belgium

(3) Flanders Heritage Agency, Brussels, Belgium

*Journal:* Dendrochronologia, volume 32

*Abstract:* The current state-of-the-art of tree-ring analysis and densitometry is still mainly limited to two dimensions and mostly requires proper treatment of the surface of the samples. In this paper we elaborate on the potential of helical X-ray computed tomography for 3D tree-ring analysis. Microdensitometrical profiles are obtained by processing of the reconstructed volumes. Correction of the structure direction, taking into account the angle of growth rings and grain, results in very accurate microdensity and precise ring width measurements. Both a manual as well as an automated methodology is proposed here, of which the MATLAB code is available. Examples are given for pine (*Pinus sylvestris* L.), oak (*Quercus robur* L.) and teak (*Tectona grandis* L.). In all, the methodologies applied here on the 3D volumes are useful for growth related studies, enabling a fast and non-destructive analysis

**28. Investigation of the Three-Dimensional Orientation of Mineralized Collagen Fibrils in Human Lamellar Bone Using Synchrotron X-Ray Phase Nano-Tomography**

*Authors:* Peter Varga (1), **Alexandra Pacureanu (2,3,4)**, Max Langer (2,3), Heikki Suhonen (3), Bernhard Hesse (1,3), Quentin Grimal (5), Peter Cloetens (3), Kay Raum (1), Françoise Peyrin (2,3)

(1) Julius Wolff Institute and Berlin-Brandenburg School for Regenerative Therapies, Charité Universitätsmedizin, Berlin, Germany

(2) Creatis, Université de Lyon, France

(3) European Synchrotron Radiation Facility, Grenoble, France

(4) Science for Life Laboratory, SciLifeLab, UU

(5) LIP, UPMC Université Pierre et Marie Curie Paris 6, Paris, France

*Journal:* Acta Biomaterialia, volume 9, number 9, pages 8118-8127

*Abstract:* We investigate the three-dimensional (3-D) organization of mineralized collagen fibrils in human cortical bone based on synchrotron X-ray phase nano-tomography images. In lamellar bone the collagen fibrils are assumed to have a plywood-like arrangement, but due to experimental limitations the 3-D fibril structure has only been deduced from section surfaces so far and the findings have been controversial. Breakthroughs in synchrotron tomographic imaging have given access to direct 3-D information on the bone structure at the nanoscale level. Using an autocorrelation-based orientation measure we confirm that the fibrils are unidirectional in quasi-planes of sub-lamellae and find two specific dominant patterns, oscillating and twisted plywoods coexisting in a single osteon. Both patterns exhibit smooth orientation changes between adjacent quasi-planes. Moreover, we find that the periodic changes in collagen fibril orientation are independent of fluctuations in local mass density. These data improve our understanding of the lamellar arrangement in bone and allow more detailed investigations of structure-function relationships at this scale, providing templates for bio-inspired materials. The presented methodology can be applied to non-destructive 3-D characterization of the sub-micron scale structure of other natural and artificial mineralized biomaterials.

**29. Postprocessing Method for Reducing Phase Effects in Reconstructed Microcomputed-Tomography Data**

*Authors:* Erik L. G. Wernersson, Matthieu N. Boone (1,2), Jan Van den Bulcke (1,3), Luc Van Hoorebeke (1,2), Cris L. Luengo Hendriks

(1) UGCT, University Ghent Centre for X-ray Tomography, Belgium

(2) Dept. Physics and Astronomy, Ghent University, Belgium

(3) Dept. Forest and Water Management, Ghent University, Belgium

*Journal:* Optical Society of America, Journal A, volume 30, number 3, pages 455-461

*Abstract:* With increased resolution in x-ray computed tomography, refraction adds increasingly to the attenuation signal. Though potentially beneficial, the artifacts caused by refraction often need to be removed from the image. In this paper, we propose a postprocessing method, based on deconvolution, that is able to remove these artifacts after conventional reconstruction. This method poses two advantages over existing projection-based (preprocessing) phase-retrieval or phase-removal algorithms. First, evaluation of the parameters can be done very quickly, improving the overall speed of the method. Second, postprocessing methods can be applied when projection data is not available, which occurs in several commercial systems with closed software or when projection data has been deleted. It is shown that the proposed method performs comparably to state-of-the-art methods in terms of image quality.

## 6.3 Refereed conference proceedings

Authors affiliated with CBA are in bold.

### 1. Cluster Detection and Field-of-View Quality Rating: Applied to Automated Pap-Smear Analysis

*Authors:* Marine Astruc (1), **Patrik Malm**, Rajesh Kumar (2), Ewert Bengtsson

(1) Ecole Centrale Nantes, France

(2) Centre for Development of Advanced Computing, Thiruvananthapuram, India

*In Proceedings:* 2nd International Conference on Pattern Recognition Applications and Methods (ICPRAM), Barcelona, Spain, pages 355-364

*Abstract:* Automated cervical cancer screening systems require high resolution analysis of a large number of epithelial cells, involving complex algorithms, mainly analysing the shape and texture of cell nuclei. This can be a very time consuming process. An initial selection of relevant fields-of-view in low resolution images could limit the number of fields to be further analysed at a high resolution. In particular, the detection of cell clusters is of interest for nuclei segmentation improvement, and for diagnostic purpose, malignant and endometrial cells being more prone to stick together in clusters than other cells. In this paper, we propose methods aiming at evaluating the quality of fields-of-view in bright-field microscope images of cervical cells. The approach consists in the construction of neighbourhood graphs using the nuclei as the set of vertices. Transformations are then applied on such graphs in order to highlight the main structures in the image. The methods result in the delineation of regions with varying cell density and the identification of cell clusters. Clustering methods are evaluated using a dataset of manually delineated clusters and compared to a related work.

### 2. An Algorithm for Parallel Calculation of Trigonometric and Exponential Functions

*Authors:* Tony Barrera (1), **Anders Hast**, Ewert Bengtsson

(1) Uppsala, Sweden

*In Proceedings:* ACM International Conference on Computing Frontiers, Ischia, Italy, paper 8

*Abstract:* We propose a new way of calculating the sine and cosine functions. The method is based on recursive applications of a modified complex power algorithm. On a machine with multiple complex multipliers the method can be used to calculate sines and cosines in logarithmic time. The serial version of the presented method requires only two precomputed constants and no tables. In the parallel versions a trade off can be made between the number of parallel processing elements and the size of tables.

### 3. A Weight Sequence Distance Function

*Authors:* Benedek Nagy (1), **Robin Strand**, Nicolas Normand (2)

(1) Department of Computer Science, University of Debrecen, Hungary

(2) Université de Nantes, France

*In Proceedings:* Mathematical Morphology and Its Applications to Signal and Image Processing (ISMM), Uppsala, Sweden, Lecture Notes in Computer Science 7883, pages 292-301

*Abstract:* In this paper, a family of weighted neighborhood sequence distance functions defined on the square grid is presented. With this distance function, the allowed weight between any two adjacent pixels along a path is given by a weight sequence. We build on our previous results, where only two or three unique weights are considered, and present a framework that allows any number of weights. We show that the rotational dependency can be very low when as few as three or four unique weights are used. An algorithm for computing the distance transform (DT) that can be used for image processing applications is also presented.

### 4. Dual B-spline Snake for Interactive Myocardial Segmentation

*Authors:* Kevin Bianchi (1), Antoine Vacant (1), **Robin Strand**, Pierre Terve (2), Laurent Sarry (1)

(1) ISIT UMR6284 CNRS, Univ. d'Auvergne, Clermont-Ferrand, France

(2) KEOSYS Company 1, Saint Herblain, France

*In Proceedings:* Medical Image Understanding and Analysis (MIUA), Birmingham, UK

*Abstract:* This paper presents a novel interactive segmentation formalism based on two coupled B-Spline snake models to efficiently and simultaneously extract myocardial walls from short-axis magnetic resonance images. The main added value of this model is interaction as it is possible to quickly and intuitively correct the result in complex cases without restarting the whole segmentation working flow. During this process, energies computed from the images guide the user to the best position of the model.

## 5. Salience-Based Parabolic Structuring Functions

**Authors:** Vladimir Curic, Cris L. Luengo Hendriks

*In Proceedings:* Mathematical Morphology and Its Applications to Signal and Image Processing, Uppsala, Sweden, Lecture Notes in Computer Science 7883, pages 183-194

**Abstract:** It has been shown that the use of the salience map based on the salience distance transform can be useful for the construction of spatially adaptive structuring elements. In this paper, we propose salience-based parabolic structuring functions that are defined for a fixed, predefined spatial support, and have low computational complexity. In addition, we discuss how to properly define adjunct morphological operators using the new spatially adaptive structuring functions. It is also possible to obtain flat adaptive structuring elements by thresholding the salience-based parabolic structuring functions

## 6. A New Quantitative Approach for Estimating Bone Cell Connections from Nano-CT Images

**Authors:** Pei Dong (1), Alexandra Pacureanu, Maria Zuluaga (2), Cecile Olivier (1), Frederique Frouin (3), Quentin Grimal (4), Francoise Peyrin (1)

(1) European Synchrotron Radiation Facility and CREATIS, Université de Lyon, France

(2) University College London, UK

(3) Faculté de Médecine Pierre et Marie Curie - Pitié Salpêtrière, Paris, France

(4) Université Pierre et Marie Curie, Paris, France

*In Proceedings:* IEEE 35th Annual International Conference on Engineering in Medicine and Biology Society (EMBC), Osaka, Japan, pages 3694-3697

**Abstract:** Recent works highlighted the crucial role of the osteocyte system in bone fragility. The number of canaliculi of osteocyte lacuna (Lc.NCa) is an important parameter that reflects the functionality of bone tissue, but rarely reported due to the limitations of current microscopy techniques, and only assessed from 2D histology sections. Previously, we showed the Synchrotron Radiation nanotomography (SR-nanoCT) is a promising technique to image the 3D lacunar-canicular network. Here we present, for the first time, an automatic method to quantify the connectivity of bone cells in 3D. After segmentation, our method first separates and labels each lacuna in the network. Then, by creating a bounding surface around lacuna, the Lc.NCa is calculated through estimating 3D topological parameters. The proposed method was successfully applied to a 3D SR-nanoCT image of cortical femoral bone. Statistical results on 165 lacunae are reported, showing a mean of 51, which is consistent with the literature.

