Centre for Image Analysis
Uppsala University

ANNUAL REPORT 2017

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Annual Report 2017

Centre for Image Analysis

Centrum för bildanalys

Cover: Illustrations from the three PhD theses presented at Centre for Image Analysis (CBA) during 2017. Further information in Section 4.2.

Kristina Lidayova — Fast Methods for Vascular Segmentation Based on Approximate Skeleton Detection
Volume rendering of bones in a 3D computed tomography angiography (CTA) image of the lower limbs (displayed in green colour) is overlayed with a detected morphological skeleton of blood arteries (printed in red colour). The morphological skeleton serves as a seed region for subsequent vascular surface extraction algorithms.

Sajith Kecheril Sadanandan — Deep Neural Networks and Image Analysis for Quantitative Microscopy
(a) Input phase contrast image of E. coli cell colony growing in a micro chamber. (b) Segmentation of individual cells using curvature based features on the image intensity landscape. The E. coli cells are tracked over time in a time-lapse sequence to study the growth pattern.

Fredrik Wahlberg — Historical Manuscript Production Date Estimation using Deep Convolutional Neural Networks
Three-dimensional t-SNE embedding showing similarity between writer hands in the Swedish medieval charter collection “Svenskt Diplomatarium”.

Cover design:
Anton Axelsson

Edited by:
Gunilla Borgefors, Filip Malmberg, Ingela Nyström, Ida-Maria Sintorn, Leslie Solorzano, **Robin Strand**

Centre for Image Analysis, Uppsala, Sweden

Contents

1 Introduction

The Centre for Image Analysis (CBA) conducts research and graduate education in computerised image analysis and perceptualisation. Our role is to develop theory in image processing as such, but also to develop better methods, algorithms and systems for various applications. We have found applications primarily in digtal humanities, life sciences, and medicine. In addition to our own research, CBA contributes to image technology promotion and application in other research units and society nationally as well as internationally.

1.1 General background

CBA was founded in 1988 and was until 2014 a collaboration between Uppsala University (UU) and the Swedish University of Agricultural Sciences (SLU). From an organisational point of view, CBA was an independent entity within our host universities until 2010. Today, we are hosted by the Disciplinary Domain of Science and Technology and belong to one of five divisions within the Department of Information Technology (IT), the Division of Visual Information and Interaction (Vi2). The organisational matters are further outlined in Section 2.

A total of 37 researchers were active at the CBA in 2017: 16 PhD students and 21 seniors. Many of us have additional duties to research – for example, teaching, appointments within the Faculty, and leave for work outside academia – so the effective work time in CBA research corresponded to about 25 full-time equivalents. The number of staff in the CBA corridor fluctuates over the year thanks to that we have world class scientists visiting CBA and CBA staff visiting their groups, for longer or shorter periods, as an important ingredient of our activities. A successful example of collaboration we have is with the Division of Radiology, where two of our staff members work part time at the Uppsala University Hospital in order to be close to radiology researchers and also have funding from there. Among our staff members, we are pleased that Filip Malmberg qualified as Docent at UU bringing the total number of CBA docents to fifteen.

The activity level in 2017 was high with a total of 72 ongoing research projects of which 20 are new for 2017. Our projects are involving as many as 57 international and around 47 national collaboration partners. One way to measure are results is to acknowledge our three PhD theses during the year as well as 27 journal papers and 18 fully reviewed conference papers.

We continue to be active in organising conferences and seminars. For example, this year we were part of organising the first Swedish Symposium on Deep Learning. The symposium was very well attended, as this is a very hot subject at present.

As usual, we participated in the annual national symposium organised by the Swedish Society for Automated Image Analysis (SSBA), which in March 2017 was hosted by Linköping University. CBA accounted for 25 of the 170 participants from academia, local students, and industry – a proof as good as any that CBA is the largest academic image analysis group in Sweden.

We are very active in international and national societies and are pleased that our leaders are recognised in these societies. Ingela Nyström is a member of the Executive Committee of the International Association of Pattern Recognition (IAPR), since 2008 (President during 2014–2016). In August, she hosted the Executive Committee at our Department in a two-day meeting. We are also closely involved in the Network of EUropean BioImage Analysis (NEUBIAS), where Natasa Sladoje and Carolina Wählby serve as members of the management committee.

Nationally, CBA currently has two board members in the Swedish Society for Automated Image Analysis (SSBA), Ida-Maria Sintorn as Vice-Chair and Anders Brun. Other examples are that Carolina Wählby serves on the board of Swedish Bioimaging and Ingela Nyström is Vice-Chair of the Council for Research Infrastructure (RFI) within the Swedish Research Council.

During the last few years, we have been active on both national and local level to establish biomedical image analysis and biomedical engineering as more well-supported strategic research areas. During 2017, the UU Faculties of Science and Technology and Medicine and Pharmacy formed the new centre Medtech Science and Innovation together with the UU Hospital. We are looking forward to the increased funding and collaboration opportunities we expect to be the results of this new structure. Our image analysis support for researchers within life science has developed into a formal national SciLifeLab facility within BioImage Informatics, with Carolina Wählby as director and Petter Ranefall as head.

CBA has several elected members of learned socities. Ewert Bengtsson, Gunilla Borgefors, Christer Kiselman, and Carolina Wählby are elected members of the Royal Society of Sciences in Uppsala. Christer Kiselman is elected member and Ingela Nyström is elected as well as board member of the Royal Society of Arts and Sciences of Uppsala. In addition, Ewert Bengtsson, Gunilla Borgefors, and Carolina Wählby are elected members of the Royal Swedish Academy of Engineering Sciences (IVA).

Gunilla Borgefors is Editor-in-Chief for the journal Pattern Recognition Letters. Researchers at CBA also serve on several other journal editorial boards, scientific organisation boards, conference committees, and PhD dissertation committees. In addition, we take an active part in reviewing grant applications and scientific papers submitted to conferences and journals.

This annual report is available in printed form as well as on the CBA webpage, see `http://www.cb.uu.se/annual_report/AR2017.pdf`.

1.2 Summary of research

The objective of CBA is to carry out research 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 in, for example, biomedicine. We also have interdisciplinary collaboration with the humanities mainly through our projects on handwritten text recognition. In addition, we develop methods for perceptualisation, combining computer graphics, haptics, and image processing. Some of our projects lead to entrepreneurial efforts, which we interpret as a strength of our resaerch.

Our research is organised in many projects of varying size, ranging in effort from a few person months to several 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. See Section 5 for details on and illustrations of all our research projects on the diverse topics.

1.3 How to contact CBA

CBA maintains a home-page (`http://www.cb.uu.se/`). The main structure contains links to a brief presentation, people, 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), the annual reports, lists of all publications since CBA was founded in 1988, and other material. In addition, staff members have their own home-pages, which are linked from the CBA "Staff" page. On these, you can usually find detailed course and project information, etc.

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

Visiting address:	Lägerhyddsvägen 2 Polacksbacken, ITC, building 2, floor 1 Uppsala
Postal address:	Box 337 SE-751 05 Uppsala Sweden
Telephone:	+46 18 471 3460

2 Organisation

From the start in 1988 until the end of 2010, CBA was an independent entity belonging to Uppsala University (UU) and Swedish University of Agricultural Sciences (SLU), administered through UU. Reorganisations in several stages at both universities have led to that CBA now belongs to only UU hosted by the Department of Information Technology in the Division for Visual Information and Interaction (Vi2) where the two subjects Computerised Image Processing and Human-Computer Interaction are joined. Ingela Nyström is currently heading both Vi2 and CBA.

The Board of the Disciplinary Domain of Science and Technology (TekNat) established an instruction for CBA in November 2016 with description of objectives, mission, organisation, board and roles of the director. The board appointed is

- Teo Asplund, Dept. of Information Technology *(PhD student representative)*
- Anders Brun, Dept. of Information Technology
- Elna-Marie Larsson, Dept. of Surgical Sciences; Radiology
- Nikolai Piskunov, Dept. of Physics and Astronomy *(Vice-chair)*
- Robin Strand, Dept. of Information Technology
- Carolina Wählby, Dept. of Information Technology *(Chair)*
- Maria Ågren, Dept. of History

The many organisational changes in the past few years have of course affected us all, to varying degrees. However, as seen in this report, we continue our high activity. Scientifically, we continue in our areas of strength:

- Theoretical image analysis, mainly based on discrete mathematics
- Digital humanities
- Quantitative microscopy
- Interactive biomedical image analysis
- Visualisation and haptics

CBA was founded in 1988 and is today Sweden's largest single academic group for image analysis and has created a strong national and international position. This successful operation shows that centre formations in special cases are worth investing in for many years. As image analysis currently is finding widespread application in research in many fields as well as in society in general, we believe there is a need for a centre with strong application profile based on equally strong roots in fundamental image analysis research.

2.1 Finances

After the re-organisation, where CBA became part of the Division of Visual Information and Interaction (Vi2) at the Department of Information Technology, the CBA economy is not separate, but integrated in activities as well as organisation. Hence, we report how this is financed as a whole. The total expenditure for Vi2 was 45.4 million SEK for 2017, where the largest cost is personnel. To cover this, 45% came from external sources, 30% from UU faculty funding, and 18% from undergraduate education. The remaining % were covered by funds balanced from previous years.

Even though CBA as a centre does not organise undergraduate education, Vi2 offers undergraduate education with several courses on Image Analysis, Computer Graphics, and Scientific Visualisation as well as Human-Computer Interaction themes. Most of us teach 10–20%, while some Senior Lecturers teach more.

The economy in Table 1 summarises the overall economy for Vi2 in 2017. 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 2017 in kSEK.

Income		**Costs**	
UU	12701	Personnel	27902
UU undergraduate education	7666	Equipment	301
Governmental grants[1]	13344	Operating expenditure[4]	2410
Non-governmental grants[2]	5685	Rent	2079
Contracts[3]	2827	University overhead	12705
Financial netto	0		
Total income	**42223**	**Total cost**	**45397**

[1] The Swedish Research Council, Vinnova, SSF, etc.

[2] Research foundations, EU

[3] Internal invoices from UU and compensations

[4] Including travel and conferences

Within UU, we have financial support from SciLifeLab, the Centre for Interdisciplinary Mathematics, eSSENCE as well as strategic funds from the IT department as a supplement to the faculty funds that came to the research program Image analysis and human-computer interaction (so-called FFF). We note that the share of external funding is increasing year by year. The funding agencies are, for example, the Swedish Research Council, the Swedish Foundation for Strategic Research, Vinnova, the European Research Council, and the Riksbankens jubileumsfond. The strong finances led to recruitments of new PhD students and PostDocs. In October 2017, we announced for a senior lecturer in computerised image analysis (with the possibility to be promoted to full professor). This is a particular strategic step to safeguard the future of our subject at the Department, Faculty as well as Uppsala University.

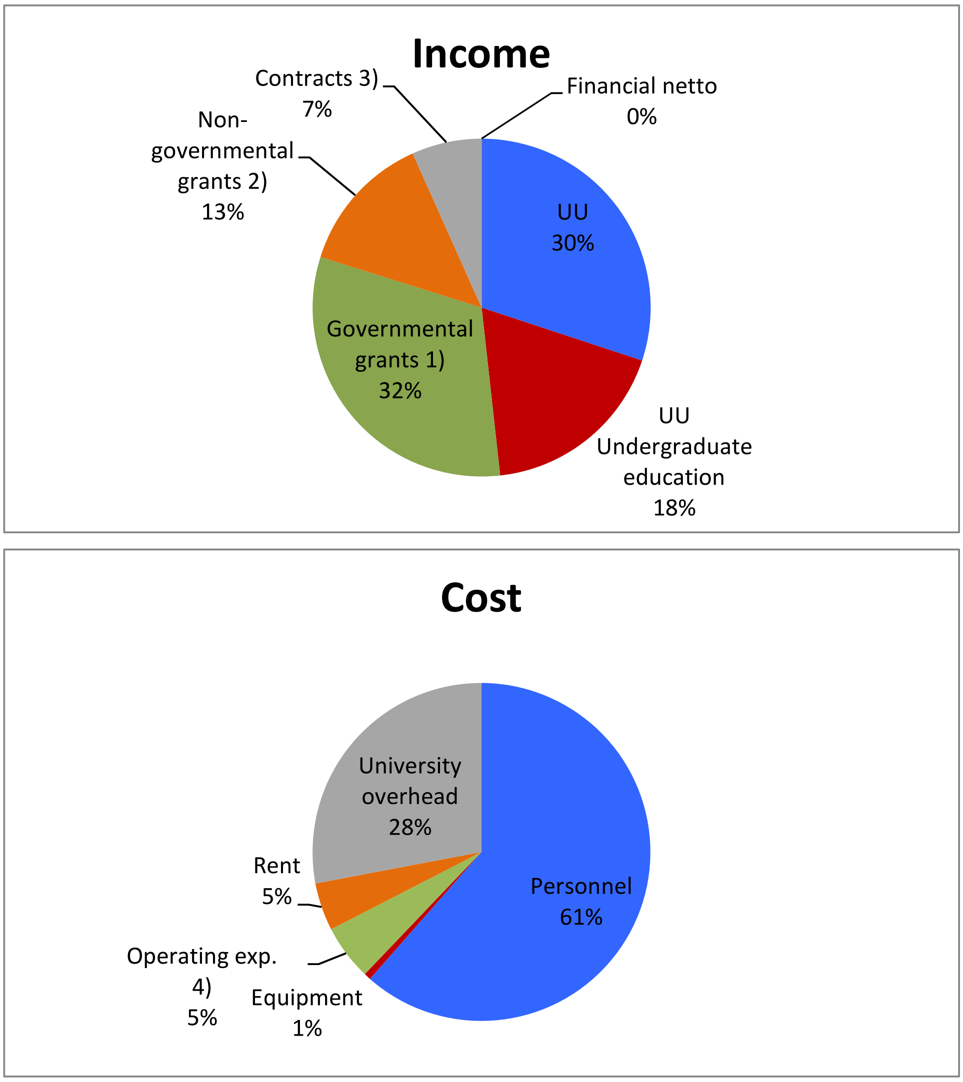

Figure 1: Vi2 income (top) and costs (bottom) for 2017.
[1] The Swedish Research Council, Vinnova, SSF, etc.
[2] Research foundations, EU
[3] Internal invoices from UU and compensations
[4] Including travel and conferences

2.2 Staff, CBA

People affiliated with CBA and employed by the Department of Information Technology during 2017:

Amin Allalou, PhD, Researcher (part time)
Teo Asplund, Graduate Student
Marine Astruc, Graduate Student, –170122
Ewert Bengtsson, Professor Emeritus
Ludovic Blache, PhD, PostDoc
Maxime Bombrun, PhD, PostDoc
Gunilla Borgefors, Professor
Eva Breznik, Graduate Student
Anders Brun, PhD, Researcher
Heung-Kook Choi, Professor, Guest Researcher, 170201–
Anders Hast, Docent and Excellent Teacher, Lecturer
Christer O. Kiselman, Professor Emeritus
Ashis Kumar Dhara, PhD, PostDoc, 170901–
Kristína Lidayová, Graduate Student, –170630
Joakim Lindblad, PhD, Researcher (part time)
Filip Malmberg, PhD, Docent, Researcher
Damian Matuszewski, Graduate Student
Marco Mignardi, PhD, PostDoc, –170930
Lena Nordström, Administrator, –170831
Fredrik Nysjö, Graduate Student
Ingela Nyström, Professor, Director
Camilla Pajunen, Administrator, 170401–
Gabriele Partel, Graduate Student
Kalyan Ram, Graduate Student
Petter Ranefall, Docent, Bioinformatician
Sajith Sadanandan Kecheril, Graduate Student
Stefan Seipel, Professor, (part time) UU and University of Gävle
Ida-Maria Sintorn, Docent, Associate Senior Lecturer
Nataša Sladoje, Docent, Researcher
Leslie Solorzano, Graduate Student
Robin Strand, Docent, Researcher
Amit Suveer, Graduate Student
Fredrik Wahlberg, Graduate Student, –170331
Elisabeth Wetzer, Graduate Student, 171001–
Ekta Vats, PhD, PostDoc, 170501–
Håkan Wieslander, Graduate Student, 170901–
Tomas Wilkinson, Graduate Student
Carolina Wählby, Professor
Johan Öfverstedt, Graduate Student, 170301–

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
13. Nataša Sladoje, 2015, UU
14. Petter Ranefall, 2016, UU
15. Filip Malmberg, 2017, UU

CBA staff appointed Excellent Teachers

1. Anders Hast 2014, UU

3 Undergraduate education

CBA is responsible for undergraduate courses in Image Analysis, Computer Graphics, and Scientific Visualisation, and Medical Informatics (course examiners in bold). In addition, we teach or give guest lectures in many other courses at UU. We also either supervise or review many Master theses, as our subjects are useful in many different industries or for other research groups and are also popular with the students. This year, we supervised five theses and reviewed ten theses. Four of them were industrial, three in medical applications, and three in more theoretical image analysis.