## 7. Epithelial Cell Segmentation in Histological Images of Testicular Tissue Using Graph-Cut

**Authors:** Azadeh Fakhrzadeh, Ellinor Spörndly-Nees (1), Lena Holm (1), Cris L. Luengo Hendriks

(1) Department of Anatomy, Physiology and Biochemistry, SLU, Uppsala

*In Proceedings:* 17th International Conference on Image Analysis and Processing, Naples, Italy, Lecture Notes in Computer Science 8157, pages 201-208

**Abstract:** Computerized image processing has provided us with valuable tools for analyzing histology images. However, histology images are complex, and the algorithm which is developed for a data set may not work for a new and unseen data set. The preparation procedure of the tissue before imaging can significantly affect the resulting image. Even for the same staining method, factors like delayed fixation may alter the image quality. In this paper we face the challenging problem of designing a method that works on data sets with strongly varying quality. In environmental research, due to the distance between the site where the wild animals are caught and the laboratory, there is always a delay in fixation. Here we suggest a segmentation method based on the structural information of epithelium cell layer in testicular tissue. The cell nuclei are detected using the fast radial symmetry filter. A graph is constructed on top of the epithelial cells. Graph-cut optimization method is used to cut the links between cells of different tubules. The algorithm is tested on five different groups of animals. Group one is fixed immediately, three groups were left at room temperature for 18, 30 and 42 hours respectively, before fixation. Group five was frozen after 6 hours in room temperature and thawed. The suggested algorithm gives promising results for the whole data set.

## 8. Epithelial Cell Layer Segmentation Using Graph-cut and Its Application in Testicular Tissue

**Authors:** Azadeh Fakhrzadeh, Ellinor Spörndly-Nees (1), Lena Holm (1), Cris L. Luengo Hendriks

(1) Department of Anatomy, Physiology and Biochemistry, SLU, Uppsala

*In Proceedings:* Medical Image Understanding and Analysis (MIUA), Birmingham, UK

**Abstract:** Computerized image processing has provided us with valuable tools for analyzing histology images. However, histology images are complex, and the algorithm which is developed for a data set may not work for a new and unseen data set. The preparation procedure of the tissue before imaging can sig-

nificantly affect the resulting image. Even for the same staining method, factors like delayed fixation may alter the image quality. In this paper we face the challenging problem of designing a method that works on data sets with strongly varying quality. In environmental research, due to the distance between the site where the wild animals are caught and the laboratory, there is always a delay in fixation. Here we suggest a segmentation method based on the structural information of epithelium cell layer in testicular tissue. The cell nuclei are detected using the fast radial symmetry filter. A graph is constructed on top of the epithelial cells. Graph-cut optimization method is used to cut the links between cells of different tubules. The algorithm is tested on five different groups of animals. Group one is fixated immediately, four groups were left at room temperature for 6, 18, 30 and 42 hours respectively, before fixation. The suggested algorithm gives promising results for the whole data set.

**9. Shortest Diagonal Triangulation of Convex Layers**

*Authors:* Anders Hast, Peter Jenke (1), Stefan Seipel

(1) University of Gävle

*In Proceedings:* The IASTED International Conference on Signal Processing, Pattern Recognition and Applications, Innsbruck, Austria, pages 1-7

*Abstract:* One problem in the field of computational geometry is the triangulation of convex layers. The rotating caliper algorithm is an alternative to the constrained Delaunay triangulation method. We present an improved triangulation algorithm, which gives a mesh quality close to that of the Constrained Delaunay but substantially faster. Each layer will be connected to the neighboring layer by edges and from the two vertices constituting an edge the proposed algorithm will select the shortest diagonal to its next neighbors in the polygonal chain on the other side, i.e. from the outer layer to the inner layer or vice versa. We discuss quality issues regarding the rotating caliper method and some improvements to it, as well as how a Constrained Delaunay can be efficiently implemented for convex layers.

**10. Rotation Invariant Feature Matching - Based on Gaussian Filtered Log Polar Transform and Phase Correlation**

*Authors:* Anders Hast, Andrea Marchetti (1)

(1) IIT, CNR

*In Proceedings:* 8th International Symposium on Image and Signal Processing and Analysis (ISPA), Trieste, Italy, pages 1-6

*Abstract:* Rotation invariance is an important property for any feature matching method and it has been implemented in different ways for different methods. The Log Polar Transform has primarily been used for image registration where it is applied after phase correlation, which in its turn is applied on the whole images or in the case of template matching, applied on major parts of them followed by an exhaustive search. We investigate how this transform can be used on local neighborhoods of features and how phase correlation as well as normalized cross correlation can be applied on the result. Thus, the order is reversed and we argue why it is important to do so. We demonstrate a common problem with the log polar transform and that many implementations of it are not suitable for local feature detectors. We propose an implementation of it based on Gaussian filtering. We also show that phase correlation generally will perform better than normalized cross correlation. Both handles illumination differences well, but changes in scale is handled better by the phase correlation approach.

**11. Automated Quantification of Zebrafish Tail Deformation for High-Throughput Drug Screening**

*Authors:* Omer Ishaq, Joseph Negri (1), Mark-Anthony Bray (1), Alexandra Pacureanu, Randall T. Peterson (2) Carolina Wählby (1)

(1) Broad Institute of Harvard and MIT, Cambridge, MA, USA

(2) Massachusetts General Hospital, Harvard Medical School, Department of Medicine, Charlestown, MA, USA

*In Proceedings:* 10th International Symposium on Biomedical Imaging : From Nano to Macro, San Francisco, CA, USA pages 902-905

*Abstract:* Zebrafish (*Danio rerio*) is an important vertebrate model organism in biomedical research thanks to its ease of handling and translucent body, enabling *in vivo* imaging. Zebrafish embryos undergo spinal deformation upon exposure to chemical agents that inhibit DNA repair. Automated image-based quantification of spine deformation is therefore attractive for whole-organism based assays for use in early-phase drug discovery. We propose an automated method for accurate high-throughput measurement of tail deformations in multi-fish micro-plate wells. The method generates refined medial representations of partial

tail-segments. Subsequently, these disjoint segments are analyzed and fused to generate complete tails. Based on estimated tail curvatures we reach a classification accuracy of 91% on individual animals as compared to known control treatment. This accuracy is increased to 95% when combining scores for fish in the same well.

## 12. Coverage Segmentation of Thin Structures by Linear Unmixing and Local Centre of Gravity Attraction

*Authors:* Kristina Lidayová, Joakim Lindblad, Nataša Sladoje, Hans Frimmel (1)

(1) Division of Scientific Computing, UU

*In Proceedings:* 8th International Symposium on Image and Signal Processing and Analysis, Trieste, Italy, pages 83-88

*Abstract:* We present a coverage segmentation method for extracting thin structures in two-dimensional images. These thin structures can be, for example, retinal vessels, or microtubules in cytoskeleton, which are often 1-2 pixels thick. There exist several methods for coverage segmentation, but when it comes to thin and long structures, the segmentation is often unreliable. We propose a method that does not shrink the structures inappropriately and creates a trustworthy segmentation. In addition, as a by-product a high-resolution crisp reconstruction is provided. The method needs a reliable crisp segmentation as an input and uses information from linear unmixing and the crisp segmentation to create a high-resolution crisp reconstruction of the object. After a procedure where holes and protrusions are removed, the high-resolution crisp image is optionally down-sampled back to its original size, creating a coverage segmentation that preserves thin structures.

## 13. Faster Fuzzy Connectedness via Precomputation

*Authors:* Filip Malmberg, Robin Strand

*In Proceedings:* Mathematical Morphology and Its Applications to Signal and Image Processing (ISSM), Uppsala, Sweden, Lecture Notes in Computer Science 7883, pages 476-483

*Abstract:* We propose a method for accelerating the computation of fuzzy connectedness. The method is based on a precomputation step - the construction of a supervertex graph whose vertices are clusters of image elements. By constructing this supervertex graph in a specific way, we can perform the bulk of the fuzzy connectedness computations on this graph, rather than on the original image, while guaranteeing exact results. Typically, the number of nodes in the supervertex graph is much smaller than the number of elements in the image, and thus less computation is required. In an experiment, we demonstrate the ability of the proposed method to accelerate the computation of fuzzy connectedness considerably.

## 14. Digital Distances and Integer Sequences

*Authors:* Nicolas Normand (1), Robin Strand

(1) LUNAM Université, Université de Nantes, France

*In Proceedings:* 17th IAPR International Conference on Discrete Geometry for Computer Imagery, Seville, Spain, Lecture Notes in Computer Science 7749, pages 169-179

*Abstract:* In recent years, the theory behind distance functions defined by neighbourhood sequences has been developed in the digital geometry community. A neighbourhood sequence is a sequence of integers, where each element defines a neighbourhood. In this paper, we establish the equivalence between the representation of convex digital disks as an intersection of half-planes ( $\mathcal{H}$ -representation) and the expression of the distance as a maximum of non-decreasing functions. Both forms can be deduced one from the other by taking advantage of the Lambek-Moser inverse of integer sequences. Examples with finite sequences, cumulative sequences of periodic sequences and (almost) Beatty sequences are given. In each case, closed-form expressions are given for the distance function and  $\mathcal{H}$ -representation of disks. The results can be used to compute the pair-wise distance between points in constant time and to find optimal parameters for neighbourhood sequences.

## 15. Precise 3D Angle Measurements in CT Wrist Images

*Authors:* Johan Nysjö, Albert Christersson (1), Ida-Maria Sintorn, Ingela Nyström, Sune Larsson (1), Filip Malmberg

(1) Dept. of Orthopaedics, UU

*In Proceedings:* Image Analysis and Processing – ICIAP 2013: Part II, Naples, Italy, Lecture Notes in Computer Science 8157, pages 479-488

*Abstract:* The clinically established method to assess the displacement of a distal radius fracture is to manually measure two reference angles, the dorsal angle and the radial angle, in consecutive 2D X-ray images of

the wrist. This approach has the disadvantage of being sensitive to operator errors since the measurements are performed on 2D projections of a 3D structure. In this paper, we present a semi-automatic system for measuring relative changes in the dorsal angle in 3D computed tomography (CT) images of fractured wrists. We evaluate the proposed 3D measurement method on 28 post-operative CT images of fractured wrists and compare it with the radiographic 2D measurement method used in clinical practice. The results show that our proposed 3D measurement method has a high intra- and inter-operator precision and is more precise and robust than the conventional 2D measurement method

#### 16. **SplineGrip - An Eight Degrees-of-Freedom Flexible Haptic Sculpting Tool**

*Authors:* Pontus Olsson, Fredrik Nysjö, Björn Aneer (1), Stefan Seipel, Ingrid B. Carlbom

(1) Independent Artist, Stockholm, Sweden

*In Proceedings:* 40th International Conference ACM SIGGRAPH 2013, Anaheim, USA, paper 50

*Abstract:* SplineGrip is a flexible haptic sculpting tool that senses the articulation and pose (position and orientation) of the sculpting hand in eight degrees-of-freedom (DOF). The tool captures the hand articulation in two DOF, and uses a commercial haptic device to track the hand pose in six DOF and to simultaneously provide three DOF haptic feedback. The eight DOF input is mapped to the pose and shape of a virtual NURBS-based sculpting tool, offering versatile interaction with a virtual model. We capture the hand articulation in two DOF using two bend sensors with curvature dependent resistance, which are attached in two directions to a flexible plastic sheet mounted on the gimbal of the haptic device. One sensor measures the plastic sheet curvature controlled by the thumb, and the other measures the curvature controlled by the middle and ring fingers. In a neutral state, when all fingers are straight, the virtual sculpting tool takes the shape of a line segment. By bending one sensor with the middle and ring fingers, the user changes the virtual tool curvature. By bending the other sensor with the thumb, the user changes the width of the virtual tool. A curvature increase at zero width turns the line into a spline, and a width increase at zero curvature creates a plane. By bending both sensors, the user may simultaneously control the curvature and width of the NURBS surface. The user may toggle between negative and positive curvatures to make convex and concave tools. We demonstrate SplineGrip with a simple sculpting system where the user starts with a block of material and uses the virtual sculpting tool to gradually remove material; the sculpting tool is not limited to subtractive modeling, but can work with other modeling paradigms.