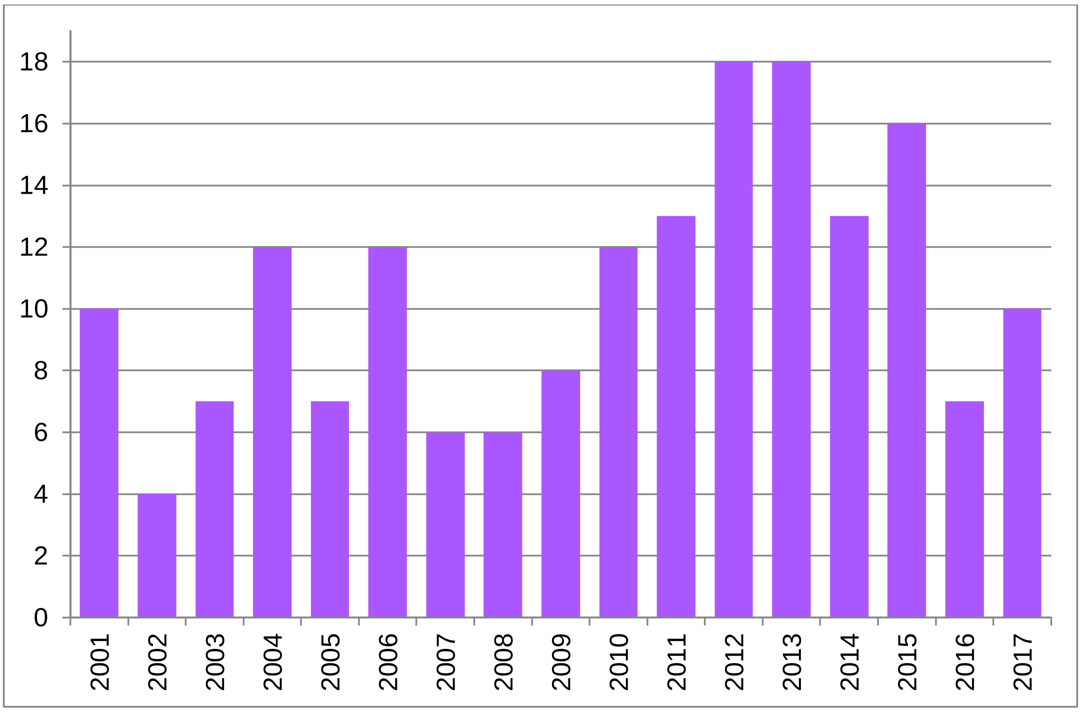

Figure 2: The number of Master theses from CBA 2001-2017.

1. **Computer Assisted Image Analysis II, 10p**
   Nataša Sladoje, Anders Brun, Maxime Bombrun, Robin Strand, Filip Malmberg, Carolina Wählby, Sajith Kecheril Sadanandan
   Period: 20170101–20170331

2. **Medical Informatics, 5p**
   Robin Strand
   Period: 20170117–0321

3. **Computer Graphics, 10p**
   Anders Hast, Filip Malmberg, Fredrik Nysjö
   Period: 20170321–0530

4. **Scientific Visualisation, 5p**
   Anders Hast, Fredrik Nysjö, Stefan Seipel
   Period: 20170828–1024

5. **Computer Programming I, 5p**
   Johan Öfverstedt
   Period: 20170831–1023

6. **Computer-Assisted Image Analysis I, 5p**
   Filip Malmberg, Damian Matuszewski, Amit Suveer, Tomas Wilkinson
   Period: 20171030–1213

7. **MSc programmes in Molecular Medicine and Medical Nuclide techniques Bioinformatics introduction**
   Ida-Maria Sintorn
   Period: 20170913–1210
   Comment: Sintorn contributed with one image analysis lecture and a computer exercise.

8. **Machine Learning, 10p**
   Teo Asplund
   Period: 20170116–0602
   Comment: Asplund was lab assistant.

9. **Advanced Interaction Design, 5p**
   Fredrik Nysjö
   Period: 20170201–0201

10. **Programming, 10p**
    Teo Asplund
    Period: 20170828–1218
    Comment: Asplund was lab assistant.

3.1 Master theses

1. **Classification of High Content Screening Data by Deep Convolutional Neural Networks**
   Student: Karl-Johan Leuchowius
   Supervisors: Liam O'Connor, O'Connor Walter and Eliza Hall; Institute of Medical Research, Australia
   Reviewer: Carolina Wählby
   Publisher: UPTEC IT
   Abstract: In drug discovery, high content screening (HCS) is an imaging-based method forcell-based screening of large libraries of drug compounds. HCS generates enormous amounts of images that need to be analysed and quantified by automated image analysis. This analysis is typically performed by a variety of algorithms segmenting cells and sub-cellular compartments and quantifying properties such as fluorescence intensities, morphological features, and textural characteristics. These quantified data can then be used to train a classifier to classify the imaged cells according to the phenotypic effects of the compounds. Recent developments in machine learning have enabled a new kind of image analysis in which classifiers based on convolutional neural networks can be trained on the image data directly, by passing the image quantification step. This has been shown to produce highly accurate predictions and simplify the analysis process. In this study, convolutional neural networks (CNNs) were used to classify HCS images of cells treated with a set of different drug compounds. A set of network architectures and hyper-parameters were explored in order to optimise the classification performance. The results were compared with the accuracies achieved with a classical image analysis pipeline in combination with a classifier. With this data set, the best CNN-based classifier achieved an accuracy of 91.3 %, where as classical image analysis combined with a random forest classifier achieved a classification accuracy of 78.8 %. In addition to the large increase in classification accuracy, CNNs have benefits such as being less biased when it comes to image quantification algorithm selection, and require less hands-on time during optimisation.

2. **Infrared image-based modeling and rendering**
   Student: Oskar Wretstam
   Supervisor: Martin Solli, Flir Systems AB, Stockholm
   Reviewer: Robin Strand
   Publisher: UPTEC F 17021
   Abstract: Image based modeling using visual images has undergone major development during the earlier parts of the 21th century. In this thesis a system for automated uncalibrated scene reconstruction using infrared images is implemented and tested. An automated reconstruction system could serve to simplify thermal inspection or as a demonstration tool. Thermal images will in general have lower resolution, less

contrast and less high frequency content as compared to visual images. These characteristics of infrared images further complicates feature extraction and matching, key steps in the reconstruction process. In order to remedy the complication preprocessing methods are suggested and tested as well. Infrared modeling will also impose additional demands on the reconstruction as it is of importance to maintain thermal accuracy of the images in the product. Three main results are obtained from this thesis. Firstly, it is possible to obtain camera calibration and pose as well as a sparse point cloud reconstruction from an infrared image sequence using the suggested implementation. Secondly, correlation of thermal measurements from the images used to reconstruct three dimensional coordinates is presented and analyzed. Lastly, from the preprocessing evaluation it is concluded that the tested methods are not suitable. The methods will increase computational cost while improvements in the model are not proportional.

3. **Automatic Recognition of Abdominal Organs in Whole-Body Water Fat MRI**
   Student: Camilla Englund
   Supervisor: Robin Strand
   Reviewer: Joel Kullberg, Dept. of Surgical Sciences, Radiology
   Publisher: UPTEC F 17036
   Abstract: As imaging has become part of the clinical routine in medicine, automatic analysis of medical images has gained increasing interest and importance. Imiomics, developed at the department of radiology, Uppsala universitet, is an application for automatic analysis of whole-body magnetic resonance (MR) images and positron emission tomography (PET) images. Imiomics gives insight into questions such as correlation between genetics and physical morphology and diseases, and could be used for following patients before and after medical treatment. Imiomics is based on image registration, which relates to matching of different image data, but registration often fails in body regions with high variability, such as the abdominal organs, which have large variations in size and shape between different subjects.

   One way of improving the registration in difficult regions is by localization of anatomical structures beforehand. However, manual localization and segmentation are often time-consuming and also subjective procedures. To this end, this thesis investigated whether machine learning could be used for automatic recognition and localization of abdominal organs from whole-body MR images by building up a computer vision system. This work aimed for recognition of a few organs in the abdomen and torso; liver, kidney, heart, spine, stomach, and fat tissue. The data set consisted of 10 subjects, where seven of them where used for training and three subjects were used for validation of the model. The algorithm chosen for the task was random forest and the computational software used was MATLAB.

   Expressive texture features were determined during a training phase by filtering the images with various kernels and by calculation of co-occurrence matrices. Also, features based on spatial position and distance were calculated. A large number of feature was employed as the baseline approach. However, the dimension of the feature space was reduced to limit computational needs. Dimension reduction was applied in order to select the most important features for the recognition task. Some experiments of feature selection were tried such as filter methods, and sequential forward feature selection, also some experiments with random forest feature importance were done. Sequential forward feature selection reduced the number of feature the most without losing predictive power of any considerable amount. The selected features were often related to position and distances, which also have low computational cost. In order to invoke more of those feature, a second layer of random forest was introduced. The first layer of classifier produced probability maps, from which estimated center of mass of the regions of interest were extracted. As a result, coordinates and distances relative these landmarks of estimated center of mass were used as features for the second layer of random forest classifier.

   In total, four variations of the classifier design were tested and compared; the baseline feature set, a reduced feature set by using feature selection, a two-layer classifier design, and a two-layer design with a second feature selection applied. The most successful design was the two layer design of random forest, which achieved an average error on the estimated of center of mass with 1.4 cm, without any post-processing applied, within an average run time of two minutes for classification of a test volume of the torso. However, there was no large difference in predictive power between the different classifier designs.

   The computer vision pipeline constructed reached reasonable performance in the localization task, and machine learning algorithms such as random forest could successfully be used to localize anatomical structures, even with such a small data set as 10 subjects. Thus, such a system is considered to be useful as a pre-step for Imiomics.

4. **Convolutional neural networks for classification of transmissionelectron microscopy imagery**
   Student: Sergii Gryshkevych
   Supervisor: Max Pihlström, Vironova, Stockholm
   Reviewer: Ida-Maria Sintorn
   Publisher: UPTEC IT 17004
   Abstract: One of Vironova's electron microscopy services is to classify liposomes. This includes determining the structure of a liposome and presence of a liposomal encapsulation. A typical service analysis contains a lot of electron microscopy images, so automatic classification is of great interest. The purpose of this project is to evaluate convolutional neural networks for solving lamellarity and encapsulation classification problems. The available data sets are imbalanced so a number of techniques toovercome this problem are studied. The convolutional neural network models have reasonable performance and offer great flexibility, so they can be an alternative to the support vector machines method which is currently used to perform automatic classification tasks. The project also includes the feasibility study of convolutional neural networks from Vironova's perspective.

5. **Comparing SIFT and SURF: Performance on patent drawings**
   Student: Christian Lindqvist
   Supervisor: Shigeru Tamaki, Intellectual property department, Semiconductor Energy Laboratory's (SEL), Atsugi, Japan
   Reviewer: Ida-Maria Sintorn
   Publisher: UPTEC IT 17020
   Abstract: In recent time, it has been found that one can use the images contained in patents in order to organize large collections of patents. This can be very helpful in order to reduce the time and resources required for handling patents. Research has resulted in systems that can find and compare specific images using content-based image retrieval (CBIR). There are plenty of CBIR algorithms available and they all have different traits. This project tests two such algorithms with regards to patent drawings. Experiments show that these algorithms can retrieve about three to four relevant images when looking at the 20 top results of a performed search, and even more if more results are considered. This in turn could potentially result in finding dozens of relevant patent documents using only the images of onespecific patent document.

6. **Semi-automatic Training Data Generation for Cell Segmentation Network Using an Intermediary Curator Net**
   Student: David Ramnerö
   Supervisors: Petter Ranedall, Sajith Kecheril Sadanandan
   Reviewer: Carolina Wählby
   Publisher: UPTEC F 17054
   Abstract: In this work we create an image analysis pipeline to segment cells from microscopy image data. A portion of the segmented images are manually curated and this curated data is used to train a Curator network to filter the whole dataset. The curated data is used to train a separate segmentation network to improve the cell segmentation. This technique can be easily applied to different types of microscopy object segmentation.

7. **Implementation of handwritten text recognition using density value of Delauney tessellation**
   Student: Adithya Ravindran
   Supervisor: Anders Hast
   Reviewer: Michael Aschcroft
   Publisher: UPTEC IT 17070
   Abstract: This paper presents a novel Word spotting technique for handwritten documentsusing density value of Delaunay triangulation. Delaunay tessellation is constructedfrom a set of data points on a query image and the density value is computed for eachdata point. This information is either directly used for training in a feed-forward neural network or used to compute the probability estimates of a class from Delaunay Tessellation Field Estimation and classification follows using naive Bayesian classifier. This paper discusses the performance of a Delaunay tessellation fieldestimation model and neural network model.

8. **Similarity of Hybrid Object Representations With Applications in Object Recognition and Classification**
   Student: Johan Öfverstedt
   Supervisor: Nataša Sladoje

Reviewer: Joakim Lindblad
Publisher: UPTEC IT 17014
Abstract: Similarity measures between images that are robust to noise and other kinds of distortion, while sensitive to transformations in a smooth and stable way, are of great importance in many image analysis problems. In this thesis a family of measures based on fuzzy set theory which combine shape and intensity, is extended to vector-valued fuzzy sets for hybrid object representations such as intensity and gradient magnitude as well as multi-spectral images such as color images. Several novel distance measures are proposed, discussed with regards to theoretical and practical properties, and evaluated empirically on both synthetic images and real-life object recognition and classification tasks. Performance metrics, such as number of local minima and size of catchment basin, which are important for distance-based local search techniques are evaluated for varying degrees of distortion by additive noise and number of discrete membership levels. The proposed distance measures are shown to enable utilization of information-rich object representations and to outperform distance measures between scalar-valued fuzzy sets on various object detection and classification tasks.

9. **Automatic Registration of Point Clouds Acquired by a Sweeping Single-Pixel TCSPC Lidar System**
Student: Mattias Mejerfalk
Supervisor: Markus Henriksson
Reviewer: Filip Malmberg
Partner(s): Swedish Defence Research Agency
Publisher: UPTEC F 17028
Abstract: This project investigates an image registration process, involving a method known as K-4PCS. This registration process was applied to a set of 16 long range lidar scans, acquired at different positions by a single pixel TCSPC lidar system. By merging these lidar scans, after having been transformed by proper scan alignments, one could obtain clear information regarding obscured surfaces. Using all available data, the investigated method was able to provide adequate alignments for all lidar scans. The data in each lidar scan was subsampled and a subsampling ratio of 50%, approximately equivalent to 9 million registrated photon detections per scan position, proved to be sufficient in order to construct sparse, representative point clouds that, when subjected to the image registration process, result in adequate alignments. Lower subsampling ratios failed to generate representative point clouds that could be used in the image registration process in order to obtain adequate alignments. Large errors followed, especially in the horisontal and elevation angles, of each alignment. The computation time for one scan pair matching at a subsampling ratio = 1.0 was, on average, approximately 120 s, and 95 s for a subsampling ratio = 0.5. To summarise, the investigated method can be used to registrate lidar scans acquired by a lidar system of TCSPC principles, and with proper equipment and code implementation, one could potentially acquire 3D images of a measurement area every second, however, at a delay depending on the efficiency of the lidar data processing.

10. **Deep Convolutional Neural Networks For Detecting Cellular Changes Due To Malignancy**
Student: Håkan Wieslander, Gustav Forslid
Supervisors: Sajith K. Sadanandan, Ewert Bengtsson,
Reviewer: Carolina Wählby
Partner(s): Jan-Michael Hirch, Institutionen för kirurgiska vetenskaper Uppsala Universitet
Christina Runow Stark, Södersjukhuset Stockholm
Publisher: UPTEC F 17039
Abstract: Discovering cancer at an early stage is an effective way to increase the chance of survival. However, since most screening processes are done manually it is time inefficient and thus costly. One way of automizing the screening process could be to classify cells using Convolutional Neural Networks. Convolutional Neural Networks have been proven to produce high accuracy for image classification tasks. This thesis investigates if Convolutional Neural Networks can be used as a tool to detect cellular changes due to malignancy in the oral cavity and uterine cervix. Two datasets containing oral cells and two datasets containing cervical cells were used. The cells were divided into normal and abnormal cells for a binary classification. The performance was evaluated for two different network architectures, ResNet and VGG. For the oral datasets the accuracy varied between 78-82% correctly classified cells depending on the dataset and network. For the cervical datasets the accuracy varied between 84-86% correctly classified cells depending on the dataset and network. These results indicates a high potential for classifying abnormalities for oral and cervical cells. ResNet was shown to be the preferable network, with a higher accuracy and a smaller standard deviation.

4 Graduate education

We usually offer several PhD courses each year, both for our own students and for others needing our expertise as tools. This year, a course in Image Segmentation was held by our guest professor from Inje University, Korea. There were three PhD dissertations at CBA in 2017. The first was also the first thesis from our large Handwritten Text Recognition project; the second one developed new methods for segmenting blood vessels in 3D medical images; and the third was our first using Deep Learning for quantitative microscopy. We also added our fifteenth Docent, Filip Malmberg.

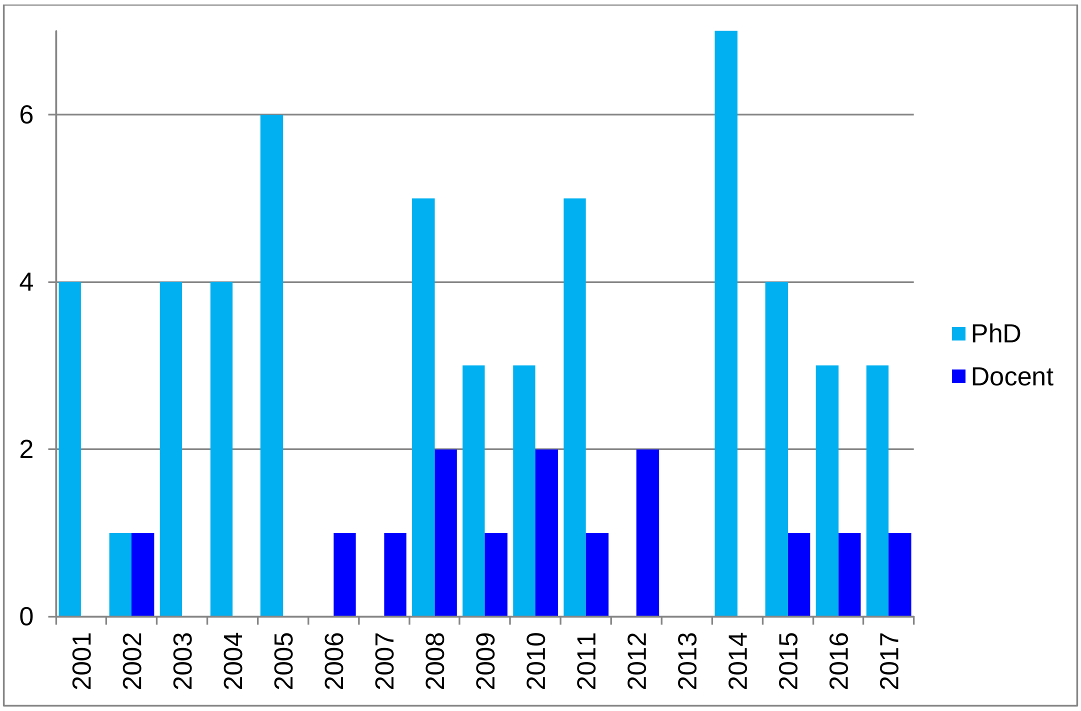

Figure 3: The number of new PhDs and docents at CBA 2001–2017.

4.1 Graduate courses

1. **Methods and Algorithms for Image Segmentation (5p)**
   Heung-Kook Choi
   Period: 201703–201705
   Venue: The course was given during Professor Choi's sabbatical year at CBA.

2. **Methods for Cell Analysis (3.5p)**
   Carolina Wählby and **Maxime Bombrun**
   Period: 20170803–20170317 and 20171004–20171013 (two instances of the same course)
   Venue: The course was organized by BioVis; the UU Biological Visualization Platform

3. **Classical and Modern Papers in Image Analysis**
   PhD students at CBA, **Nataša Sladoje**
   Period: During the whole year
   Venue: The course was given at CBA.
   Description: Presentations and discussions of classical or modern papers in image processing.

4. **Advanced Electron Microscopy (5p)**
Ida-Maria Sintorn
Period: 20170213–0310
Comment: Sintorn contributed with one lecture on image processing and one group assignment.

4.2 Dissertations

1. *Date:* 20170324
Interpreting the Script: Image Analysis and Machine Learning for Quantitative Studies of Pre-modern Manuscripts
Student: **Fredrik Wahlberg**
Supervisor: Anders Brun
Assistant Supervisor: Lasse Mårtensson (1), Ewert Bengtsson
(1) University of Gävle
Opponent: Apostolos Antonacopoulos(1)
(1) University of Salford, Manchester, UK
Committee: Lena Klasén (1), Anders Heyden (2), Atsuto Maki (3), Beáta Megyesi (4), Klas Nordberg (1)
(1) Dept. of Electrical Engineering, Linköping University
(2) Department of Mathematics, Lund Institute of Technology
(3) School of Computer Science and Communication, Royal Institute of Technology
(4) Department of Linguistics and Philology, UU
Publisher: Acta Universitatis Upsaliensis, ISBN: 978-91-554-9814-6
Abstract: The humanities have for a long time been a collection of fields that have not gained from the advancements in computational power, as predicted by MooreÂ´s law. Fields like medicine, biology, physics, chemistry, geology and economics have all developed quantitative tools that take advantage of the exponential increase of processing power over time. Recent advances in computerized pattern recognition, in combination with a rapid digitization of historical document collections around the world, is about to change this.

   The first part of this dissertation focuses on constructing a full system for finding handwritten words in historical manuscripts. A novel segmentation algorithm is presented, capable of finding and separating text lines in pre-modern manuscripts. Text recognition is performed by translating the image data of the text lines into sequences of numbers, called features. Commonly used features are analysed and evaluated on manuscript sources from the Uppsala University library Carolina Rediviva and the US Library of Congress. Decoding the text in the vast number of photographed manuscripts from our libraries makes computational linguistics and social network analysis directly applicable to historical sources. Hence, text recognition is considered a key technology for the future of computerized research methods in the humanities.

   The second part of this thesis addresses digital palaeography, using a computers superior capacity for endlessly performing measurements on ink stroke shapes. Objective criteria of character shapes only partly catches what a palaeographer use for assessing similarity. The palaeographer often gets a feel for the scribe's style. This is, however, hard to quantify. A method for identifying the scribal hands of a pre-modern copy of the revelations of saint Bridget of Sweden, using semi-supervised learning, is presented. Methods for production year estimation are presented and evaluated on a collection with close to 11000 medieval charters. The production dates are estimated using a Gaussian process, where the uncertainty is inferred together with the most likely production year.

   In summary, this dissertation presents several novel methods related to image analysis and machine learning. In combination with recent advances of the field, they enable efficient computational analysis of very large collections of historical documents.

2. *Date:* 20170522
Fast Methods for Vascular Segmentation Based on Approximate Skeleton Detection
Student: **Kristina Lidayova**
Supervisor: Hans Frimmel, Dept. of Information Technology, UU
Assistant Supervisor: Ewert Bengtsson, Örjan Smedby (1)
(1) Department of Science and Technology (ITN), Linköping University
Opponent: Alejandro F. Frangi (1)

(1) The University of Sheffield, UK.
Committee: Gunilla Borgefors, Josef Bigun (1), Johan Wikström (2), Anna Fabijańska (3), Antoine Vacavant (4)
(1) Halmstad University
(2) Dept. of Surgical Sciences, Radiology, UU
(3) Lodz University of Technology, Lodz, Poland
(4) Université Clermont Auvergne, Le Puy-en-Velay, France
Publisher: Acta Universitatis Upsaliensis, ISBN: 978-91-554-9874-0
Abstract: Modern medical imaging techniques have revolutionized health care over the last decades, providing clinicians with high-resolution 3D images of the inside of the patient's body without the need for invasive procedures. Detailed images of the vascular anatomy can be captured by angiography, providing a valuable source of information when deciding whether a vascular intervention is needed, for planning treatment, and for analyzing the success of therapy. However, increasing level of detail in the images, together with a wide availability of imaging devices, lead to an urgent need for automated techniques for image segmentation and analysis in order to assist the clinicians in performing a fast and accurate examination.

To reduce the need for user interaction and increase the speed of vascular segmentation, we propose a fast and fully automatic vascular skeleton extraction algorithm. This algorithm first analyzes the volume's intensity histogram in order to automatically adapt the internal parameters to each patient and then it produces an approximate skeleton of the patient's vasculature. The skeleton can serve as a seed region for subsequent surface extraction algorithms. Further improvements of the skeleton extraction algorithm include the expansion to detect the skeleton of diseased arteries and the design of a convolutional neural network classifier that reduces false positive detections of vascular cross-sections. In addition to the complete skeleton extraction algorithm, the thesis presents a segmentation algorithm based on modified onion-kernel region growing. It initiates the growing from the previously extracted skeleton and provides a rapid binary segmentation of tubular structures. To provide the possibility of extracting precise measurements from this segmentation we introduce a method for obtaining a segmentation with subpixel precision out of the binary segmentation and the original image. This method is especially suited for thin and elongated structures, such as vessels, since it does not shrink the long protrusions. The method supports both 2D and 3D image data.

The methods were validated on real computed tomography datasets and are primarily intended for applications in vascular segmentation, however, they are robust enough to work with other anatomical tree structures after adequate parameter adjustment, which was demonstrated on an airway-tree segmentation.

3. *Date:* 201711100
Deep Neural Networks and Image Analysis for Quantitative Microscopy
Student: **Sajith Kecheril Sadanandan**
Supervisor: Carolina Wählby
Assistant Supervisor: Petter Ranefall
Opponent: Jeroen van der Laak
Committee: Josephine Sullivan (1), Kaj Nyström (2), Claes Lundström (3), Kristian Eurén (4), Erik Meijering (5)
(1) School of Computer Science and Communication, Royal Institute of Technology
(2) Department of Mathematics, UU
(3) Department of Science and Technology (ITN), Linköping University
(4) ContextVision, Stockholm
(5) Biomedical Imaging Group Rotterdam, Erasmus University Medical Center, Rotterdam, the Netherlands
Publisher: Acta Universitatis Upsaliensis, ISBN: 978-91-513-0080-1
Abstract: Understanding biology paves the way for discovering drugs targeting deadly diseases like cancer, and microscopy imaging is one of the most informative ways to study biology. However, analysis of large numbers of samples is often required to draw statistically verifiable conclusions. Automated approaches for analysis of microscopy image data makes it possible to handle large data sets, and at the same time reduce the risk of bias. Quantitative microscopy refers to computational methods for extracting measurements from microscopy images, enabling detection and comparison of subtle changes in morphology or behavior induced by varying experimental conditions. This thesis covers computational methods for segmentation and classification of biological samples imaged by microscopy.

Recent increase in computational power has enabled the development of deep neural networks (DNNs) that perform well in solving real world problems. This thesis compares classical image analysis algorithms for segmentation of bacteria cells and introduces a novel method that combines classical image analysis and DNNs for improved cell segmentation and detection of rare phenotypes. This thesis also demonstrates a novel DNN for segmentation of clusters of cells (spheroid), with varying sizes, shapes and textures imaged by phase contrast microscopy. DNNs typically require large amounts of training data. This problem is addressed by proposing an automated approach for creating ground truths by utilizing multiple imaging modalities and classical image analysis. The resulting DNNs are applied to segment unstained cells from bright field microscopy images. In DNNs, it is often difficult to understand what image features have the largest influence on the final classification results. This is addressed in an experiment where DNNs are applied to classify zebrafish embryos based on phenotypic changes induced by drug treatment. The response of the trained DNN is tested by ablation studies, which revealed that the networks do not necessarily learn the features most obvious at visual examination. Finally, DNNs are explored for classification of cervical and oral cell samples collected for cancer screening. Initial results show that the DNNs can respond to very subtle malignancy associated changes. All the presented methods are developed using open-source tools and validated on real microscopy images.