#### 17. **Snap-to-fit, a Haptic 6 DOF Alignment Tool for Virtual Assembly**

*Authors:* Pontus Olsson, Fredrik Nysjö, Jan-Michaél Hirsch (1), Ingrid B. Carlbom

(1) Oral and Maxillofacial Surgery, UU

*In Proceedings:* IEEE World Haptics (WHC), Daejeon, South Korea, pages 205-210

*Abstract:* Virtual assembly of complex objects has application in domains ranging from surgery planning to archaeology. In these domains the objective is to plan the restoration of skeletal anatomy or archaeological artifacts to achieve an optimal reconstruction without causing further damage. While graphical modeling plays a central role in virtual assembly, visual feedback alone is often insufficient since object contact and penetration is difficult to discern due to occlusion. Haptics can improve an assembly task by giving feedback when objects collide, but precise fitting of fractured objects guided by delicate haptic cues similar to those present in the physical world requires haptic display transparency beyond the performance of today's systems. We propose a haptic alignment tool that combines a 6 Degrees of Freedom (DOF) attraction force with traditional 6 DOF contact forces to pull a virtual object towards a local stable fit with a fixed object. The object forces are integrated into a virtual coupling framework yielding a stable haptic tool. We demonstrate the use of our system on applications from both cranio-maxillofacial surgery and archaeology, and show that we can achieve haptic rates for fractured surfaces with over 5000 points.

#### 18. **Dual-Domain Visual Exploration of Urban Solar Potential**

*Authors:* Stefan Seipel, David Lingfors (1), Joakim Widén (1)

(1) Solid State Physics, Dept. Engineering Sciences, UU

*In Proceedings:* Eurographics Workshop on Urban Data Modelling and Visualisation, Girona, Spain, pages 21-24

*Abstract:* This project aims to improve the planning and design of solar electricity installations in the urban environment. One major objective of these studies is to enable a highly detailed temporal and spatial analysis of the expected solar yield, which becomes increasingly important for optimal load balance in electric power networks. In our research we develop a 3D simulation model that integrates geographical data and detailed 3D urban models with temporal solar irradiance and climate data. According to our model the predicted

solar yield becomes a multi-dimensional function of several design-specific parameters that are interactively explored by a human expert. This project is an interdisciplinary initiative that involves researchers from Energy Systems and from Computer Science at Uppsala University and the University of Gävle. During the first year, a demonstrator system for the interactive exploration of the design parameter space has been developed. Our method and the demonstrator system have been published in two international conferences in 2013. Forthcoming research in this project will concern the refinement and validation of computational models, as well new methods for interactive visual exploration.

**19. A Probabilistic Template Model for Finding Macromolecules in MET Volume Images**

**Authors:** Lennart Svensson, Ida-Maria Sintorn

*In Proceedings:* 6th Iberian Conference on Pattern Recognition and Image Analysis (IbPRIA), Madeira, Portugal, Lecture Notes in Computer Science 7887, pages 855-962

*Abstract:* We introduce and investigate probabilistic templates with particular focus on the application of protein identification in electron tomography volumes. We suggest to create templates with a weighted averaging operation of several object instances after alignment of an identified subpart. The subpart to be aligned should, ideally, correspond to a rigid and easily identifiable part of the object. The proposed templates enable common rigid template matching methods to also find different shape variations without increasing time complexity in the actual search procedure, since a static template is still used. We present general ideas on how to perform the object instance alignment and look specifically at how to do it for the antibody macromolecule IgG.

**20. Feature Weight Optimization and Pruning in Historical Text Recognition**

**Authors:** Fredrik Wahlberg, Anders Brun

*In Proceedings:* 9th International Symposium on Visual Computing, Advances in Visual Computing, Rethymnon, Crete, Greece, Lecture Notes in Computer Science 8034, pages 98-107

*Abstract:* In handwritten text recognition, "sliding window" feature extraction represent the visual information contained in written text as feature vector sequences. In this paper, we explore the parameter space of feature weights in search for optimal weights and feature selection using the coordinate descent method. We report a gain of about 5% AUC performance. We use a public dataset for evaluation and also discuss the effects and limitations of "word pruning," a technique in word spotting that is commonly used to boost performance and save computational time.

**21. Feature Space Denoising Improves Word Spotting**

**Authors:** Fredrik Wahlberg, Anders Brun

*In Proceedings:* 2nd International Workshop on Historical Document Imaging and Processing, Washington DC, USA, pages 59-66

*Abstract:* Some of the sliding window features commonly used in off-line handwritten text recognition are inherently noisy or sensitive to image noise. In this paper, we investigate the effects of several de-noising filters applied in the feature space and not in the image domain. The purpose is to target the intrinsic noise of these features, stemming from the complex shapes of handwritten characters. This noise is present even if the image has been captured without any kind of artefacts or noise. An evaluation, using a public database, is presented showing that the recognition of word-spotting can be improved considerably by using de-noising filters in the feature space.

## 6.4 Non-refereed conferences and workshops

Authors affiliated with CBA are in bold.

### 1. Case Specific Finite Element Analysis of the Strains Experienced by Osteocytes

*Authors:* Peter Varga(1), **Alexandra Pacureanu** (2), Max Langer(3), Bernhard Hesse (1), Francoise Peyrin (3), Kay Raum (1)

(1) Julius Wolff Institute & Berlin-Brandenburg School for Regenerative Therapies, Charité, Berlin, Germany

(2) SciLifeLab, UU

(3) European Synchrotron Radiation Facility, Creatis, Université de Lyon, France

*In Proceedings:* International Conference on Computational Bioengineering, Leuven, Belgium

*Comment:* Abstract review

### 2. The 3D Orientation of Mineralized Collagen Fibrils in Human Lamellar Bone and Its Mechanical Consequences

*Authors:* Peter Varga (1), **Alexandra Pacureanu** (2), Max Langer (3), Heikki Suhonen (3), Bernhard Hesse (1), Quentin Grimal (4), Peter Cloetens, Kay Raum, Francoise Peyrin

(1) Julius Wolff Institute & Berlin-Brandenburg School for Regenerative Therapies, Charité, Berlin, Germany

(2) SciLifeLab, UU

(3) European Synchrotron Radiation Facility, Creatis, Université de Lyon, France

(4) LIP, Université Pierre et Marie Curie, Paris, France

*In Proceedings:* 19th Congress of the European Society of Biomechanics, Patras, Greece

*Comment:* Abstract review

### 3. Interactive Visual Simulation for Photovoltaic Design and Planning in the Built Environment

*Authors:* David Lingfors, Joakim Widén, **Stefan Seipel**

*In Proceedings:* 28th European Photovoltaic Solar Energy Conference, Paris, France

### 4. Movement on Uneven Surfaces Displays Characteristic Features of Hop Diffusion

*Authors:* Ingela Parmryd (1), Jeremy Adler (2), **Ida-Maria Sintorn, Robin Strand**

(1) Department of Medical Cell Biology, UU

(2) Cancer and Vascular Biology, UU

*In Proceedings:* 57th Biophysical Society Annual Meeting, Philadelphia, USA, Biophysical Journal, volume 104, number 2, page 524A

*Comment:* Abstract review

### 5. Viewing and Analyzing Slide Scanner Data Using CellProfiler (Work in Progress)

*Authors:* Petter Ranefall (1), **Alexandra Pacureanu** (1), Carolin Wählby (1,2)

(1) Science for Life Laboratory, SciLifeLab, UU

(2) Imaging Platform, Broad Institute of Harvard and MIT, Cambridge, MA, USA

*In Proceedings:* European BioImage Analysis Symposium 2013, Barcelona, Spain, page 58

### 6. Towards Automated Virus Detection and Identification Using TEM

*Author:* **Ida-Maria Sintorn** (1), Gustaf Kylberg, Rickard Nordström (1), Lars Haag (1), Eva Coufalova (2), Michal Drstka (2)

(1) Vironova AB, Stockholm, Sweden

(2) Delong Instruments, Brno, Czech Republic

*In Proceedings:* Microscopy Conference 2013, Regensburg, Germany, Part II, pages 397-398

### 7. Factors Influencing High Quality Low Voltage TEM Imaging of Biological Routinely Stained Specimen

*Authors:* **Ida-Maria Sintorn** (1), Rickard Nordström (1), Lars Haag (1), Eva Coufalova (2), Michal Drstka (2)

(1) Vironova AB, Stockholm, Sweden

(2) Delong Instruments, Brno, Czech Republic

*In Proceedings:* Microscopy Conference 2013, Regensburg, Germany, part I, pages 321-322

## **8. Large-Scale Analysis of Live Cells**

*Authors:* **Sajith Kecheril Sadanandan** (1), **Carolina Wählby** (1)

(1) Science for Life Laboratory, SciLifeLab, UU

*In Proceedings:* poster at eSSENCE Academy Workshop 2013, Lund

## **9. Debris Removal in Pap-Smear Images**

*Authors:* **Patrik Malm**, Byju N. Balakrishnan (1), Vilayil K. Sujathan (2), Rajesh Kumar (1), **Ewert Bengtsson**

(1) Centre for Development of Advanced Computing, Thiruvananthapuram, India

(2) Regional Cancer Centre, Thiruvananthapuram, India

*In Proceedings:* Swedish Symposium on Image Analysis (SSBA), Göteborg (electronic publication)

## **10. Creating Templates for Finding Proteins in MET Volume Images**

*Authors:* **Lennart Svensson, Ida-Maria Sintorn**

*In Proceedings:* Swedish Symposium on Image Analysis (SSBA), Göteborg (electronic publication)

## **11. Chromatin Pattern Analysis of Cell Nuclei for Improved Cervical Cancer Screening**

*Authors:* Ramin Moshavegh (1,2), Babak Ehteshami Bejnordi (1,2), K. Sujathan (3), **Patrik Malm, Ewert Bengtsson**, Andrew Mehnert (1,2)

(1) Department of Signals and Systems, Chalmers University of Technology, Göteborg

(2) MedTech West, Sahlgrenska University Hospital, Göteborg

(3) Department of Pathology, Regional Cancer Centre (RCC), Thiruvananthapuram, India

*In Proceedings:* Swedish Symposium on Image Analysis (SSBA), Göteborg (electronic publication)