5 Research

We have tried to list our research activities as a number of separate projects in this Chapter. Some projects are large and some are small and many are related, but all are unique in some way. Even though our own subjects can be loosely described as Image Analysis, Visualization, and Pattern Recognition most of our projects are medical and life science applications. Such applications are of great interest to our researchers, and offer possibilities to get external grants for image analysis and visualization. Another reasonably large application area is Digital Humanities in the form of analysis of old, handwritten manuscripts. In almost all application projects we co-operate with experts in the application area. Of course we also develop new mathematics and new algorithms in our own subjects, both independently of applications but also as a result of new, challenging application problems.

In Section 5.1, we list projects that use a microscope, optical or electronic, for imaging and cell biology as the application. Many of the projects are generated by our participation in the large Swedish co-operation project SciLifeLab, where we provide image analysis support to researchers within life science via our SciLifeLab BioImage Informatics facility. In Section 5.2, microscopes are also the imaging tool, but here the objects are tissues and whole model organisms, such as zebrafish. Again, many are performed within SciLifeLab. Our contributions to 5.1 and 5.2 projects is almost exclusively image analysis. Section 5.3 also lists medical applications, but now nearer to the patient, including diagnosis and surgical planning. Here, we use many different imaging modalities and the tools used are 3D image analysis, haptics, and visualization. In Section 5.4, we list the theoretical projects that develop image analysis, to generate new useful mathematics for arbitrary applications. Finally in Section 5.5, we list various projects involving humanities. As mentioned above, the largest one is analysing old, handwritten documents using Image Analysis and Pattern Recognition, but there are also a few "odd" small ones.

In Section 5.6, we have collected all our research partners, international and national, with whom we had active co-operation, in the form of either a joint project or a joint publication, during 2017.

5.1 Microscopy, cell biology

1. **Automated Quantification of Axonal Growth**
   Petter Ranefall, Carolina Wählby
   Partner: Sarah Pan, Alexander Ossinger, Nils Hailer, Nikos Schizas - Dept. of Surgical Sciences, UU.
   Funding: SciLifeLab BioImage Informatics Facility (www.scilifelab.se/facilities/bioimage-informatics)
   Period: 20161004–
   Abstract: The aim of this project is to establish a standardised method for measuring axonal growth from spinal cord slice cultures using ImageJ and CellProfiler softwares. To measure the area of axons outside the explant body, pictures of spinal cord slice cultures are captured through a light microscope and then analysed in ImageJ and CellProfiler. Our plan is to use this method in future experiments on axonal regeneration and growth from the spinal cord. See Figure 4.

2. **Assessing Bacterial Growth Kinetics and Morphology Using Time-lapse Microscopy Data**
   Petter Ranefall, Carolina Wählby
   Partner: Elisabet Nielsen - Dept. of Pharmaceutical Bioscience, UU, Pikkei Yuen, Pernilla Lagerbäck, Thomas Tängdén Otto Cars - Dept. of Medical Sciences, UU
   Funding: SciLifeLab BioImage Informatics Facility (www.scilifelab.se/facilities/bioimage-informatics)
   Period: 20160603–
   Abstract: In vitro methods are often used to study the concentration-effect relationship for antimicrobial agents. Time-kill curve experiments have long been the standard methodology, with bacterial counts followed over time using viable count assessments on agar plates. This method is labor-intensive and recently

digital time-lapse microscopy methods have become available which might allow a more rapid assessment of antibiotic activity. Additionally, these methods could add information related to drug-induced morphological changes. The aim of this project is to integrate information obtained from time-lapse microscopy in the characterization of antibiotic effect on bacterial growth and morphology. See Figure 5.

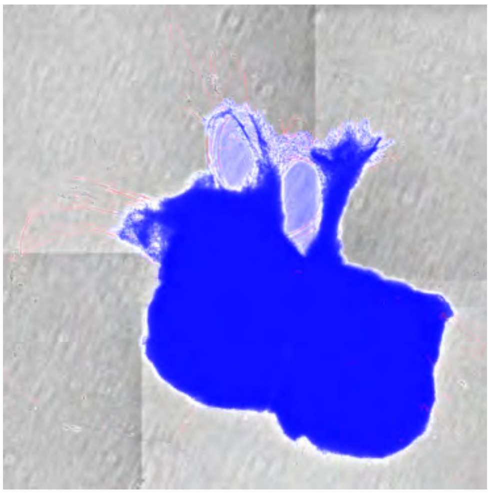

Figure 4: Automated quantification of axonal growth

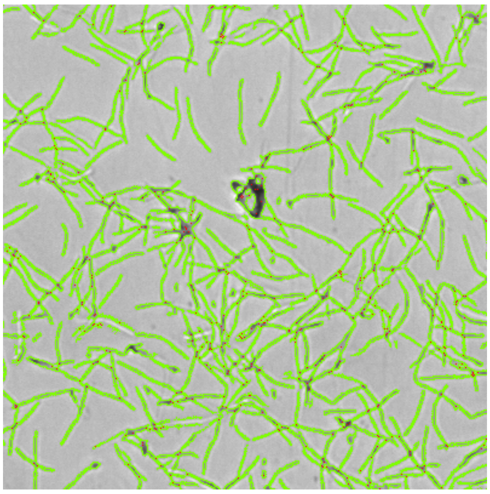

Figure 5: Assessing Bacterial Growth Kinetics and Morphology Using Time-lapse Microscopy Data

3. **Amyotrophic Lateral Sclerosis**
   Petter Ranefall, Carolina Wählby
   Partner: Jordi Carreras Puigvert, Oskar Fernandez-Capetillo - Division of Translational Medicine and Chemical Biology, Dept. of Medical Biochemistry and Biophysics, Karolinska Institute, SciLifeLab, Stockholm
   Funding: SciLifeLab BioImage Informatics Facility (www.scilifelab.se/facilities/bioimage-informatics)
   Period: 20160113–
   Abstract: Amyotrophic lateral sclerosis is a neurodegenerative disease characterized by the loss of motor neurons in the cortex brain stem and spinal chord. The incidence is 1 in 50 000 combining US and EU populations. The disease is fatal in approximately 5 years and there is currently no cure for AL. Morover, given the low incidence of case, finding new treatments for ALS is not a priority of the Pharma industry. At SciLifeLab, we are developing several image based assays to discover strategies that can alleviate the death of ALS-motor neurons. See Figure 6.

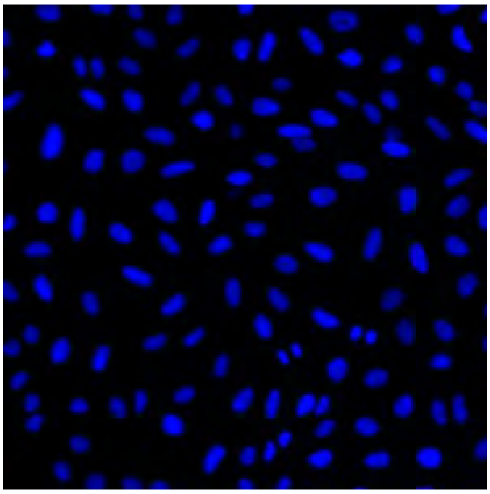

Figure 6: Amyotrophic lateral sclerosis

4. **Quantification of Lipid Droplets in Human Pre-Adipocyte**
   Maxime Bombrun, Petter Ranefall, Carolina Wählby
   Partner: Hui Gao, Niklas Mejhert, Mikael Ryden, Peter Arner - Dept. of Medicine (H7) Karolinska Institute
   Funding: SciLifeLab BioImage Informatics Facility (www.scilifelab.se/facilities/bioimage-informatics)
   Period: 20160311–
   Abstract: Adipocytes store lipids, predominantly triglycerides (TGs), in lipid droplets (LDs). Upon energy shortage, TGs are hydrolyzed into non-esterified fatty acids and glycerol in an enzymatic process termed lipolysis. LDs are highly dynamic and undergo fragmentation or fusion under lipolytic and lipogenic conditions, respectively. The aim of this project is to unravel the molecular mechanisms governing LD formation and investigate connections between LD morphology and lipolysis rate. We will perform a high throughput image analysis of TG (BODIPY)-stained adipocytes treated with siRNAs that target lipolysis regulating genes. Images will be acquired by an automated microphotography pipeline. Using the proposed image analysis, we aim to quantitatively measure the effects on LD morphology and lipolysis rate for each gene. The results from this screen are compared with clinical measures in our cross-sectional and prospective cohorts. This will constitute an invaluable resource for in-depth and hypothesis-driven analyses, which will improve our understanding of the mechanisms controlling human adipocyte lipolysis. See Figure 7.

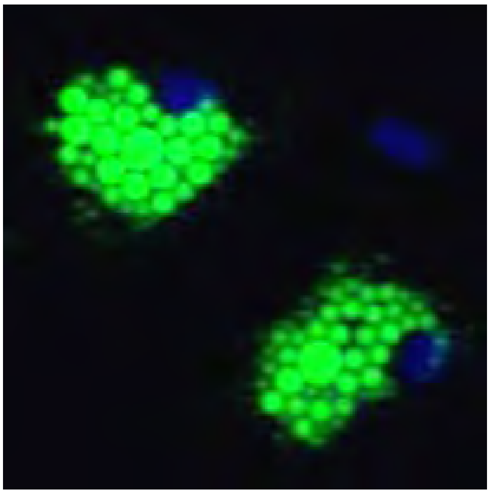

Figure 7: Quantification of lipid droplets in human pre-adipocyte

5. **Ubiquitin Screen**
   Carolina Wählby, Petter Ranefall
   Partner: Johan Boström, Jordi Carreras Puigvert, Mikael Altun, Dept. of Medical Biochemistry and Biophysics, Karolinska Institute
   Funding: SciLifeLab BioImage Informatics Facility (www.scilifelab.se/facilities/bioimage-informatics)
   Period: 201502—-
   Abstract: Ubiquitin is a small protein that is found in almost all cellular tissues in humans and other eukaryotic organisms, which helps to regulate the processes of other proteins in the body. Cultured cells respond to treatments such as silencing of genes or exposure to radiation and/or drugs by changing their morphology, giving us hints on mechanisms of action. We develop methods for image-based high-throughput screening to identify subtle changes in individual cells, not accessible by bulk-methods, here focusing on the ubiquitin pathway. See Figure 8.

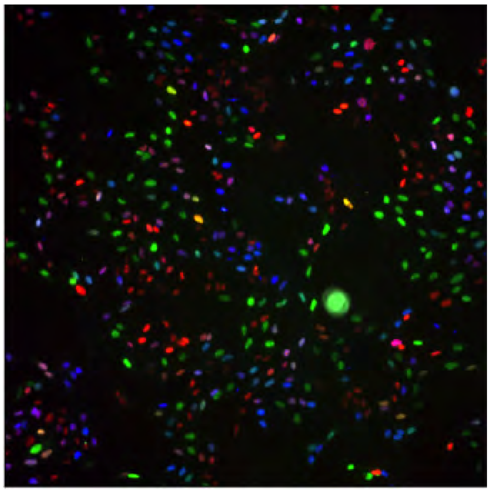

Figure 8: Ubiquitin Screen

6. **Analysis of Keratin Aggregates**
   Petter Ranefall, Carolina Wählby
   Partner: Hanqian Zhang and Hans Törmä, Dept. of Medical Sciences, UU
   Funding: SciLifeLab BioImage Informatics Facility (www.scilifelab.se/facilities/bioimage-informatics)
   Period: 201510—-
   Abstract: Epidermolytic hyperkeratosis (EH) is a rare genetic skin disorder caused by mutation of keratin 1 or 10, and characterized by blistering in the epidermis and hyperkeratosis. The skin may blister easily following mechanical injury and exposure to heat etc. Immortalized keratinocyte cell lines were established by our collaborators at the Dept. of Medical Sciences, Dermatology and Venereology, and these cell lines show promise as a screening model to test new potential drugs for treating EH patients. Large-scale screening requires robust, efficient and effective image analysis methods, and we are currently developing methods to analyze keratin aggregates in cultured EH cells. See Figure 9.

7. **Vascular Networks**
   Petter Ranefall, Carolina Wählby
   Partner: Elisabet Olin, Ross Smith, Chiara Testini, Lena Claesson-Welsh, Dept of Immunology, Genetics and Pathology, UU
   Funding: SciLifeLab BioImage Informatics Facility (www.scilifelab.se/facilities/bioimage-informatics)
   Period: 201406—-
   Abstract: In this project we analyze vascular networks in the mouse brain, retina networks and cell junction activations. We have several applications where we skeletonize the networks and extract branch points in the skeleton. For the cell junction activations we have initially used an approach where we compute the area of the activated junctions (green) between the cells and use that as a measurement of activation. See Figure 10.

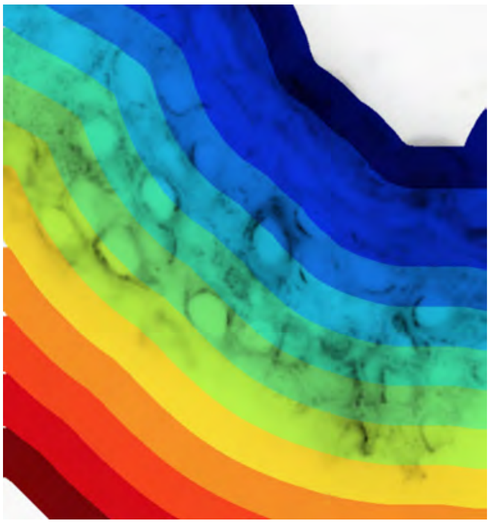

Figure 9: Analysis of Keratin Aggregates

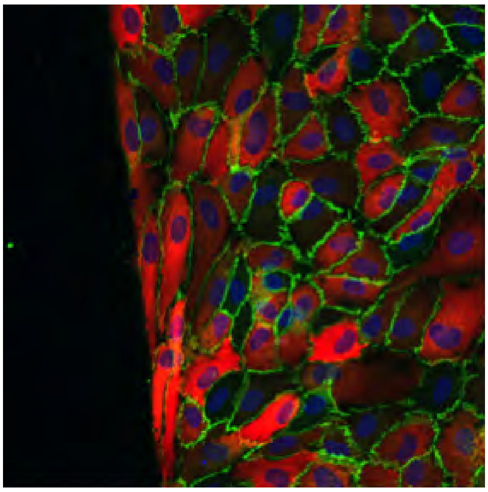

Figure 10: Vascular Networks

8. **Segmentation and Tracking of E.coli Bacteria in Bright-Field Microscopy Images**
   Sajith Kecheril Sadanandan, Carolina Wählby, Petter Ranefall
   Partner: Johan Elf, David Fange, Alexis Boucharin, Dept. of Cell and Molecular Biology, UU; Klas E. G. Magnusson, Joakim Jalden, ACCESS Linnaeus Centre, KTH.
   Funding: SciLifeLab, eSSENCE, VR junior researcher grant to CW
   Period: 201210—-
   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. We developed a novel method for the E.coli cell segmentation using deep neural networks. This new method was able to detect irregular and unusually large cells present in the sample. The methods and results were published in a paper in the Bioimaging workshop as part of European Conference on Computer Vision 2016. See Figure 11.

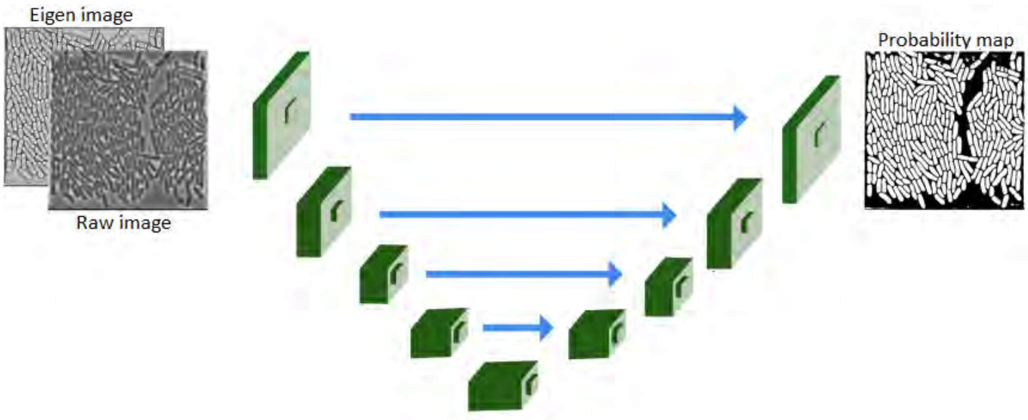

Figure 11: Segmentation and Tracking of E.coli Bacteria in Bright-Field Microscopy Images

9. **SciLifeLab Cancer Stem Cell Program**
Damian Matuszewski, Petter Ranefall, Carolina Wählby, Ida-Maria Sintorn, Andre Liebscher
Partner: Sven Nelander, Ingrid Lönnstedt, Cecilia Krona, Linnéa Schmidt, Karin Forsberg-Nilsson, Irina Alafuzoff, Ulf Landegren, Anna Segerman, Tobias Sjöblom, Lene Urborn, and Bengt Westermark - Dept. of Immunology, Genetics and Pathology and SciLifeLab, UU; Bo Lundgres - Karolinska Institute and SciLifeLab, Stockholm; Rebecka Jörnsten - Mathematical Sciences, Chalmers, Gothenburg; and Göran Hesselager - Dept. of Neuroscience, UU
Funding: AstraZeneca-SciLifeLab Joint Research Program
Period: 201303—-
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 characterized 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. Patient data is continously collected, and close to one hundred primary cell lines have been established. The cultured cells are exposed to known and novel drug compounds at varying doses, and imaged by fluorescence as well as bright-field microscopy. In 2016 algorithms for cell cycle analysis and automatic selection of potentially effective treatments were developed. See Figure 12.

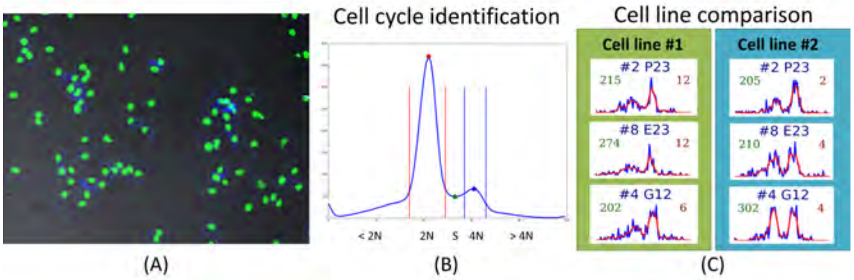

Figure 12: SciLifeLab Cancer Stem Cell Program

10. **A Smart and Easy Platform to Facilitate Ultrastructural Pathologic Diagnoses**
Amit Suveer, Nataša Sladoje, Joakim Lindblad
Partner: Ida-Maria Sintorn - Vironova AB, Stockholm; Anca Dragomir - Dept. of Immunology, Genetics and Pathology, UU; Kjell Hultenby - Dept. of Laboratory Medicine, Karolinska Institute, Stockholm

Funding: MedTech4Health, Vinnova; TN-Faculty, UU
Period: 20160109–
Abstract: TEM is an essential diagnostic tool for screening human tissues at the *nm*-scale. It is the only option in some cases and considered as gold standard for diagnosing several disorders, e.g. cilia and renal diseases, rare cancers to name a few. The high resolution of TEM provides unique morphological information, significant for diagnosis and personalized care management. However, the microscope is expensive, technically complex, bulky, needs a high level of expertise to operate, and still diagnosis is subjective and time-consuming. In this project we are collaborating with microscope manufacturers, pathologists, and microscopists, to develop the next generation smart software and easy platform that will significantly simplify and enhance the TEM imaging and analysis experience. The work includes automated steering of a TEM microscope for the search for regions of interest, followed by automatic multiscale imaging and processing of the images of acquired regions. The results for cilia detection using CNN at low-resolution is reported in SCIA'17 with an area under PR-curve reaching 0.71 and a significant reduction in false-positives. And the result of super-resolution cilium reconstruction by registering multiple high-resolution cilia cross-sectional cut-outs is also reported in SCIA'17 with 2.35±1.82 pixels as the average pixel alignment error during the registration. See Figure 13.

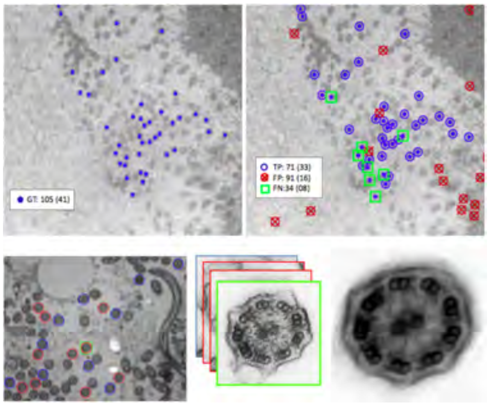

Figure 13: A smart and easy platform to facilitate ultrastructural pathologic diagnoses

11. **Advanced Methods for Reliable and Cost Efficient Image Processing in Life Sciences**
Nataša Sladoje, Joakim Lindblad, Ewert Bengtsson, Ida-Maria Sintorn
Partner: Marija Delić, Buda Bajić, Faculty of Technical Sciences, University of Novi Sad, Serbia
Funding: VINNOVA; TN-Faculty; Swedish Research Council
Period: 201308—-
Abstract: Within this project our goal is to increase reliability, efficiency, and robustness against variations in sample quality, of computer assisted image analysis in two particular research tracks, related to two applications: (1) Chromatin distribution analysis for cervical cancer diagnostics, and (2) Virus detection and recognition in TEM images. Efficient utilization of available image data to characterize barely resolved structures, is crucial in both the considered applications. We rely on theoretical work in discrete mathematics, which provides methods which enable preservation and efficient usage of information, aggregate information of different types, improve robustness of the developed methods and increase precision of the analysis results. During 2017, we have developed, applied and evaluated (quantitatively and qualitatively) several denoising methods on TEM images. This study is summarized in a paper accepted for the IEEE International Symposium on Biomedical Imaging (ISBI) 2018. We have presented our developed distance measures between multi-channel representations of image objects at two international conferences (ISMM and IWCIA). We have presented our results on developing a pipeline for automated detection and analysis of TEM images of cilia at SCIA 2017. We have continued with developing texture descriptors suitable for TEM images, which offer a good balance between simplicity and performance. See Figure 14.

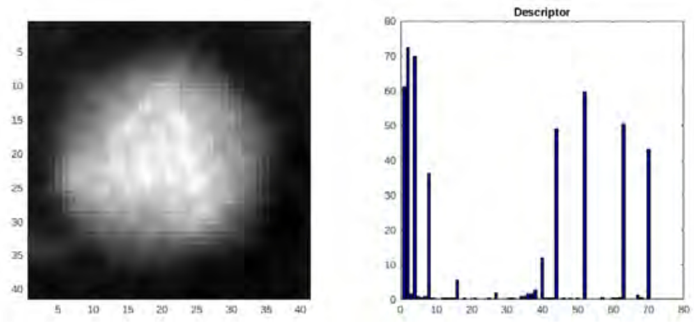

Figure 14: Advanced Methods for Reliable and Cost Efficient Image Processing in Life Sciences

12. **Visualization of Uncharacterized Archaea in Lake and Marine Sediments**
Petter Ranefall, Carolina Wählby
Partner: Disa Bäckström, Thijs Ettema, Dept. of Cell and Molecular Biology, UU.
Funding: SciLifeLab
Period: 20170302–
Abstract: Most of the archaea found in marine and lake sediments have only been characterized by their 16S sequences or by metagenomic binning. The goal of the current project is to assess the archaeal diversity in sediments from Århus Bay, Lake Erken and Lake Plåten and visualize the cells through fluorescent in situ hybridization (FISH). This allows us to study the morphology of poorly characterized archaeal lineages. Once a reliable protocol for has been developed it opens up for the possibility to proceed with targeted cell sorting and single cell genomics. It is difficult to analyse the images by eye in a standardized and objective way, so CellProfiler will be used to process the images and determine the ratio of cells with positive hybridization signal. See Figure 15.

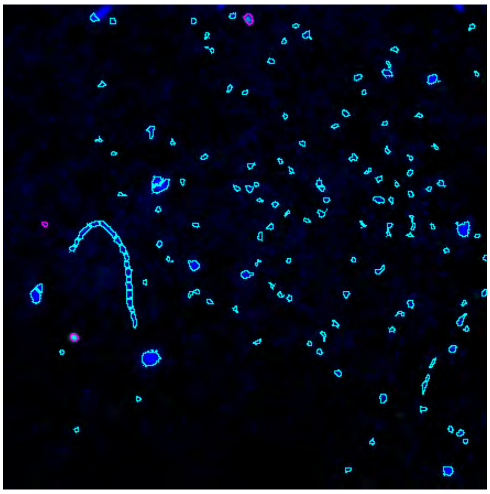

Figure 15: Visualization of uncharacterized archaea in lake and marine sediments

13. **Protein Inheritance in Asymmetric Cell Division**
Petter Ranefall, Carolina Wählby
Partner: Alexander Julner-Dunn(1), Zhijian Li(2), Charles Boone(2) and Victoria Menendez-Benito(1), (1)Dept. of Biosciences and Nutrition, Karolinska Institute, Stockholm; (2)The Donelly Center, University of Toronto, Canada
Funding: SciLifeLab
Period: 20170428–
Abstract: In some cells, such as yeast and stem cells, proteins are asymmetrically inherited during cell division. By doing this, cells can control cell fate and protect specific progeny from aging. Examples of

age-dependent symmetric inheritance include centrosomes, histones, oxidized proteins and old mitochondria. Yet, we do not have a global view on which proteins in the cell are asymmetrically inherited. In this project, we address this question by developing a systems-based approach to explore protein inheritance in yeasts. We use a technique, named recombination induced epitope tag (RITE), which is a living pulse-chase that allows tracking old (maternal) and new proteins by genetic switching between two fluorescent protein fusions. Our specific goals are: 1. To create the first yeast library for single-cell analysis of protein inheritance, by tagging each gene with RITE at its chromosomal location. 2. To generate a map of the proteome inheritance in budding yeast, by measuring the abundance and localization of old/new proteins in the yeast RITE library, using high-content microscopy and automated image analyses. We will generate resources, data and novel information that will facilitate the discovery of new asymmetries in protein inheritance that control cell fate, epigenetic memory and/or cellular ageing. See Figure 16.

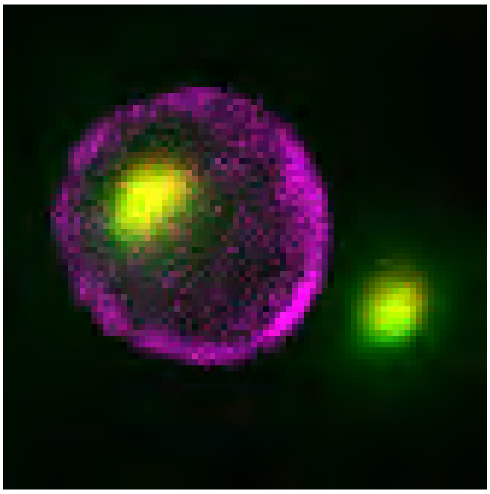

Figure 16: Protein inheritance in asymmetric cell division

14. **Influence of the Extracellular Matrix on the Epithelial Cell Microenvironment**
Petter Ranefall, Carolina Wählby
Partner: Katie Hansel, Molly Stevens(1,2), (1)Dept. of Medical Biochemistry and Biophysics, Karolinska Institute, Stockholm, (2) Imperial College, London
Funding: SciLifeLab
Period: 20170517–
Abstract: The collaborators are studying the influence of the extracellular matrix (ECM) on the epithelial cell microenvironment, since the ECM influences the bulk, shape and strength of many tissues in vivo. The basement membrane (BM) is a thin layer of specialised ECM consisting primarily of laminin and collagen that lines all epithelia and guides cell adhesion, polarity and differentiation. During the epithelial-to-mesenchymal transition (EMT), polarized epithelial cells lose their adherens junctions and tight junctions and transition to a migratory mesenchymal phenotype which is able to disrupt and penetrate through the BM, an event at the onset of cancer metastasis and tissue fibrosis. This transition is associated with the formation of prominent stress fibres and mature focal adhesions, along with a change in matrix metalloproteinase (MMP) expression and activation of multiple signalling pathways. The group has identified a biologically-active fragment of the $\beta 1$-chain of laminin that is released by matrix metalloproteinase 2 (MMP2) in the course of EMT. This laminin-$\beta 1$ fragment has been shown to modulate EMT signalling via $\alpha 3 \beta 1$–integrin expressed on the surface of epithelial cells. See Figure 17.