## **12. Image-based Screening of Zebrafish**

*Authors:* **Omer Ishaq** (1), **Alexandra Pacureanu** (1), **Carolina Wählby** (1)

(1) Science for Life Laboratory, SciLifeLab, UU

*In Proceedings:* Swedish Symposium on Image Analysis (SSBA), Göteborg (electronic publication)

## **13. Worms and Digital Image Processing in the Search for Novel Drugs**

*Authors:* **Carolina Wählby** (1), Lee Kamentsky (1), Zihan H. Liu (1), Tammy Riklin-Raviv (2), Annie L. Conery (3), Eyleen J. O'Rourke (3), Katherine L. Sokolnicki (1), Orane Visvikis (4), Vebjorn Ljosa (1), Javier E. Irazoqui (4), Polina Golland (2), Gary Ruvkun (3), Frederick M. Ausubel (3), and Anne E. Carpenter (1)

(1) Imaging Platform, Broad Institute of MIT and Harvard, Cambridge, MA, USA

(2) Computer Science and Artificial Intelligence Laboratory, MIT, Cambridge, MA, USA

(3) Dept. of Molecular Biology and Center for Computational and Integrative Biology, MGH, Boston, MA, USA

(4) Developmental Immunology Program, Dept. of Pediatrics, Mass. General Hospital, Boston, MA

*In Proceedings:* Swedish Symposium on Image Analysis (SSBA), Göteborg (electronic publication)

## **14. Identifying All Individuals in a Honeybee Hive – Progress Towards Mapping All Social Interactions**

*Authors:* **Cris L. Luengo Hendriks, Zi Quan Yu**, Antoine Lecocq (1,2), Teatske Bakker (1), Barbara Locke (1), Olle Terenius (1)

(1) Department of Ecology, SLU, Uppsala

(2) Currently at: Department of Agriculture & Ecology, University of Copenhagen

*In Proceedings:* Swedish Symposium on Image Analysis (SSBA), Göteborg (electronic publication)

## **15. Towards Faster Fuzzy Connectedness**

*Authors:* **Filip Malmberg, Robin Strand**

*In Proceedings:* Swedish Symposium on Image Analysis (SSBA), Göteborg (electronic publication)

## **16. Priors for X-Ray in-Line Phase Tomography of Heterogeneous Objects**

*Authors:* Max Langer (1,2), Bernhard Hesse (1,2,3), **Alexandra Pacureanu** (4), Heikki Suhonen (1), Peter Cloetens (1), Kay Raum (2), Francoise Peyrin (1,2)

(1) European Synchrotron Radiation Facility, Grenoble, France

(2) Creatis, Université de Lyon, Lyon, France

(3) Julius Wolff Institute & Berlin-Brandenburg School for Regenerative Therapies, Charité, Berlin, Germany

(4) SciLifeLab, Uppsala University  
*In Proceedings:* Swedish Symposium on Image Analysis (SSBA), Göteborg (electronic publication)

## 6.5 Other publications

Authors affiliated with CBA are in bold. See also Section 3.2 for Master theses finished during 2012.

1. **ISMM 2013 - 11th International Symposium on Mathematical Morphology**  
*Author:* **Gunilla Borgefors**  
*Journal:* IAPR Newsletter, volume 35, number 4, pages 15-16
2. **Pre-Study on Automatically Determining Road Condition with a Camera**  
*Author:* **Cris Luengo**  
*Publisher:* Centre for Image Analysis, External Report No. 35, 16 pages
3. **Multi-resolution Cervical Cell Dataset**  
*Author:* **Patrik Malm**  
*Publisher:* Centre for Image Analysis, External Report No. 37, 9 pages
4. **CBA Annual Report 2012**  
*Editors:* **Vladimir Curic, Omer Ishaq, Lena Nordström, Ingela Nyström, Ida-Maria Sintorn, Robin Strand**  
*Publisher:* Centre for Image Analysis, 97 pages

## 7 Activities

### 7.1 ICPR 2014

The 22nd International Conference on Pattern Recognition (ICPR 2014) was held on August 24–28, 2014, at the Stockholm Waterfront Congress Centre in Stockholm, Sweden. Despite its long history — the ICPR conference series started in 1973 — this was the first time it was held in Sweden. The conference was hosted by the Swedish Society for Automated Image Analysis (SSBA) and supported by Linköping University, Lund University, and Uppsala University. The organisation engaged a majority of the CBA staff. It was concluded that ICPR 2014 was a successful event with as many as 1215 participants from 58 countries attending.

Scientifically, ICPR 2014 had five tracks: Computer Vision; Pattern Recognition and Machine Learning; Image, Speech, Signal and Video Processing; Document Analysis, Biometrics and Pattern Recognition Applications; and Biomedical Image Analysis. For each track, there was an Invited Speaker and all together there was approximately 200 oral presentations and 600 poster presentations.

#### 7.1.1 Organizing committee

**General Chair:** Professor Magnus Borga, Linköping University

**Program Chair:** Professor Anders Heyden, Lund University

**Program Co-Chair:** Professor Denis Laurendeau, Université Laval

**Local Arrangements Chair:** Professor Ingela Nyström, Uppsala University

**Local Arrangements Co-Chair:** Professor Aysin Baytan Ertuzun, Bogaziçi University

**Finance Chair:** Professor Ewert Bengtsson, Uppsala University

**Invited Speakers Chair:** Professor Gunilla Borgefors, Uppsala University

**International Liaison Chair:** Professor Kim Boyer, Rensselaer Polytechnic Institute

**Workshops, Tutorials and Contests Co-Chairs:** Assoc. Professor Cris Luengo, Uppsala University; Dr. Ola Friman, SICK IVP

**Publicity Chair:** Assoc. Professor Hedvig Kjellström, KTH Royal Institute of Technology

**Sponsor and Exhibitions Chair:** Dr. Anders Åström, Combitech AB

**Publications Chair:** Professor Michael Felsberg, Linköping University

**Poster Session Chair:** PhD student Elisabeth Linnér, Uppsala University

**Awards Chair:** Assoc. Professor Robin Strand, Uppsala University

**Webmaster:** PhD student Johan Nysjö, Uppsala University

**Official Photographer:** PhD student Kristína Lidayová, Uppsala University

**Volunteers from CBA:** Christophe Avenel, Anders Brun, Vladimir Curic, Azadeh Fahkrzadeh, Filip Malmberg, Damian Matuszewski, Kalyan Ram, Petter Ranefall Sajith Sadanandan Kecheril, Fredrik Wahlberg Tomas Wilkinson

### 7.2 Organized conferences and workshops

#### 1. Principles of Evolution

*Organisers:* Gunilla Borgefors

*Address:* EBC, UU

*Date:* 20140214

*Comment:* Organised by the Celsius-Linné committee the day after the Celsius-Linné lectures. Borgefors is its Chair. See <http://www.teknat.uu.se/research/celsius-linnaeus/?languageId=1>.

#### 2. Scifest 2014

*Organisers:* Uppsala University and Uppsala Kommun

*Address:* Fyrishov, Uppsala

*Date:* 20140217–20140301

*Comment:* Pontus Olsson, Fredrik Nysjö, and Ingrid Carlbom ran a booth showing haptics and its applications

### **3. ISBI 2014**

*Organisers:* Carolina Wählby, Alexandra Pacureanu and Ingrid Carlbom

*Address:* Renaissance Beijing Capital Hotel in Beijing, China

*Date:* 20140429–20140502

*Comment:* We organized a special session on Advances in Computer-Aided Histopathology. Ewert Bengtsson was one of the invited speakers.

### **4. 22nd International Conference on Pattern Recognition**

*Organisers:* Cris Luengo

*Address:* Stockholm

*Date:* 20140824–20140828

*Attendees:*

*Topic:*

*Comment:* Organizing Committee, and Workshops, Tutorials and Contests Co-Chair

### **5. 22nd International Conference on Pattern Recognition**

*Organisers:* Ingela Nyström

*Address:* Stockholm Waterfront Congress Centre

*Date:* 20140824–20140828

*Attendees:*

*Topic:*

*Comment:* Local Arrangements Chair and Member of IAPR Executive Committee

### **6. ICPR 2014**

*Organisers:* Ewert Bengtsson finance chair

*Address:* Waterfront Stockholm

*Date:* 20140824–20140828

*Attendees:*

*Topic:*

### **7. ICPR 2014**

*Organisers:* Gunilla Borgefors

*Address:* Stockholm

*Date:* 20140824–20140829

*Attendees:*

*Topic:*

*Comment:* Borgefors was Invited Speakers Chair

### **8. ICPR 2014**

*Organisers:* SSBA

*Address:* Stockholm, Sweden

*Date:* 20140824–20140828

*Comment:* Webmaster

### **9. Tutorial, "Digital Geometry, Topology and Applications" in conjunction with ICPR**

*Organisers:* Robin Strand

*Address:* Waterfront Congress Center, Stockholm

*Date:* 20140824

*Comment:* Presentations by Gunilla Borgefors, Robin Strand, Punam Saha and Gabriella Sanniti di Baja

### **10. 3rd eSENCE Academy**

*Organisers:* Ingela Nyström, eSENCE

*Address:* Umeå University

*Date:* 20141015–20141016

*Comment:* 90 researchers within the e-Science community gathered for this workshop to present, discuss, and find synergies among researchers from Lund University, Umeå University, and Uppsala University.

## 11. CIM Workshop on Mathematics in Medicine

*Organisers:* Carolina Wählby and Robin Strand

*Address:* Polacksbacken, Uppsala, Sweden

*Date:* 20141106–20141107

*Comment:* Main organizer: Elisabeth Larsson, CIM. Other members of the scientific committee: Alexander Medvedev and Stefan Engblom

## 7.3 Seminars held outside CBA

### 1. Ewert Bengtsson

*Date:* 20140129

*Address:* Uppsala University Hospital

*Title:* Medical engineering in Uppsala

*Comment:* Meeting to form the network "Uppsala Forum för Medicinsk Teknik"

### 2. Ewert Bengtsson

*Date:* 20140129

*Address:* BlåKorset, Akademiska sjukhuset

*Title:* Uppsala Forum för Medicinsk Teknik

### 3. Anders Hast

*Date:* 20140425

*Title:* Swedish eScience Education

*Comment:* Fifth annual SeRC meeting 24-25 of April

### 4. Olof Lindahl

*Date:* 20140508

*Title:* UFMT - Uppsala Forum on Medical Engineering

*Comment:* A second seminar for the newly formed UFMT, Olof was one of the invited speakers, Bengtsson was co-chair of the event

### 5. Elisabeth Linnér

*Date:* 20140514

*Address:* Ångströmlaboratoriet

*Title:* ForskarFika

*Comment:* Seminar arranged by the students of the Master of Science in Engineering Physics program, to familiarize themselves with researchers and research at an early stage in their education.

### 6. several, Chaired by Örjan Smedby

*Date:* 20140519

*Address:* Svenska Lägaresällskapet, Stockholm

*Title:* SBI - Swedish Bioimaging strategic seminar day

*Comment:* A whole day seminar to discuss future strategy for Swedish Bioimaging with several invited speakers. Ewert Bengtsson participated as a member of the board.