15. **qUTI - a Point-Of Care Test for Fast Diagnosis of Urinary Tract Infections**
Petter Ranefall
Partner: Özden Baltekin, Johan Elf, Ove Öhman, Astrego Diagnostics AB, Uppsala
Funding: Astrego Diagnostics AB
Period: 20170404–
Abstract: The emergence and spread of antibiotic-resistant bacteria are aggravated by incorrect prescription

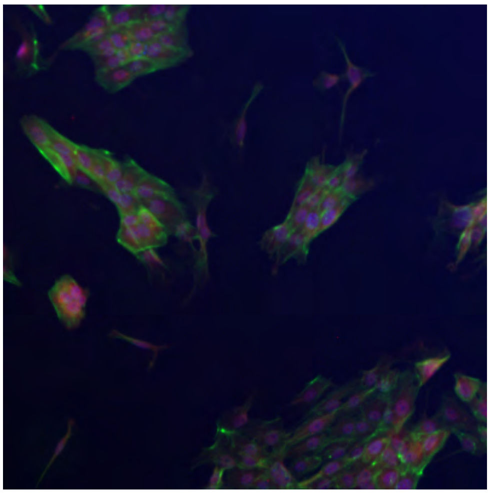

Figure 17: Influence of the extracellular matrix on the epithelial cell microenvironment

and use of antibiotics. A core problem is that there is no sufficiently fast diagnostic test to guide correct antibiotic prescription at the point of care. Here, we investigate if it is possible to develop a point-of-care susceptibility test for urinary tract infection, a disease that 100 million women suffer from annually and that exhibits widespread antibiotic resistance. We capture bacterial cells directly from samples with low bacterial counts (104 cfu/mL) using a custom-designed microfluidic chip and monitor their individual growth rates using microscopy. By averaging the growth rate response to an antibiotic over many individual cells, we can push the detection time to the biological response time of the bacteria. We find that it is possible to detect changes in growth rate in response to each of nine antibiotics that are used to treat urinary tract infections in minutes. In a test of 49 clinical uropathogenic Escherichia coli (UPEC) isolates, all were correctly classified as susceptible or resistant to ciprofloxacin in less than 10 min. The total time for antibiotic susceptibility testing, from loading of sample to diagnostic readout, is less than 30 min, which allows the development of a point-of-care test that can guide correct treatment of urinary tract infection. See Figure 18.

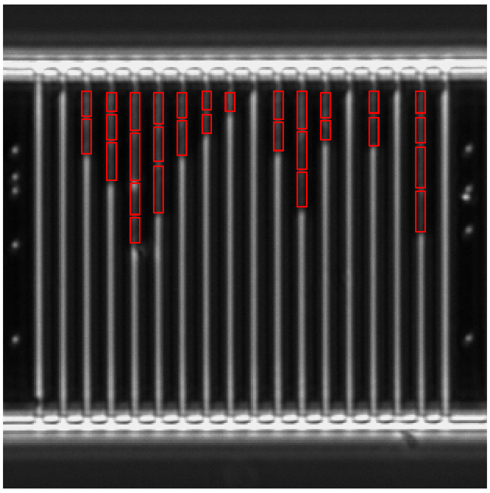

Figure 18: qUTI - A point-of care test for fast diagnosis of urinary tract infections

16. **Applying Semi-Automated Histology-To-Radiology Co-Registration in en Bloc Resected Gliomas**
Petter Ranefall
Partner: Kenney Roodakker, Anja Smits, Dept. of Neurology, UU
Funding: SciLifeLab BioImage Informatics Facility (www.scilifelab.se/facilities/bioimage-informatics)
Period: 20171130–

Abstract: Gliomas are heterogeneous tumors in terms of imaging appearances, and a deeper understanding of the histopathological tumor characteristics that underlie the signal abnormalities on PET and MRI is needed. Here we used histology-to-radiology co-registration of gliomas with the aim to correlate local changes in tumor perfusion and 11C-methionine uptake with cell density, vascularity and proliferation in these areas. See Figure 19.

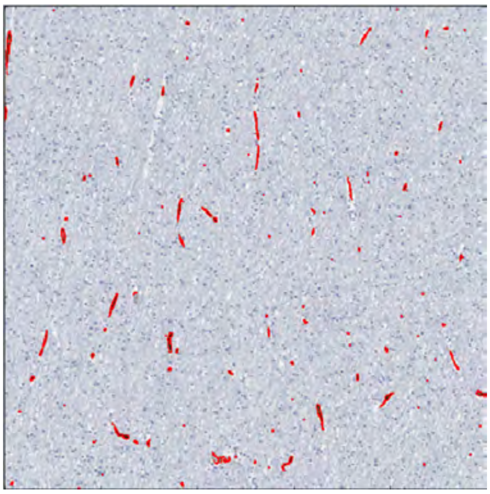

Figure 19: Applying semi-automated histology-to-radiology co-registration in en bloc resected gliomas

17. **Intracellular Trafficking Pathways of PDGFRβ**
Petter Ranefall, Carolina Wählby
Partner: Natalia Papadopoulos, Carl-Henrik Heldin, Dept. of Medical Biochemistry and Microbiology, Uppsala Universiyty
Funding: SciLifeLab BioImage Informatics Facility (www.scilifelab.se/facilities/bioimage-informatics)
Period: 20171204–
Abstract: This project investigates trafficking pathways of PDGFRβ from the cell surface upon activation with PDGF-BB ligand. PDGFRβ is known to form dot-like clusters upon activation that only partially co-localize with the known markers of intracellular organelles. This project is designed to identify novel markers and trafficking pathways of PGDFRβ. In order to distinguish between the PDGFRβ localized at the cell surface and the intracellular pools, the cell surface PDGFRβ is labelled with biotin. Thus, confocal microscopy with triple staining is used to estimate the co-localization of signals between the three types of molecules: biotin, PDGFRβ and organelle marker. The pipeline is used to analyze the images and estimate the presence of biotinylated PDGFRβ within a given organelle.

18. **Imaging Protein Synthesis in Primary Cortical Neuronal Culture Using Click-It-Registered Plus OPP Protein Synthesis Assay Kits**
Petter Ranefall
Partner: Rekha Tripathi, Dept. of Pharmaceutical Biosciences, UU
Funding: SciLifeLab BioImage Informatics Facility (www.scilifelab.se/facilities/bioimage-informatics)
Period: 20171201–
Abstract: The goal of this project is to analyze protein translation rate in mouse primary cortical neurons and astrocytes. The aim is to assess the protein synthesis by using the OPP Kit in primary cortical cultures of wild type and SLC38A10-/- Knockout mice. To understand role of SLC38A10 in protein regulation in neurons and astrocytes. We are using Cell Profiler to measure fluorescence intensity. See Figure 20.

19. **HASTE: Hierarchical Analysis of Spatial and Temporal Data**
Carolina Wählby, Håkan Wieslander
Partner: Andreas Hellander, Salman Toor, Ben Blamey and Lovisa Lugnegård, Dept. of Information Technology, UU, Ola Spjuth, Niharika Gauraha and Phil Harrison, Dept. of Pharmaceutical Biosciences, UU, Markus M. Hilscher, SciLifeLab, Dept. of Biochemistry and Biophysics, Stockholm University, Ida-Maria Sintorn, Vironova AB, Lars Carlsson, Johan Karlsson, Alan Sabirsh and Ola Engkvist, AstraZeneca AB,

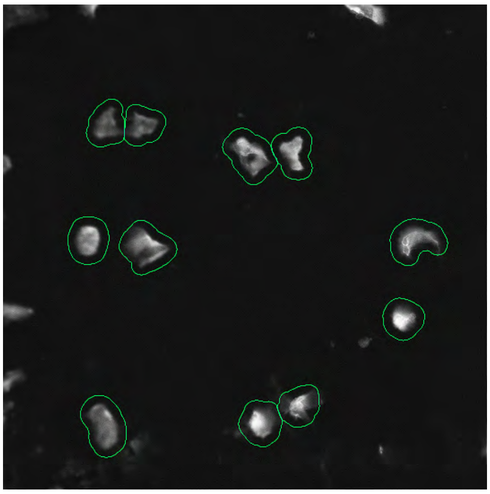

Figure 20: Imaging protein synthesis in primary cortical neuronal culture using Click-iT-registered Plus OPP Protein Synthesis Assay Kits

Mölndal, Mats Nilsson, Dept. of Biochemistry and Biophysics, Stockholm University
Funding: Swedish Foundation for Strategic Research (SSF)
Period: 20170103–
Abstract: Images contain very rich information, and digital cameras combined with image processing and analysis can detect and quantify a range of patterns and processes. The valuable information is however often sparse, and the ever increasing speed at which data is collected results in data-volumes that exceed the computational resources available. The HASTE project takes a hierarchical approach to acquisition, analysis, and interpretation of image data. We develop computationally efficient measurements for data description, confidence-driven machine learning for determination of interestingness, and a theory and framework to apply intelligent spatial and temporal information hierarchies, distributing data to computational resources and storage options based on low-level image features. At Vi2 we focus on developing the efficient measurements that will identify non-informative data early on in the analysis process; either online at data collection, or off-line prior to full data analysis. The challenge is to use minimal computational time and power to extract a broad range of informative measurements from spatial-, temporal-, and multi-parametric image data, useful as input for conformal predictions and efficient enough to work well in a streaming setting. http://haste.research.it.uu.se/ See Figure 21.

20. **Multi-Layer Object Representations for Integrated Shape and Texture Analysis with Applications in Biomedical Image Processing**
Elisabeth Wetzer, Natasa Sladoje, Joakim Lindblad
Partner: Ida-Maria Sintorn, Lars Haag - Vironova AB
Funding: Centre for Interdisciplinary Mathematics, TN-Faculty, UU
Period: 20171001–
Abstract: The aim of the project is to develop the theoretical foundation for a class of methods applicable to multi-layered heterogeneous object representations and to apply and evaluate these methods in clinical biomedical applications. In particular, texture descriptors are applied to multi-scale data in order to allow for the search of candidate areas that are likely to hold objects of interest in low resolution images. Classical machine Learning techniques as well as deep learning will provide a tool for feature selection to reduce the high dimensional feature space of the data. Optimization routines and similarity measures will be adapted or derived to improve the classification. The framework will be used for automatic object detection, classification and registration among many applications. A close collaboration with Vironova AB provides an environment to implement, test and validate the obtained theoretical concepts by providing samples, images, as well as the miniTEM, a transmission electron microscope developed by Vironova. See Figure 22.

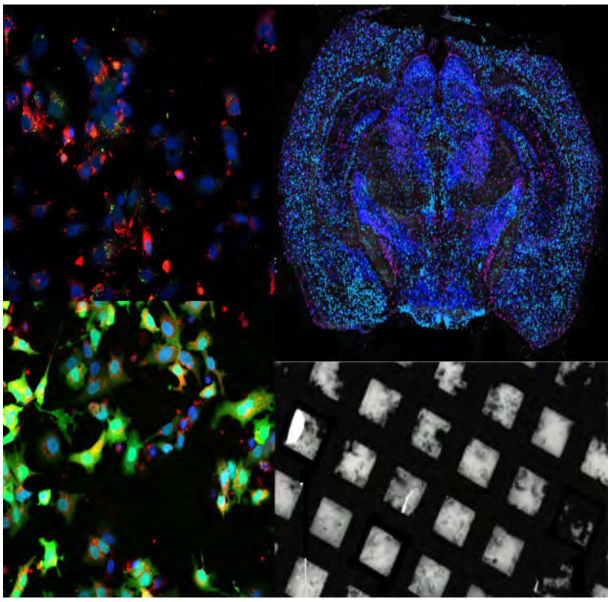

Figure 21: HASTE: Hierarchical Analysis of Spatial and Temporal Data

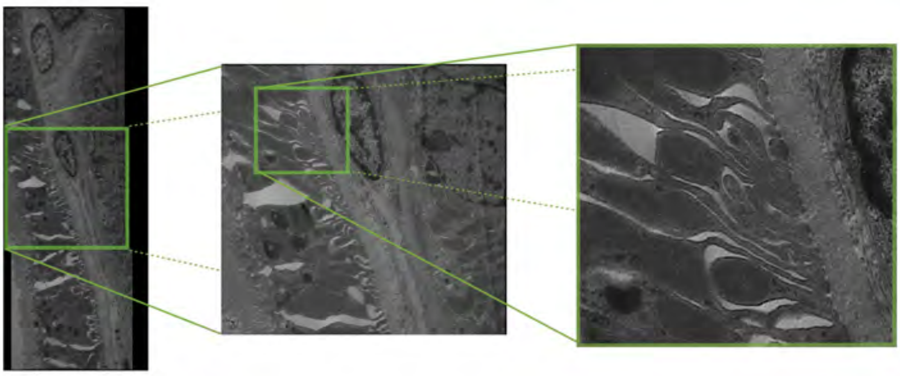

Figure 22: Multi-layer object representations for integrated shape and texture analysis with applications in biomedical image processing

21. **Human Induced Pluripotent Cells Derived Neuroepithelial-Like Cells Differentiation Potential in the Presence of the Mouse Auditory Brainstem Milieu**
    Petter Ranefall, Carolina Wählby
    Partner: Andreas Kaiser, Ekaterina Novozhilova, Petri Olivius, Dept. of Surgical Sciences, UU
    Funding: SciLifeLab BioImage Informatics Facility (www.scilifelab.se/facilities/bioimage-informatics)
    Period: 20170120–
    Abstract: Stem cell therapy has been proposed as an option to treat sensorineural hearing loss since auditory system as well as the most of the central nervous system has a limited regenerative potential. The treatment of neurodegenerative diseases has been studied through the cell-based approach over the past years. Replacement of the damaged spiral ganglion neurons in the inner ear, the first-order neurons of the auditory pathway, with precursor cells would be a way to improve hearing function in patients with malfunctions of the auditory system including patients in need of a cochlear implant. In our project we use mouse organotypic auditory brainstem slice culture as a screening platform for donor cells differentiation potential to further proceed with in vivo studies. See Figure 23.

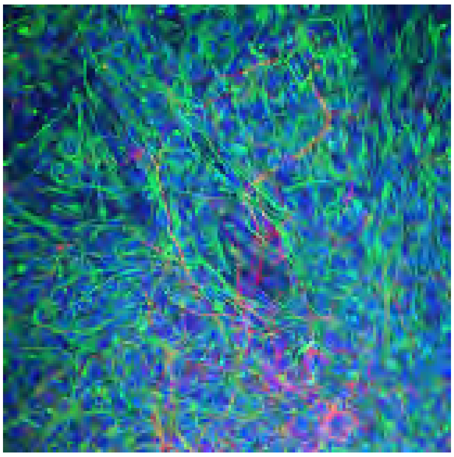

Figure 23: Human induced pluripotent cells derived neuroepithelial-like cells differentiation potential in the presence of the mouse auditory brainstem milieu

22. **Image- and AI-Based Cytological Cancer Screening**
    Joakim Lindblad, Ewert Bengtsson, Carolina Wählby
    Partner: Dr Christina Runow Stark - Medicinsk Tandvård, Folktandvården AB, Stockholm; Dr Eva Ramquist - Karolinska Hospital, Stockholm; Prof. Jan-Michaél Hirsch - Medicinsk Tandvård, Södersjukhuset; Dr. Kunjuraman Sujathan - Regional Cancer Centre, Kerala, India
    Funding: VINNOVA through MedTech4Health, AIDA
    Period: 20171001–
    Abstract: Oral cancer incidence is rapidly increasing worldwide, with over 450,000 new cases found each year. The most effective way of decreasing cancer mortality is early detection, which makes routine screening of patient risk groups highly desired. However, screening for oral cancer is not feasible with today's methods that rely on painful tissue sampling and laborious manual examination by a medical expert. A consequence is that oral cancer is often discovered as late as when it has metastasized to another location. Prognosis at this stage of discovery is significantly worse than when it is caught in a localized oral area. Within this project, we aim to develop a system that uses artificial intelligence (AI) to automatically detect oral cancer in microscopy images of brush samples, which can quickly and without pain be routinely taken at ordinary dental clinics. We expect that the proposed approach will be crucial for introducing a screening program for oral cancer at dental clinics, in Sweden and the world. The project, which involves researchers from UU, Karolinska University Hospital, Folktandvården Stockholms län AB, and the Regional Cancer Center in Kerala, India, will greatly benefit from AIDA to turn developed methods into clinically useful tools. See Figure 24.