7. **Cris Luengo**  
*Date:* 20140603  
*Address:* Division of Wood Science and Engineering, Luleå University of Technology, Skellefteå, Sweden  
*Title:* Image analysis with mathematical morphology  
*Comment:* Invited seminar in conjunction with a Licentiate defence
8. **Vladimir Curic**  
*Date:* 20140610  
*Address:* University of Rennes, France  
*Title:* Distance functions and adaptive mathematical morphology
9. **Cris Luengo**  
*Date:* 20140624  
*Address:* Institute for Research in IT and Random Systems (IRISA), University of Bretagne Sud, Vannes, France  
*Title:* Image-based measurement with mathematical morphology
10. **Filip Malmberg**  
*Date:* 20140820  
*Address:* Elekta AB, Uppsala  
*Title:* Image Processing using Graphs
11. **Petter Ranefall**  
*Date:* 20140911  
*Address:* BMC, Uppsala  
*Title:* Quantitative Microscopy  
*Comment:* A delegation from the Eurasian National University in Kazakhstan visited BMC.
12. **Anders Hast**  
*Date:* 20141016  
*Title:* Swedish eScience Education  
*Comment:* eSENCE academy in Umeå, 15-16 of October

## 7.4 Seminars at CBA

1. **Gunilla Borgefors**  
*Date:* 20140113  
*Title:* Choosing colours for scientific data presentation
2. **Alexandra Pacureanu**  
*Date:* 20140120  
*Title:* Analyzing gene expression in preserved tissue and imaging in 3D semi-transparent biological samples on a low budget
3. **Petter Ranefall**  
*Date:* 20140127  
*Title:* Experiences from working in the industry
4. **Patrik Malm**  
*Date:* 20140203  
*Title:* Rehearsal before the public defense of the thesis
5. **Dr. Calum MacAuley**  
*Date:* 20140206  
*Title:* Biomedical Optics for the Detection of Early Cancers

6. **Gustaf Kylberg**  
*Date:* 20140317  
*Title:* Automatic Virus Identification using TEM - Image Segmentation and Texture Analysis
7. **Walter Kropatsch**  
*Date:* 20140320  
*Title:* Presentation of the Pattern Recognition and Image Processing (PRIP) Group
8. **Ingrid Carlbom**  
*Date:* 20140324  
*Title:* Picro-Sirius-HTX stain for blind color decomposition of histopathological prostate tissue
9. **Kalyan Ram Ayyalasomayajula**  
*Date:* 20140331  
*Title:* Document binarization using topological clustering guided Laplacian Energy Segmentation
10. **Azadeh Fakhrzadeh**  
*Date:* 20140407  
*Title:* Studying Arabidopsis cell structures using Image analysis techniques
11. **Anant Madabhushi**  
*Date:* 20140410  
*Title:* Computational pathology: Squeezing the most out of digitized histopathology
12. **Anders Brun**  
*Date:* 20140414  
*Title:* From quill to bytes, datamining collections of historical documents
13. **Fredrik Nysjö**  
*Date:* 20140505  
*Title:* Custom Mandibular Implant Design with Deformable Models and Haptics
14. **Vladimir Curic**  
*Date:* 20140512  
*Title:* Distance Functions and Their Use in Adaptive Mathematical Morphology
15. **Ida-Maria Sintorn**  
*Date:* 20140519  
*Title:* MiniTEM - for fast and easy TEM imaging and analysis
16. **Richard Szeliski**  
*Date:* 20140528  
*Title:* Reflections on Image-Based Modeling and Rendering
17. **Stefan Seipel**  
*Date:* 20140602  
*Title:* Not quite perfect spherical triangles and what they are good for
18. **Thu Tran**  
*Date:* 20140602  
*Title:* An interactive interface for multiple-resolution analysis of large images
19. **Erik Wernersson**  
*Date:* 20140609  
*Title:* Local orientation in images
20. **Elisabeth Linnér**  
*Date:* 20140616  
*Title:* Anti-Aliased Euclidean Distance Transform on 3D Sampling Lattices
21. **Several speakers**  
*Date:* 20140818  
*Title:* ICPR poster and oral presentation rehearsals

22. **Fredrik Nysjö and Anders Hast**  
*Date:* 20140901  
*Title:* Our new 2D and 3D projector
23. **Fillipe Dias Moreira de Souza**  
*Date:* 20140902  
*Title:* Pattern Theory-Based Interpretation of Activities
24. **Omer Ishaq**  
*Date:* 20140908  
*Title:* Ground-truth annotation for real data sets
25. **Pontus Olsson**  
*Date:* 20140915  
*Title:* A Novel Virtual Planning of Bone, Soft tissue and Vessels in Fibula Osteocutaneous Free Flap with the Uppsala Haptics-Assisted Surgery Planning (UHASP) System
26. **Cris Luengo**  
*Date:* 20140922  
*Title:* Path Openings
27. **Carolina Wählby**  
*Date:* 20140929  
*Title:* An open-source platform for integration, automated analysis, and interactive visualization of tissue image data: TissueMaps
28. **Tomas Wilkinson**  
*Date:* 20141006  
*Title:* Visualizing Document Images using Image-based Word Clouds
29. **Marco Loog**  
*Date:* 20141021  
*Title:* Scale Selection for Supervised Image Segmentation
30. **Bettina Selig**  
*Date:* 20141027  
*Title:* The Evolution of the Stochastic Watershed
31. **Lennart Thurfjell**  
*Date:* 20141103  
*Title:* Decision support in neurodegenerative diseases
32. **Ginevra Castellano**  
*Date:* 20141110  
*Title:* Socially intelligent robots: closing the loop in human-robot interaction
33. **Willy Wriggers**  
*Date:* 20141125  
*Title:* From Atoms to Living Organisms: Emergent Complexity of Multiscale Computational Modeling
34. **Erik Wernersson**  
*Date:* 20141126  
*Title:* Rehearsal before the public defense of the thesis Modeling
35. **Christophe Avenel**  
*Date:* 20141208  
*Title:* Uppsala Automatic Prostate Malignancy Grading System: An Overview
36. **Alicia Fornés**  
*Date:* 20141215  
*Title:* Recognition of the Historical Marriage License Books of the Cathedral of Barcelona

## 7.5 Conference participation

### 7.5.1 Special invited speaker

1. *Conference:* Swedish Natural History Museum Digitization Symposium  
**Anders Brun**  
*Date:* 20140109–20140109  
*Address:* Stockholm, Sverige  
*Title:* Challenges and advances in OCR and handwriting recognition
2. *Conference:* ISBI IEEE International Symposium on Biomedical Imaging  
**Ewert Bengtsson**  
*Date:* 20140428–20140502  
*Address:* Renaissance Beijing, Capital Hotel, Beijing, China  
*Title:* Quantitative and Automated Microscopy – Where Do We Stand after 80 Years of Research?
3. *Conference:* Swedish Bioimaging 5th National Meeting  
**Ingela Nyström**  
*Date:* 20140507  
*Address:* Rudbecklaboratoriet, Uppsala  
*Title:* The Council for Research Infrastructures (RFI) –a decision-taking body within the Swedish Research Council (VR)
4. *Conference:* Symposium for Lars-Olof Sundelöf  
**Christer Kiselman**  
*Date:* 20140604  
*Address:* Ångström Laboratory  
*Title:* Mathematical spaces (“Matematiska rum”)  
*Comment:* The talk will be published in a proceedings volume honoring Lars-Olof Sundelöf
5. *Conference:* Constructive Approximation of Functions  
**Christer Kiselman**  
*Date:* 20140630–20140705  
*Address:* Bedlewo, Poland  
*Title:* Weak Lineal Convexity
6. *Conference:* Universala Kongreso de Esperanto  
**Christer Kiselman**  
*Date:* 20140725–20140802  
*Address:* Buenos Aires, Argentina  
*Title:* Akademio de Esperanto fronte al novaj taskoj
7. *Conference:* IMC  
**Carolina Wählby**  
*Date:* 20140907–20140910  
*Address:* International Microscopy Congress (IMC) in Prague, Czech Republic.  
*Title:* Quantitative microscopy – extracting relevant information from biomedical image data
8. *Conference:* SBI2  
**Carolina Wählby**  
*Date:* 20140911–20140912  
*Address:* Society of Biomolecular Imaging and Informatics SBI2, at the JB Martin Conference Center at Harvard Medical School, Boston, MA, USA.

*Title:* Combining image-based in situ RNA screening with quantitative analysis of cell and tissue morphology

*Comment:* Carolina Wählby was honored with the 'SBI2 President's innovation award' for her presentation.

9. *Conference:* Analysis Day in Memory of Mikael Passare

**Christer Kiselman**

*Date:* 20140924

*Address:* Stockholm University

*Title:* Discrete convolution operators, the Fourier transformation, and its tropical counterpart: the Fenchel transformation

10. *Conference:* BMTL

**Carolina Wählby**

*Date:* 20141027–20141029

*Address:* 'Bringing Maths To Life' in Naples, Italy

*Title:* Image processing and analysis in microscopy and life science

11. *Conference:* 2nd High Throughput Cell Biology: from screening to applications

**Carolina Wählby**

*Date:* 20141117–20141118

*Address:* Institut Curie - Research Centre, Paris, France.

*Title:* Characterizing solid tumors by image-based high throughput screening of cancer stem cells

12. *Conference:* Meeting of Swedish university IT directors

**Ewert Bengtsson**

*Date:* 20141125

*Address:* University of Karlstad

*Title:* Research data storage system planned for Uppsala university

## 7.5.2 Oral presentations – refereed conferences

1. *Conference:* ISBI' 2014

**Ingrid Carlbom**

*Date:* 20140428–20140502

*Address:* Beijing China

*Title:* Picro-Sirius-HTX Stain for Blind Color Decomposition of Histopathological Prostate Tissue

*Comment:* Carlbom also organized a special session on "Advances in Computer-Aided Histopathology"

2. *Conference:* Swedish Bioimaging Annual Meeting

**Carolina Wählby**

*Date:* 20140507

*Address:* Rudbeck Laboratory and SciLifeLab Navet, Uppsala, Sweden

*Title:* The Centre for Image Analysis

*Comment:* Carolina Wählby organized the meeting together with Lena Claesson-Welsh. Several other members of CBA attended the meeting.