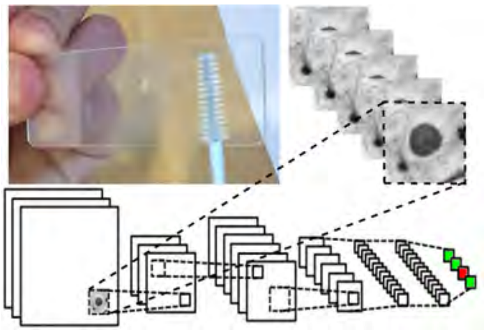

Figure 24: Image- and AI-based cytological cancer screening

5.2 Microscopy, model organisms and tissues

23. **Effects of Mixtures of Endocrine Disrupting Compounds (EDC) on Wnt/Beta-Catenin Signaling in Developing Zebrafish**
Petter Ranefall, Carolina Wählby
Partner: Maria Jönsson - Dept. of Organismal Biology, Environmental Toxicology, UU
Funding: SciLifeLab BioImage Informatics Facility (www.scilifelab.se/facilities/bioimage-informatics)
Period: 20160902–
Abstract: Wnt/beta-catenin signaling is involved in proliferation and fate of cells thus playing fundamental roles during embryo development. The specific aims of this part of the EU project are to 1) develop methods for detection of chemically induced changes in Wnt/beta-catenin signaling and to 2) determine developmental effects of EDC mixtures on Wnt/beta-catenin signaling. EDC-induced changes in Wnt/beta-catenin signaling are visualized and studied by transgenic zebrafish carrying a beta-catenin signaling fluorescent reporter (Tcf/Lef-miniP: d2EGFP). See Figure 25.

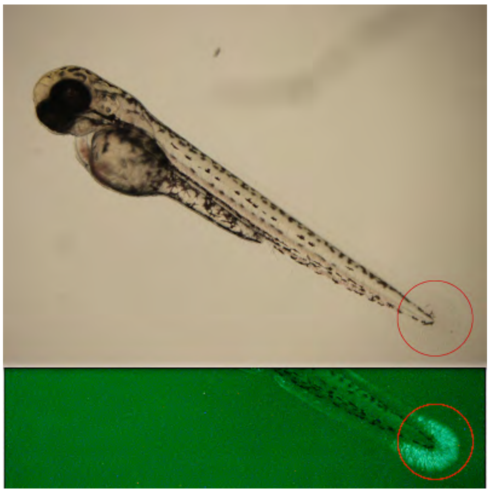

Figure 25: Effects of mixtures of endocrine disrupting compounds (EDC) on Wnt/beta-catenin signaling in developing zebrafish

24. **Kidney Morphology and Topology of the Glomerular Filtration Barrier**
Petter Ranefall, Carolina Wählby
Partner: David Unnersjö Jess, Hans Gunnar Blom - Dept. of Applied Physics, KTH
Funding: SciLifeLab BioImage Informatics Facility (www.scilifelab.se/facilities/bioimage-informatics)
Period: 20151008–
Abstract: Our collaborators have developed a super-resolution immunofluorescence microscopy protocol for the study of the filtration barrier in the kidney. The aim of the project is to quantitatively evaluate the morphology and topology of the glomerular filtration barrier in the kidney. See Figure 26.

25. **Cell Distribution and Protein Expression in the Ectocervix**
Petter Ranefall, Carolina Wählby
Partner: Anna Gibbs, Gabriella Edfeldt, Maria Röhl, Annelie Tjernlund - Dept. of Medicine, Karolinska Institute, Stockholm
Funding: SciLifeLab BioImage Informatics Facility (www.scilifelab.se/facilities/bioimage-informatics)
Period: 20150401–
Abstract: This research project is focused on mucosal immunology in the female genital tract and HIV. The female genital mucosa presents a comprehensive natural immune defense against HIV infection, although during exposure to a high dose of virus this is not enough to protect the individual against viral transmission. Some individuals have a stronger resistance against HIV than others and therefore it is highly important to investigate which factors that contribute to an effective local protection against sexual infection. The aim of this study is to quantify gene expression in the target cells of HIV in ectocervix, and measure the distance to

the vaginal lumen, as well as epithelial thickness. These parameters will be compared in women involved in sex work between the groups of HIV-infected, highly HIV exposed HIV-uninfected that seems to be resistant, and HIV-uninfected women who have been involved in sex work for a short period. See Figure 27.

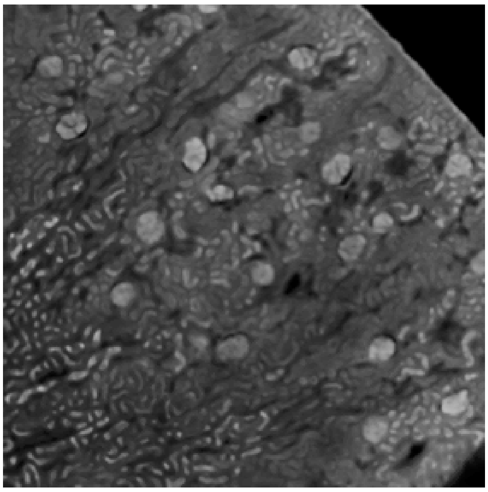

Figure 26: Kidney Morphology and Topology of the Glomerular Filtration Barrier

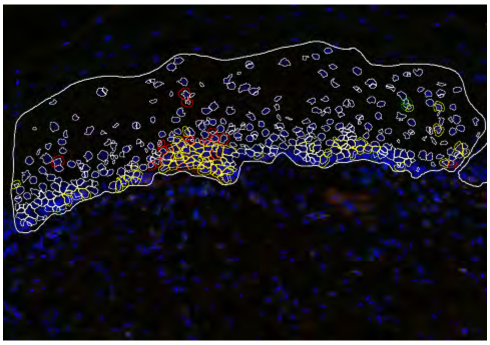

Figure 27: Cell Distribution and Protein Expression in the Ectocervix

26. **Quantification of Zebrafish Lipid Droplets**
Petter Ranefall, Carolina Wählby
Partner: Marcel den Hoed, Manoj Bandaru, Anastasia Emmanouilidou - Dept. of Medical Sciences and SciLifeLab, UU
Funding: SciLifeLab BioImage Informatics Facility (www.scilifelab.se/facilities/bioimage-informatics)
Period: 20130801–
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 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. We have also developed methods for length and volume measurements as well as quantification of macrophages, neutrophils, IK17 and the overlap with these expressions and stationary lipids. Our results confirm that zebrafish larvae represent a promising model system for early-stage atherosclerosis. See Figure 28.

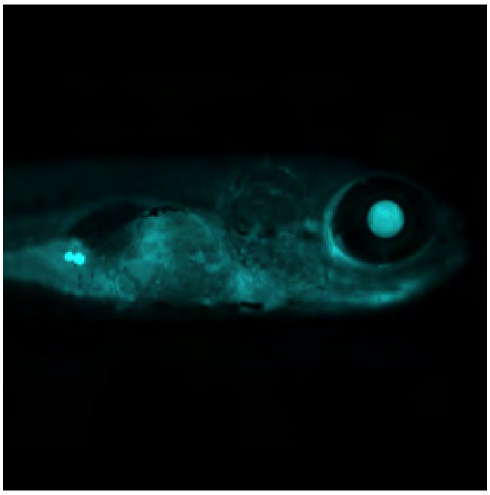

Figure 28: Quantification of Zebrafish Lipid Droplets

27. **Pigment Gene Expression in the Early Developing Crow Feather**
    Petter Ranefall, Carolina Wählby
    Partner: Chi-Chih Wu, Axel Klaesson, Ola Söderberg, Jochen Wolf - Dept. of Immunology, Genetics and Pathology, UU
    Funding: SciLifeLab
    Period: 20161108–
    Abstract: The project is to quantify and compare pigment-associated gene expressions between two closest related crow species that carrion crow has black feathers and hooded crow has gray feathers in the belly. The cooperators have adapted in situ PLA with padlock probes to label targeted mRNAs across varied developmental stages of melanocytes in feathers. We are developing a CellProfiler pipeline and scripts to recognize and quantify signals across complex tissues with strong autofluorescence. See Figure 29.

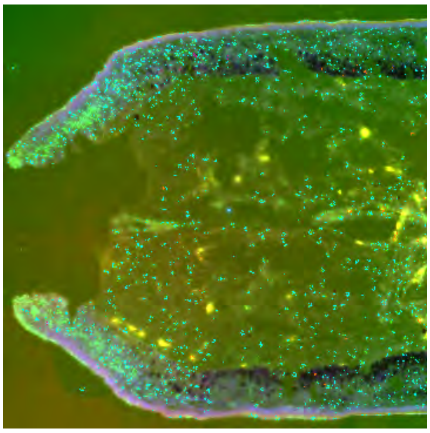

Figure 29: Pigment gene expression in the early developing crow feather

28. **In Vivo Modeling of High Grade Glioma for Oncology Drug Developments**
    Petter Ranefall, Carolina Wählby
    Partner: Riasat Islam, Cecilia Krona and Sven Nelander. Dept. of Immunology, Genetics and Pathology, UU
    Funding: SciLifeLab BioImage Informatics Facility (www.scilifelab.se/facilities/bioimage-informatics)
    Period: 20161007–
    Abstract: The main goal of this study was to develop a platform for quantifying the tumor-initiating capacity of a large panel of glioma-stem cell cultures (GSCs) in adult mouse brain to define the cancer stem-cell like

property of the individual cultures and to integrate the result with genomic and transcriptional profiling of the GSCs. In order to achieve this, adherently grown GFP-luciferase GSC cultures were dissociated and injected stereotactically into the brain of immunodeficient mice. Tumor growth was monitored in vivo by bioluminescence imaging for up to 40 weeks and brains were collected for histopathological and immunohistochemical stainings. Automatic quantification and growth pattern analysis of tumor cells in brain sections was set up based on human cell specific staining using NuMa antibodies and a CellProfiler Analyst machine learning classifier with a manual observer correlation of 0.86. Tumors were identified in brains from mice injected with 15/29 GSC cultures, suggesting these cells as a valuable resource for future preclinical therapeutic studies targeting predicted vulnerabilities for individual glioma patients. See Figure 30.

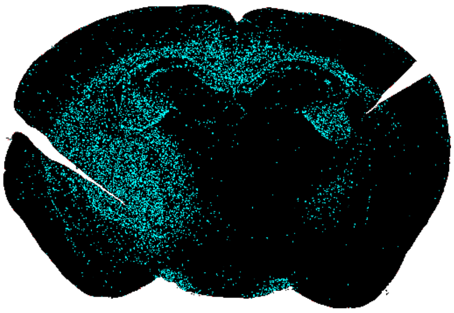

Figure 30: In vivo modeling of high grade glioma for oncology drug developments

29. **Effect of Perfluorononanoic Acid (PFNA) on Early Embryo Development in Vitro**
    Petter Ranefall, Carolina Wählby
    Partner: Ida Hallberg, Ylva Sjunnesson, Dept. of Clinical Sciences, SLU
    Funding: SciLifeLab
    Period: 20170119–
    Abstract: For the last decades a concern has been raised that female fertility is declining more than could be explained by the fact that we choose to have children later in life and possible genetic effects. Subfertility and infertility is a devastating experience for those who are affected and as the subject is also somewhat of a taboo the numbers affected are most likely higher than perceived among the general public. In our environment, we are continuously exposed to a number of exogenous chemicals, originating from industries, agriculture and other. As many of these chemicals show persistence and are very bio-accumulative, they will concentrate higher up in the food-chain, in both wildlife and humans. Many of the chemicals are new and have yet not been investigated regarding their full toxicological potential.Perfluorononanoic acid (PFNA) This project aim to further investigate perfluorononanoic acid (PFNA) and its effect on the early embryo development. This chemical is closely related to know toxic substances such as PFOS and PFOA, but is in contrary to those little research has yet been done regarding PFNAs potential toxicological effects. We have used a bovine model, where we collect material from the slaughter-house. See Figure 31.

30. **Objective Automated Quantification of Fluorescence Labeling in Histologic Sections of Rat Lens**
    Carolina Wählby
    Partner: Per Söderberg and Nooshin Talebizadeh, Dept. of Neuroscience, UU
    Funding: SciLifeLab
    Period: 20150101–20170501
    Abstract: The lens epithelium of the eye is a single layer of cells covering the anterior face of the lens. In this project we study how UV light affects the lens epithelial cells by quantitatively analyzing fluorescent signal from biomarkers in cell nuclei and cytoplasms. We have developed an automated method to delineate lens epithelial cells and to quantify expression of fluorescent signal of biomarkers in each nucleus and cytoplasm of lens epithelial cells in a histological section. A paper was published in Cytometry in May 2017. See Figure 32.

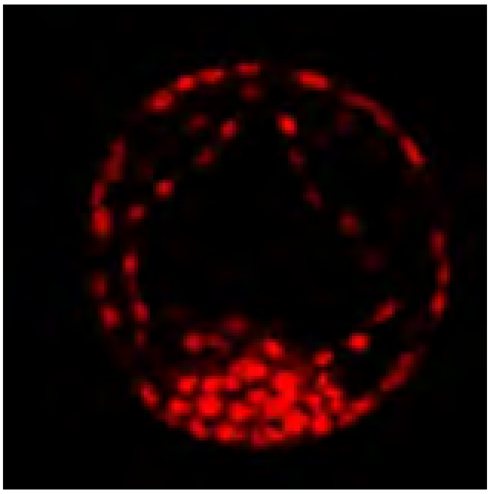

Figure 31: Effect of perfluorononanoic acid (PFNA) on early embryo development in vitro

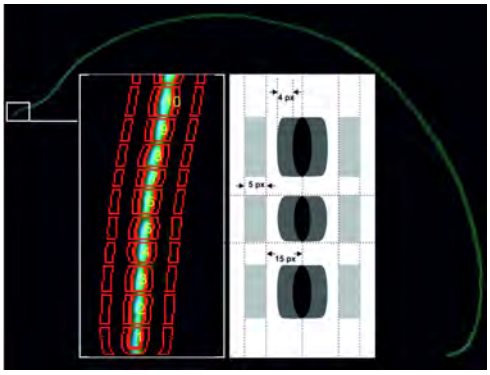

Figure 32: Objective Automated Quantification of Fluorescence Labeling in Histologic Sections of Rat Lens

31. **A Model System for Analysis of Spinal Cord Injury**
    Carolina Wählby
    Partner: Nils Hailer and Nikos Schizas, Dept. of Surgical Sciences, UU
    Funding: SciLifeLab
    Period: 20150101–
    Abstract: Following spinal cord injury neurons die due to neurotoxicity and inflammation. We study these effects in a model system with spinal cord slice cultures, aiming to find methods to reduce neurotoxicity. Our focus is quantitative image analysis methods that delineate activated cells and quantify protein expression as a response to injury and treatment. See Figure 33.