3. *Conference:* WSCG

**Anders Hast**

*Date:* 20140602–20140605

*Address:* Plzen, Czech Rep

*Title:* Invariant Interest Point Detection Based on Variations of the Spinor Tensor

4. *Conference:* Computer Assisted Radiology and Surgery  
**Fredrik Nysjö**  
*Date:* 20140625–20140628  
*Address:* Fukuoka, Japan  
*Title:* Custom Mandibular Implant Design with Deformable Models and Haptics
  
5. *Conference:* ICGG  
**Anders Hast**  
*Date:* 20140805–20140808  
*Address:* Innsbruck, Austria  
*Title:* How to Promote Student Creativity and Learning using Tutorials in Teaching Graphics and Visualization
  
6. *Conference:* 22nd International Conference on Pattern Recognition  
**Omer Ishaq**  
*Date:* 20140824–20140828  
*Address:* Stockholm, Sweden  
*Title:* An Evaluation of the Faster STORM Method for Super-resolution Microscopy
  
7. *Conference:* DGCI2014  
**Elisabeth Linnér**  
*Date:* 20140910–20140912  
*Address:* Siena  
*Title:* Anti-Aliased Euclidean Distance Transform on 3D Sampling Lattices
  
8. *Conference:* Discrete Geometry for Computer Imagery  
**Filip Malmberg**  
*Date:* 20140910–20140912  
*Address:* Siena, Italy  
*Title:* Exact Evaluation of Stochastic Watersheds: From Trees to General Graphs
  
9. *Conference:* International Conference on Image Analysis and Recognition (ICCIAR 2014)  
**Nataša Sladoje**  
*Date:* 20141022–20141024  
*Address:* Vilamoura, Algarve, Portugal  
*Title:* An evaluation of potential functions for regularized image deblurring  
*Comment:* Buda Bajic, PhD student and co-author of the paper, gave this oral presentation

### 7.5.3 Poster presentations – refereed conferences

1. *Conference:* ICPR2014  
**Elisabeth Linnér**  
*Date:* 20140824–20140828  
*Address:* Stockholm  
*Title:* A Graph-Based Implementation of the Anti-Aliased Euclidean Distance Transform
  
2. *Conference:* ICPR  
**Anders Hast**  
*Date:* 20140825–20140828  
*Address:* Stockholm  
*Title:* Robust and Invariant Phase Based Local Feature Matching

3. *Conference:* International Conference on Frontiers in Handwriting Recognition  
**Kalyan Ram**  
*Date:* 20140901–20140904  
*Address:* Crete, Greece  
*Title:* Document binarization using topological clustering guided Laplacian Energy Segmentation
  
4. *Conference:* International Conference on Frontiers in Handwriting Recognition  
**Fredrik Wahlberg**  
*Date:* 20140901–20140904  
*Address:* Crete, Greece  
*Title:* Scribal Attribution using a Novel 3-D Quill-Curvature Feature Histogram
  
5. *Conference:* DGCI 2014  
**Robin**  
*Date:* 20140910–20140912  
*Address:* Siena, Italy  
*Title:* The Minimum Barrier Distance – Stability to seed point position
  
6. *Conference:* BioImage Informatics 2014  
**Sajith Sadanandan Kecheril**  
*Date:* 20141008–20141010  
*Address:* Provinciehuis, Leuven, Belgium  
*Title:* Segmentation and tracking of E.coli bacteria in phase contrast microscopy images

#### 7.5.4 Oral presentations – non-refereed conferences

1. *Conference:* Swedish Symposium on Image Analysis (SSBA 2014)  
**Anders Hast**  
*Date:* 20140310–20140312  
*Address:* LuleåUniversity of Technology  
*Title:* A Feature Detector based on the Structure Tensor with a Scale Space Dimension
  
2. *Conference:* Swedish Symposium on Image Analysis (SSBA 2014)  
**Kristina Lidayova**  
*Date:* 20140310–20140312  
*Address:* LuleåUniversity of Technology  
*Title:* Fast Vessel Centerline Tree Extraction Algorithm
  
3. *Conference:* Swedish Symposium on Image Analysis (SSBA 2014)  
**Sajith Sadanandan Kecheril**  
*Date:* 20140310–20140312  
*Address:* LuleåUniversity of Technology  
*Title:* Segmentation of E.coli bacteria in brightfield microscopy images
  
4. *Conference:* Swedish Symposium on Image Analysis (SSBA 2014)  
**Petter Ranefall**  
*Date:* 20140311–20140312  
*Address:* LuleåUniversity of Technology  
*Title:* The Giga-pixel Challenge: Full Resolution Image Analysis – Without Losing the Big Picture

5. *Conference:* Swedish Symposium on Image Analysis (SSBA 2014)  
**Anders Hast**  
*Date:* 20140311–20140312  
*Address:* LuleåUniversity of Technology  
*Title:* A Feature Detector based on the Structure Tensor with a Scale Space Dimension
  
6. *Conference:* Swedish Symposium on Image Analysis (SSBA 2014)  
**Filip Malmborg**  
*Date:* 20140311–20140312  
*Address:* LuleåUniversity of Technology  
*Title:* An Interactive Tool for Deformable Registration of Volume Images
  
7. *Conference:* Swedish Symposium on Image Analysis (SSBA 2014)  
**Johan Nysjö**  
*Date:* 20140311–20140312  
*Address:* LuleåUniversity of Technology  
*Title:* Analyzing orbital size and shape before and after surgical correction
  
8. *Conference:* Swedish Symposium on Image Analysis (SSBA 2014)  
**Ida-Maria Sintorn**  
*Date:* 20140311–20140312  
*Address:* LuleåUniversity of Technology  
*Title:* miniTEM - a desk-top TEM for fast and easy image acquisition and analysis

### 7.5.5 Poster presentations – non-refereed conferences

1. *Conference:* Veterinary Sciences' Faculty Research Day  
**Cris Luengo**  
*Date:* 20140129–20140129  
*Address:* Ultuna  
*Title:* A sampling of bio-medical projects at the Centre for Image Analysis  
*Comment:* Went here to meet people at SLU's Faculty for Veterinary Sciences, and find future collaborators
  
2. *Conference:* Swedish Bioimaging Meeting  
**Ida-Maria Sintorn**  
*Date:* 20140507  
*Address:* Rudbecklaboratoriet, Uppsala  
*Title:* miniTEM- fast and easy TEM imaging and analysis
  
3. *Conference:* 8th International BioImage Informatics Meeting  
**Damian Matuszewski**  
*Date:* 20141008–20141010  
*Address:* Leuven, Belgium  
*Title:* Investigating phenotypic differences and drug response among glioblastoma stem cell cultures from patients
  
4. *Conference:* BioImage Informatics  
**Petter Ranefall**  
*Date:* 20141008–20141010  
*Address:* Leuven, Belgium

*Title:* Full Resolution Image Analysis – Without losing the Big Picture

5. *Conference:* SciLife Day October 2014

**Omer Ishaq**

*Date:* 20141010–20141010

*Address:* Uppsala, Sweden

*Title:* Quantification of Zebrafish Tail Deformation

6. *Conference:* Medicinteknikdagarna

**Kristina Lidayova**

*Date:* 20141014–20141016

*Address:* Svenska Mässan,

Göteborg, Sweden

*Title:* Fast Vessel Centerline Tree Extraction Algorithm

7. *Conference:* eSSENCE

**Petter Ranefall**

*Date:* 20141015–20141016

*Address:* Umeå

*Title:* Large-Scale Analysis of Cells and Tissue

8. *Conference:* 10th IEEE International Conference on e-Science

**Damian Matuszewski**

*Date:* 20141020–20141024

*Address:* Guarujá, SP, Brazil

*Title:* Investigating phenotypic differences and drug response among glioblastoma stem cell cultures from patients

9. *Conference:* Nordic Symposium on Digital Pathology

**Petter Ranefall**

*Date:* 20141105–20141106

*Address:* Linköping

*Title:* Combining image-based *in situ* RNA sequencing with quantitative analysis of cell and tissue morphology

10. *Conference:* Nordic Symposium on Digital Pathology 2014

**Anders Hast**

*Date:* 20141105–20141106

*Address:* Linköping

*Title:* Multi-instance learning as a useful tool in grading histopathological tissues

11. *Conference:* Frontiers in Cell migration

**Sajith Sadanandan Kecheril**

*Date:* 20141212–20141212

*Address:* ScilifeLab, Husargatan 3, Uppsala University

*Title:* Segmentation and tracking of E.coli bacteria in phase contrast microscopy images

### 7.5.6 Attended conferences

1. *Conference:* Informations-och kontaktmöte om industriellt forskningssamarbete

**Ingrid Carlbom**

*Date:* 20140130

*Address:* Canadian Embassy  
Stockholm

2. *Conference:* Swedish Symposium on Image Analysis (SSBA 2014)  
**Christophe Avenel, Ewert Bengtsson, Omer Ishaq, Elisabeth Linnér, Robin Strand, Gunilla Borgefors, Carolina W'ahlby, Cris Luengo, Ingela Nyström**  
*Date:* 20140310–20140312  
*Address:* Luleå University of Technology, Sweden
3. *Conference:* COSCH management committee meeting  
**Anders brun**  
*Date:* 20140330–20140401  
*Address:* Joensuu, Finland
4. *Conference:* Inauguration of Interactive Institute in Uppsala  
**Ewert Bengtsson**  
*Date:* 20140401  
*Address:* Hotel Gillet, Uppsala  
*Comment:* NITA, Nationellt IT Användarcentrum, that was formed in 2001 with Bengtsson as chair of the planning group was transformed into a unit within the Interactive Institute
5. *Conference:* MULTISPECTRAL TISSUE IMAGING & INTELLIGENT ANALYSIS  
**Petter Ranefall**  
*Date:* 20140402  
*Address:* Fluorescence Tissue Profiling Facility at SciLifeLab
6. *Conference:* SciLife Day April 2014  
**Omer Ishaq, Petter Ranefall**  
*Date:* 20140410  
*Address:* Solna, Sweden
7. *Conference:* Big data and e-Science in Medical Science  
**Petter Ranefall**  
*Date:* 20140423  
*Address:* Ehrling-Persson hall, Aula Medica, Karolinska Institutet
8. *Conference:* Phenotypic based drug discovery industry saviour or wasteful distraction  
**Petter Ranefall**  
*Date:* 20140429  
*Address:* Apotekarsocieteten, Wallingatan 26A, Stockholm
9. *Conference:* Swedish Bioimaging 5th National Meeting  
**Petter Ranefall**  
*Date:* 20140507  
*Address:* Rudbecksalen, IGP and Navet, SciLifeLab, Uppsala,
10. *Conference:* Swedish Bioimaging Meeting  
**Cris Luengo**  
*Date:* 20140507  
*Address:* Rudbecklaboratoriet, Uppsala

11. *Conference:* ISMRM 2014  
**Robin Strand**  
*Date:* 20140510–20140516  
*Address:* Milano, Italy
12. *Conference:* Sundelöf symposium  
**Gunilla Borgefors**  
*Date:* 20140604  
*Address:* Ångström, UU  
*Comment:* Organized by Royal Society of Sciences in Uppsala to celebrate Sundelöf's 31 years as its secretary,
13. *Conference:* ILEI Conference  
**Christer Kiselman**  
*Date:* 20140723–20140725  
*Address:* Montevideo, Uruguay
14. *Conference:* Mathematics in Emerging Nations: Achievements and Opportunities (MENAO)  
**Christer Kiselman**  
*Date:* 20140812  
*Address:* Seoul, South Korea
15. *Conference:* International Congress of Mathematicians (ICM)  
**Christer Kiselman**  
*Date:* 20140813–20140821  
*Address:* Seoul, South Korea
16. *Conference:* 22nd International Conference on Pattern Recognition (ICPR 2014)  
**Damian Matuszewski, Christophe Avenel, Filip Malmberg, Kristina Lidayova, Elisabeth Linnér, Carolina Wählby, Robin Strand, Gunilla Borgefors**  
*Date:* 20140824–20140828  
*Address:* Stockholm, Sweden
17. *Conference:* International Conference on Frontiers in Handwriting Recognition  
**Anders Brun, Tomas Wilkinson**  
*Date:* 20140901–20140904  
*Address:* Crete, Greece
18. *Conference:* Discrete Geometry for Computer Imagery (DGCI)  
**Gunilla Borgefors, Christer Kiselman**  
*Date:* 20140910–20140912  
*Address:* Siena, Italy  
*Comment:* Borgefors participated in the Steering Committee Meeting
19. *Conference:* BioImage Informatics 2014  
**Petter Ranefall, Sajith Sadanandan and Damian Matuszewski**  
*Date:* 20141008–20141010  
*Address:* Leuven, Belgium
20. *Conference:* SciLifeLab Day  
**Carolina Wählby and Ida-Maria Sintorn**

*Date:* 20141010–20141010

*Address:* Main university building, Uppsala University, Uppsala, Sweden

21. *Conference:* Medicinteknikdagarna Medical Engineering Days  
**Ewert Bengtsson**  
*Date:* 20141014–20141016  
*Address:* Gothenburgh Congress Centre  
*Comment:* Served on program committee and was organizer and session chair/co-chair for two sessions
22. *Conference:* 10th IEEE International Conference on e-Science  
**Ingela Nyström**  
*Date:* 20141020–20141024  
*Address:* Guaruja, Sao Paulo, Brazil  
*Comment:* Nyström was chairing the session "Cyberinfrastructure".
23. *Conference:* SSF The Foundation for Strategic Research 20 year celebration  
**Ewert Bengtsson**  
*Date:* 20141029–20141029  
*Address:* Museum of modern art, Stockholm  
*Comment:* Presentations on research funding strategies historically and today. SSF was the most important financing body in the development of CBA in the 90-ies.
24. *Conference:* Nordic Pathology Symposium  
**Ewert Bengtsson**  
*Date:* 20141105–20141106  
*Address:* Linköping Conference Centre  
*Comment:* Bengtsson was on the program committee for this second symposium of this kind
25. *Conference:* Nordic symposium on Digital Pathology  
**Carolina Wählby, Ida-Maria Sintorn, Ewert Bengtsson, Petter Ranefall**  
*Date:* 20141105–20141105  
*Address:* Linköping, Sweden
26. *Conference:* CIM Workshop on math and medicine  
**Cris Luengo, Nataša Sladoje, Filip Malmberg, Gunilla Borgefors, Ingela Nyström**  
*Date:* 20141106–20141107  
*Address:* Uppsala University
27. *Conference:* IT Department research strategy day  
**Ewert Bengtsson, Ingela Nyström, Robin Strand**  
*Date:* 20141117–20141117  
*Address:* Blåsenhus Uppsala  
*Comment:* Bengtsson was responsible for the organisation of this full day event and chaired half the day. Nyström was responsible for the brain storming on quality of PhD education.
28. *Conference:* Prostate Cancer Research Meeting  
**Ingrid Carlbom**  
*Date:* 20141124–20141125  
*Address:* The Royal Palace of Rosersberg Conference Hotel, Stockholm  
*Comment:* Christophe Avenel gave a talk on our Prostate Malignancy Grading research

29. *Conference: AimDay Imaging*

**Carolina Wählby**

*Date: 20141216–20141216*

## 7.6 Visiting scientists

### 1. Alicia Fornés

*Address:* Computer Center Vision, Edificio O, Campus UAB, 08193 Bellaterra (Cerdanyola), Barcelona, Spain

*Host:* Anders Brun

*Date:* 20141101–20141221

*Number of visitors:* 1

*Topic:* Handwritten Text Recognition

## 7.7 Visits to other research groups

### 1. Vladimir Curic

*Host:* Sébastien Lefevre

*Address:* University of South Brittany, Vannes, France

*Date:* 20140601–20140630

*Topic:* Mathematical morphology and applications

### 2. Cris Luengo

*Host:* Sébastien Levèvre

*Address:* Institute for Research in IT and Random Systems (IRISA), University of Bretagne Sud, Vannes, France

*Date:* 20140617–20140626

*Comments:* Visit financed by the Frö programme of the French Embassy in Stockholm

## 7.8 Committees



Figure 32: Journals with CBA staff in the editorial board.

### Ewert Bengtsson

International:

- Senior lifetime member of the Institute of Electrical and Electronics Engineers (IEEE), 2004–  
*Comment:* Member since 1974. Elevated to Lifetime Fellow as per 20150101.
- Member of the International Society for Optical Engineering (SPIE), ~2004–
- Member of the International Society for Analytical Cytology (ISAC), 2000–
- Associate Editor of *Computer Methods and Programs in Biomedicine*, 2012-2014  
*Comment:* Published by Elsevier. Bengtsson was Editorial Board member 1995-2011.
- Editorial Board member of *Machine Graphics & Vision*, 1994–  
*Comment:* Published by the Polish Academy of Sciences.
- Program Committee Bioimaging 2015, 12-15 January 2015, Lisbon, Portugal
- Program Committee, 21st International Conference on Computer Graphics, Visualization and Computer Vision (WSCG 2013), Plzen, Czech Republic, June 2013.
- Management Committee, EU COST Action TD1201: “Colour and Space in Cultural Heritage, COSCH” 201305–  
*Comment:* Bengtsson is responsible for coordinating the Swedish participation.
- Finance chair ICPR2014, International Conference on Pattern Recognition, Stockholm, August 2014
- Expert evaluator for proposals to the Italian Ministry of Education, Industry and Research, Office V, February–November 2014

National:

- Member of the Royal Swedish Academy of Engineering Sciences (IVA), 2006–  
*Comment:* Division VII: Basic and Interdisciplinary Engineering Sciences.
- Member of the Royal Society of Sciences in Uppsala (Kungliga Vetenskaps-Societeten), 1998–  
*Comment:* Elected member of the oldest scientific society in Sweden (founded 1710).
- Coordinating group of Medtech4Health, 201201-201406  
*Comment:* Medtech4Health is a national Swedish initiative to build a Strategic Innovation Area in medical engineering. And to apply for Vinnova Funding. The application was turned down in June 2014
- Board of Swedish Bioimaging, 201203–  
*Comment:* A Swedish network for researchers in biomedical imaging and image analysis.

- Scientific board of Swedish Association for Medical Engineering and Physics, "Svensk fÃ¶rmedicinsk teknik och fysik" 2013–
- Program committee of Swedish Medical Engineering Days, "Medicinteknikdagarna", Gothenburgh, October 14-16, 2014.  
*Comment:* A Swedish foundation that accepts applications and gives out research grants for urology research.
- Board of UpGIS, the network for Geographical Information Systems at UU, 1999–
- UU Library Council member, 2011–
- IT strategy group at UU, 201206–201310  
*Comment:* A committee headed by the university director to create a new strategy for support of administrative IT at UU.
- Chair of Uppsala University committee to propose a new strategy for handling long term storage of scientific data. 201309–201403
- Chair of a joint committee by the Faculty of science and technology and the Faculty of medicine and pharmacy to develop a strategic plan for medical engineering research and education at Uppsala University. 201409–201501
- Representative of Uppsala University IT on the ICT committee of Uppsala Municipality, 2013–2014
- Expert advisor to the head of the Information Technology Unit of UU administration, 2013–
- Board of the Dept. of Information Technology, UU, 201207–
- Head of Research ("forskningsprefekt") at the Dept. of Information Technology, UU, 2013–
- Head of the research program "Image analysis and man-machine interaction," Dept. of Information Technology, UU, 1996-2014
- PhD education responsible professor for "Computerized Image Processing", 1996-2014
- Licentiate Thesis, Matilda Landgren, Opponent, 20140131–20140131
- Expert for evaluating chair in medical engineering for Linköping University, 20141022–20141022  
*Comment:* Telephone conference deciding which of the 52 candidates were to be called to interview
- Expert evaluator of Dr Rodrigo Morenos application to become docent at Linköping university . Finished April 16, 2014

### **Gunilla Borgefors**

International:

- Fellow of the International Association for Pattern Recognition (IAPR), 1998–  
*Comment:* 1st Vice President 1994-96, Secretary 1990-94, etc., etc.
- Fellow of the Institute of Electrical and Electronics Engineers, Inc. (IEEE), 2007–  
*Comment:* Member since 1997. Senior member 1998.
- Editor-in-Chief of *Pattern Recognition Letters*, 2011–  
*Comment:* Published by Elsevier. PRL is an official journal of the International Association of Pattern Recognition. Borgefors was Associate Editor/Area Editor 2004-2010.
- Editorial Board member of *Image Processing and Communications*, 1994–  
*Comment:* Published by the Institute of Telecommunications, Bydgoszcz, Poland.
- Editorial Board member of *Pattern Recognition and Image Analysis: Advances in Mathematical Theory and Applications*, 1993–  
*Comment:* Published by Interperiodica Publishing in cooperation with the Russian Academy of Sciences.

- Editorial Board of the book series Computational Imaging and Vision, 2003–  
*Comment:* Published by Springer.
- Steering committee for Discrete Geometry for Computer Imagery (DGCI) conferences, 2000–
- Steering committee for International Symposium on Mathematical Morphology (ISMM), 2011–
- Dissertation committee of Darryl McClymont, School of Information Technology and Electrical Engineering, University of Queensland, Brisbane, Australia, 20140901–20141016  
*Comment:* Title: Computer assisted detection and characterisation of breast cancer in MRI

National:

- Member of the Royal Swedish Academy of Engineering Sciences (IVA), 2011–  
*Comment:* Division VII: Basic and Interdisciplinary Engineering Sciences.
- Member No. 19 of the Royal Society of Sciences in Uppsala (Kungliga Vetenskaps-Societeten), 2000–  
*Comment:* Elected member of the oldest scientific society in Sweden (founded 1710).
- Member of Swedish Parliamentarians and Scientists, 1987–  
*Comment:* Members are elected. Only one scientist per field admitted.
- Board/Steering Committee for Onsala Space Observatory, 2011–
- Chair of the Celsius-Linné committee, TN-faculty, UU, 201306–  
*Comment:* The committee selects the speakers for the annual Celsius and Linné lectures and organizes the following one-day Symposium. Member since 2007.
- Advisory Board for CBA 2012-2014  
*Comment:* One of two representatives for SLU.
- Expert evaluator for the application of Andrew Mehnert to become associate professor (docent) at Chalmers, Göteborg, 20140401–20140512
- Expert evaluator for an Associate Professor (lektor) in Image reproduction at Dept. of Science and Technology, Linköping University, Campus Norrköping, 20140601–20140707
- Dissertation committee of Patrik Boberg, LuleåTechnical University, Luleå, 20140612  
*Comment:* Title: Imaging and Analysis Methods for Automated Weld Inspection
- Dissertation committee of Jimmy Azar, Dept. of Information Technology, UU, 20141020  
*Comment:* Title: Automated Tissue Image Analysis Using Pattern Recognition

National:

- Board member, SSBA, 2014–  
*Comment:* Elected at SSBA yearly meeting

### **Ingrid Carlbom**

International:

- Member of the Institute of Electrical and Electronics Engineers (IEEE), 1987–
- Member of Association for Computing Machinery (ACM), 1971–
- Member of ACM Special Interest Group on Computer Graphics and Interactive Techniques (SIGGRAPH), 1976–
- Member of SIGMA XI, The Scientific Research Society ~1979–
- Programme committee member, IEEE International Symposium on Biomedical Imaging (ISBI), 2014, 20140429–20140502
- Session organizer: "Advances in Computer-Aided Histopathology" at IEEE International Symposium on Biomedical Imaging (ISBI'14) held in Beijing, China, 20140428-20140502

**Anders Hast**

National:

- Dissertation Committee Member, Andreas Kårsnäs, 20140412

*Comment:* PhD Thesis title: "mage Analysis Methods and Tools for Digital Histopathology Applications Relevant to Breast Cancer Diagnosis"

National:

- Dissertation Committee of Erik Sintorn, Dept. of Computer Science and Engineering, Chalmers University of Technology, Göteborg, 20130226

*Comment:* Title: Efficient real-time visibility testing

**Christer Kiselman**

International:

- Program Committe for Discrete Geometry for Computer Imagery (DGCI 2014), 20140101–20140912

- Reference Group of the International Science Programme, 20140811

*Comment:* Meeting in Seoul, South Korea

- Evaluation of research at LIRIS, Lyon, 20140901–20150108

*Comment:* LIRIS is the acronym of Laboratoire d'InfoRmatique en Image et Systèmes d'information. Appointed by l'Agence d'évaluation de la recherche et de l'enseignement supérieur (AERES) (from 20141114 Haut Conseil d'évaluation de la recherche et de l'enseignement supérieur (HCERES)).

National:

- Dissertation Committee of Vladimir Curic, Dept. of Information Technology, UU, 20140523

*Comment:* Thesis title: Distance Functions and Their Use in Adaptive Mathematical Morphology

**Cris Luengo**

International:

- Senior member of the Institute of Electrical and Electronics Engineers (IEEE) 2010–  
*Comment:* Member since 2001.

- Member of the International Society for Analytical Cytology (ISAC), 2006–

- Area Editor for Pattern Recognition Letters 2013-01–

*Comment:* Published by Elsevier. PRL is an official journal of the International Association of Pattern Recognition. Luengo was Associate Editor 2011-06–2012-12.

- Steering Committee, International Symposium on Mathematical Morphology, 2013–

- Organizing Committee; Workshops, Tutorials and Contests Co-Chair; and Programme committee, 22nd International Conference on Pattern Recognition, Stockholm, 2014-08-24–28.

- Programme Committee, 22nd International Conference on Intelligent Systems for Molecular Biology, Boston, MA, 2014-07-11–15.

- Programme Committee 22nd Int. Conf. on Pattern Recognition, 20140824–20140828

National:

- Advisory Board for CBA 2012–

*Comment:* One of two representatives for SLU.

- Search Committee for a junior faculty member in Machine Learning for the Department of Information Technology, UU, 2014–2015

- Oponent for licentiate defence of Tobias Pahlberg, Division of Wood Science and Engineering, Luleå University of Technology, Skellefteå, 2014-02-14

*Comment:* Title: Wood Fingerprints: Recognition of Sawn Wood Products. Supervisor: Olle Hagman.

- Dissertation committee of Janne West, Division of Radiological Sciences, Linköping University, 2014-02-14  
*Comment:* Title: Quantitative Magnetic Resonance Imaging of the Brain: Applications for Tissue Segmentation and Multiple Sclerosis. Supervisor: Örjan Smedby.
- Dissertation committee of Richard Nordenskjöld, Dept. of Radiology, Oncology and Radiation Science, UU, 2014-06-10  
*Comment:* Title: Analysis of Human Brain MRI: Contributions to Regional Volume Studies. Supervisor: Joel Kullberg.
- PhD Evaluation Committee, Susanne Bornelöv, 20141003  
*Comment:* Supervisor: Jan Komorowski  
Title: Rule-based models of transcriptional regulation and complex diseases  
Dept. Cell and Molecular Biology, Computational and Systems Biology, Uppsala University
- PhD Evaluation Committee, Scott Holcombe, 20141216  
*Comment:* Supervisor: Staffan Jacobsson Svärd  
Title: Gamma spectroscopy and gamma emission tomography for fuel performance characterization of irradiated nuclear fuel assemblies  
Dept. of Physics and Astronomy, Applied Nuclear Physics, Uppsala University

### **Kristina Lidayova**

International:

- Programme committee member, 1st International Conference on Bioimaging, BIOIMAGING 2014,Eseo, Angers, Loire Valley, France, 20140303–20140306

### **Ingela Nyström**

International:

- President of the Executive Committee of International Association for Pattern Recognition (IAPR) 2014–  
*Comment:* 2nd Vice President 2008–2010, Secretary 2010–2014
- Local Arrangements Chair of the 22nd International Conference on Pattern Recognition (ICPR 2014), Stockholm, Sweden, August 2014
- Program Committee Member of the 10th IEEE International Conference on e-Science, São Paulo, Brazil, October 2014

National:

- Member of the Royal Society of Arts and Sciences of Uppsala (Kungliga Vetenskapssamhället i Uppsala), 2012–
- Member of the Board of the Faculty of Science and Technology, UU, 2011–2014
- Member of the Docent committee of the Faculty of Science and Technology, UU, 2011–2014
- Chair of the Advisory Board for the Centre for Image Analysis 2012–  
*Comment:* One of two representatives for UU.
- Member of the Council for Research Infrastructure (RFI), Vetenskapsrådet, 2014–
- Evaluation Panel for grant applications to the Swedish Research Council: Infrastructures for e-Science (“Beredningsgrupp 4”), 2011—
- Expert evaluator for the application of Claes Lundström to become Associate Professor (Docent) at Linköping University, 20140301–20140407
- Dissertation committee of Khoa Tan Nguyen, Dept. of Science and Technology, Linköping University, Norrköping, 20140307  
*Comment:* Title: Supporting Quantitative Visual Analysis in Medicine and Biology in the Presence of Data Uncertainty

**Alexandra Pacureanu**

International:

- Programme committee member, IEEE International Symposium on Biomedical Imaging (ISBI), 2014, 20140429–20140502

**Stefan Seipel**

International:

- Program Committee, 21st International Conference on Computer Graphics, Visualization and Computer Vision (WSCG 2013), Plzen, Czech Republic, June 2013.
- Program committee, 17th International Conference on Information Visualisation (iV 2013), London, U.K., July 2013.

National:

- Chair of the Swedish Computer Graphics Association (SIGRAD), 201206–
- Expert evaluator for the Swedish Higher Education Authority (“Universitetskanslersämbetet”), subject IT& New Media, 201209–201306.
- Scientific program committee, SIGRAD 2013, Norrköping, July 2013.
- Dissertation committee of Quan Ho, Norrköping, Dept. of Science and Technology, Linköping University, Campus Norrköping, 20130529  
*Comment:* Title: Architecture and Applications of a Geovisual Analytics Framework
- Dissertation committee of Patrik Lundblad, Dept. of Science and Technology, Linköping University, Campus Norrköping, 20130530  
*Comment:* Title: Applied Geovisual Analytics and Storytelling

**Ida-Maria Sintorn**

International:

- Programme committee, 18th Iberoamerican Congress on Pattern Recognition (CIARP 2013), Havanna, Cuba, Nov. 2013.
- Dissertation examiner of Swamidoss Isaac Niwas, Dept. of Electronics and Communication Engineering, National Institute of Technology, Tiruchirappalli, India, 201306  
*Comment:* Title: Complex Wavelet based Multiresolution Texture Analysis of Microscopic Images for Breast Cancer Diagnosis.

National:

- Treasurer of Swedish Society for Automated Image Analysis (SSBA), 2009–  
*Comment:* Board member 2008–.

**Natasa Sladoje**

National:

- Dissertation Committee of Lennart Svensson, Swedish University of Agricultural Sciences, 20141124  
*Comment:* Title: Image Analysis and Interactive Visualization Techniques for Electron Microscopy Tomograms
- Dissertation Committee of Anders Landström, LuleåUniversity of Technology, 20141125  
*Comment:* Title: Elliptical Adaptive Structuring Elements for Mathematical Morphology

**Robin Strand**

International:

- Editorial Board member of *Journal of Discrete Mathematics*, 2013–  
*Comment:* Open access. Published by Hindawi Publishing Corporation.
- Chair of local organization and Programme committee member, 11th International Symposium on Mathematical Morphology (ISMM 2013), Uppsala, Sweden, May 2013.

- International advisory committee, International Conference on Signal Processing, Image Processing and Pattern recognition (ICSIPR13), Karunya Nagar Coimbatore, Tamil Nadu, India, Feb. 2013.
- Programme committee, 17th International Conference on Discrete Geometry for Computer Imagery (DGCI 2013), Sevilla, Spain, Mar. 2013.
- Programme committee, 9th Workshop on Graph-based Representations in Pattern Recognition (GbR2013), Vienna, Austria, May 2013.
- Programme committee, 18th Iberoamerican Congress on Pattern Recognition (CIARP 2013), Havanna, Cuba, Nov. 2013.

National:

- Member of the Electoral Board (“elektorsförsamlingen”) of the Faculty of Science and Technology, UU, 2011-2013

### **Carolina Wählby**

International:

- Dissertation committee of Barathy Mayurathan, Department of Statistics and Computer Science, Faculty of Science, University of Peradeniya, Sri Lanka , 20141104  
*Comment:* Title: Super resolution optical imaging – image analysis, multicolor development and biological applications
- Programme committee member, IEEE International Symposium on Biomedical Imaging (ISBI), 2014, 20140429–20140502

National:

- Dissertation committee of Daniel Rönnlund, Dept. of Experimental Biomolecular Physics, KTH, 20140228  
*Comment:* Title: Efficient and Compact Codebook Design for Scene Analysis and Object Localisation
- Dissertation committee of Arash Sanamrad, Dept. of Cell and Molecular Biology, UU, 20140905  
*Comment:* Title: Biological Insights from Single-Particle Tracking in Living Cells
- Member of the Electoral Board (“elektorsförsamlingen”) of the Faculty of Science and Technology, UU, 2014-2016