32. **Automated Quantification of Zebrafish Tail Deformation for High-throughput Drug Screening**
    Sajith Kecheril Sadanandan, Omer Ishaq, Alexandra Pacureanu, Carolina Wählby
    Partner: Joseph Negri, Mark-Anthony Bray, Randall T. Peterson, Broad Institute of Harvard and MIT, Boston
    Funding: SciLifeLab Uppsala
    Period: 20160301–20170101
    Abstract: Zebrafish (Danio rerio) is an important vertebrate model organism in biomedical research, especially suitable for morphological screening due to its transparent body during early development. In this project we use deep learning approach for accurate high-throughput classification of whole-body zebrafish deformations in multifish microwell plates. Deep learning uses the raw image data as an input, without the need of expert knowledge for feature design or optimization of the segmentation parameters. We trained the

deep learning classifier on as few as 84 images (before data augmentation) and achieved a classification accuracy of 92.8% on an unseen test data set that is comparable to the previous state of the art (95%) based on user-specified segmentation and deformation metrics. Ablation studies by digitally removing whole fish or parts of the fish from the images revealed that the classifier learned discriminative features from the image foreground, and we observed that the deformations of the head region, rather than the visually apparent bent tail, were more important for good classification performance. A paper describing the methods and results is published in the Journal of Biomolecular screening in 2016. See Figure 34.

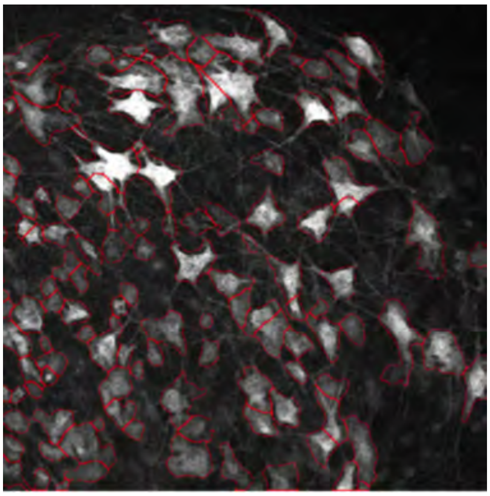

Figure 33: A Model System for Analysis of Spinal Cord Injury

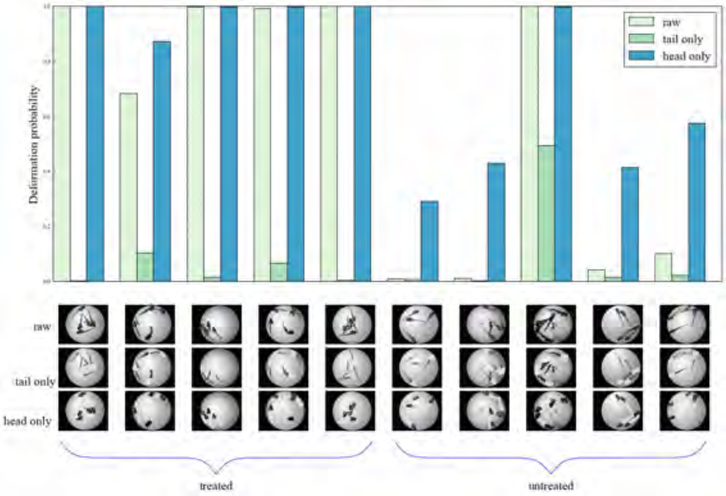

Figure 34: Automated Quantification of Zebrafish Tail Deformation for High-throughput Drug Screening

33. **CerviScan**
Ewert Bengtsson, Joakim Lindblad
Partner: Rajesh Kumar, Centre for Development of Advanced Computing (CDAC), Thiruvananthapuram, Kerala, India; K. Sujathan, Regional Cancer Centre, Thiruvananthapuram, Kerala
Funding: Swedish Governmental Agency for Innovation Systems (VINNOVA); Swedish Research Council; SIDA
Period: 20080101–
Abstract: Cervical cancer is a disease that annually kills over a quarter of a million women world-wide. This number could be reduced by screening for signs of cancer precursors using the well-established Pap-

test. However, visual screening requires highly trained cytotechnologists and is time consuming. 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, run by CDAC and RCC in Kerala and CBA in Sweden, aimed at creating a low cost, automated screening system. 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 funding applications in India and Sweden. In the meantime we have funding for our collaboration from the Swedish Research Links Programme. See Figure 35.

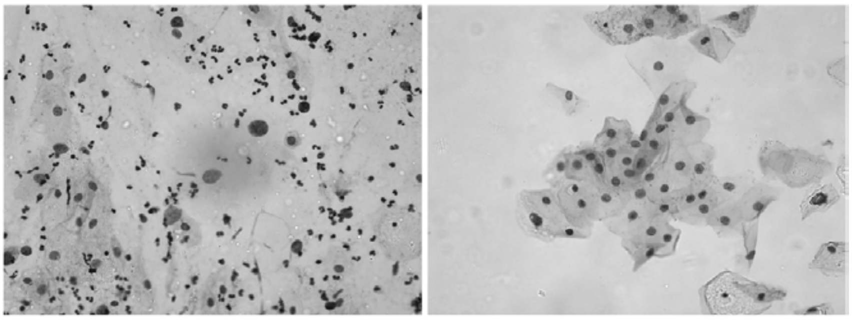

Figure 35: CerviScan

34. **Image Analysis in the ExDIN Digital Pathology Networks**
Ewert Bengtsson, Carolina Wählby, Petter Ranefall
Partner: RxEye, Stockholm, Groups at Karolinska Institute plus county council pathology labs.
Funding: Vinnova
Period: 20161231–20170630
Abstract: The ExDIN project aims at developing an operational collaborative network structure for doing routine histopathological diagnoses using digital images transmitted over networks rather than the traditional way, optically through a microscope. When the histopathological slides are scanned and made available over the network it becomes much easier to apply various computer assisted image analysis approaches than when the routine analysis is done directly in a microscope in which case computer analysis requires separate scanning steps. Our role in the project is to investigate the state-of-the-art in computer assisted image analysis applied to histopathological diagnosis. Are there any methods available today that are sufficiently mature and robust to be applied routinely in this way? We have carried out a literature study to answer this question which was documented in a report. The main result of the project was a special issue in June 2017 of the Cytometry journal addressing this question. It contained seven contributed papers and an editorial written by Bengtsson. A small pilot study demonstrating image analysis on whole immunohistochemistry stained histopathology sections in order to detect Ki67 positive cells was also carried out.

35. **Zebrafish as a Model for Cerebral Palsy and Intellectual disability**
Amin Allalou, Carolina Wählby
Partner: Marcel den Hoed, Marta Martín Martínez, Aida Hoshiar, Dept. of Immunology, Genetics and Pathology and SciLifeLab, UU
Funding: SciLifeLab
Period: 20161001–
Abstract: The zebrafish (Danio rerio) is a good model organism for vertebrate development. The organization of the embryo is simple and the body is transparent, making it easy to study with many different microscopy techniques. In this project we are using the VAST (Vertebrate Automated Screening Technology) and fluorescent imaging with OPT (Optical Tomography) to do a preliminary screen to investigate if we can detect any phenotypes for a number of candidate genes for cerebral palsy and intellectual disability. We are also performing behavioral screening to see if there are any behavioral phenotypes that can associated with the genes of interest. See Figure 36.

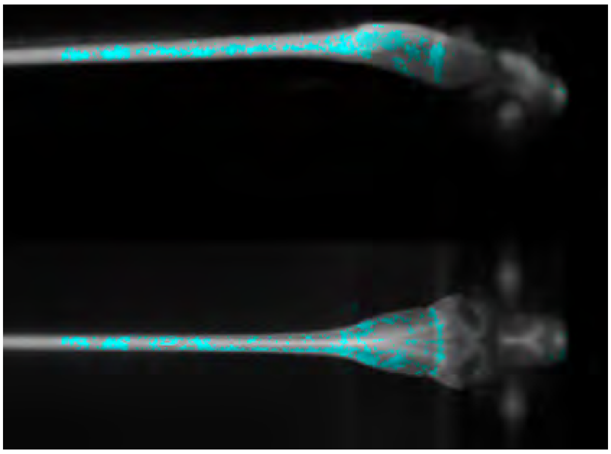

Figure 36: Zebrafish as a Model for Cerebral Palsy and Intellectual Disability

36. **Heart Rate Analysis in Zebrafish**
    Amin Allalou, Carolina Wählby
    Partner: Marcel den Hoed, Benedikt von der Heyde, Dept. of Medical Sciences and SciLifeLab, UU
    Funding: SciLifeLab
    Period: 20161001–
    Abstract: Due to the transparency of the young zebrafish the heart is easily accessible for optical analysis without any invasive procedures. Video-based quantification of heart rate and rhythm is a non-invasive method that can give important information on many phenotypic changes in heart. We have developed an analysis method to quantify the heart rate and rhythm based on video recordings of zebrafish from the VAST (Vertebrate Automated Screening Technology) system.

37. **TissueMaps – Integrating Spatial and Genetic Information via Automated Image Analysis and Interactive Visualization of Tissue Data**
    Carolina Wählby, Maxime Bombrun, Gabriele Partel, Leslie Solorzano, Petter Ranefall, Joakim Lindblad, and Amin Allalou
    Partner: Mats Nilsson - Stockholm University/SciLifeLab, Xiaoyan Qian - Stockholm University/SciLifeLab
    Funding: ERC consolidator grant to Carolina Wählby
    Period: 201109—-
    Abstract: Digital imaging of tissue samples and genetic analysis by next generation sequencing are two rapidly emerging fields in pathology. Digital pathology will soon be as common as digital images in radiology, and genetic analysis is rapidly evolving thanks to the impressive development of next generation sequencing technologies. However, most of today's available technologies result in a genetic analysis that is decoupled from the morphological and spatial information of the original tissue sample, while many important questions in tumor- and developmental biology require single cell spatial resolution to understand tissue heterogeneity. In this project, we develop computational methods that bridge these two emerging fields. We combine spatially resolved high-throughput genomics analysis of tissue sections with digital image analysis of tissue morphology. Together with collaborators from the biomedical field, we work with advanced digital image processing methods for spatially resolved genomics (Ke et al, Nature Methods 2013). In 2016, the project attracted an ERC consolidator grant and led to two review-type publications in the Proceedings of the IEEE and Nature Methods. The project has been enriched by decoding gene expression in 3D, and a novel image analysis pipeline that combines a learning approach and a graphical model to increase recall. See Figure 37.

38. **Effects of Repeated Islet Transplantation on Islet Engraftment in a Mouse Model**
    Petter Ranefall
    Partner: Hanna Liljebäck, Per-Ola Carlsson, Dept. of Medical Cell Biology, UU
    Funding: SciLifeLab
    Period: 20171016–
    Abstract: The outcome of islet transplantation has improved progressively. However, the lack of organ

donors makes islet transplantation available only to type I diabetes patients with the most severe glycemic lability. In the clinic, a second transplantation is often required to boost graft function and extend the time until recurrence of insulin dependence. Often, the second graft proves to work better than the initial islet transplant. In this study, we aimed to, in a mouse model with GFP positive islets, investigate whether this reflected differences in engraftment is caused by the repeated islet infusion procedure. See Figure 38.

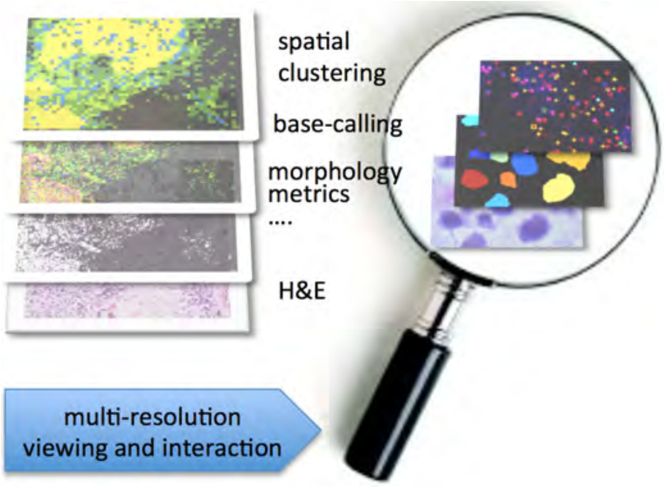

Figure 37: TissueMaps - Integrating spatial and genetic information via automated image analysis and interactive visualization of tissue data

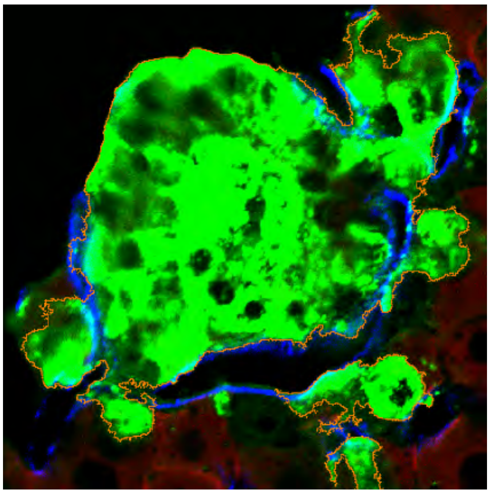

Figure 38: Effects of repeated islet transplantation on islet engraftment in a mouse model

5.3 Medical image analysis, diagnosis and surgery planning

39. **Imiomics – Large-Scale Analysis of Medical Volume Images**
Robin Strand, Filip Malmberg
Partner: Joel Kullberg, Håkan Ahlström, Simon Ekström, Therese Sjöholm, Dept. of Surgical Sciences, Radiology, UU Hospital
Funding: Faculty of Medicine, UU
Period: 20120801–
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 a large scale analysis method, which is enabled by image registration methods. These methods utilize, for example, segmented tissue and anatomical landmarks. Based on this idea, we have developed Imiomics (imaging omics) – an image analysis concept, including image registration, that allows statistical and holistic analysis of whole-body image data. The Imiomics concept is holistic in three respects: (i) The whole body is analyzed, (ii) All collected image data is used in the analysis and (iii) It allows integration of all other collected non-imaging patient information in the analysis. During 2017 a new registration method based on combinatorial optimization was developed, and a manuscript describing this method was submitted for publication. Our work was also presented at ESMO and ISMRM conferences. See Figure 39.

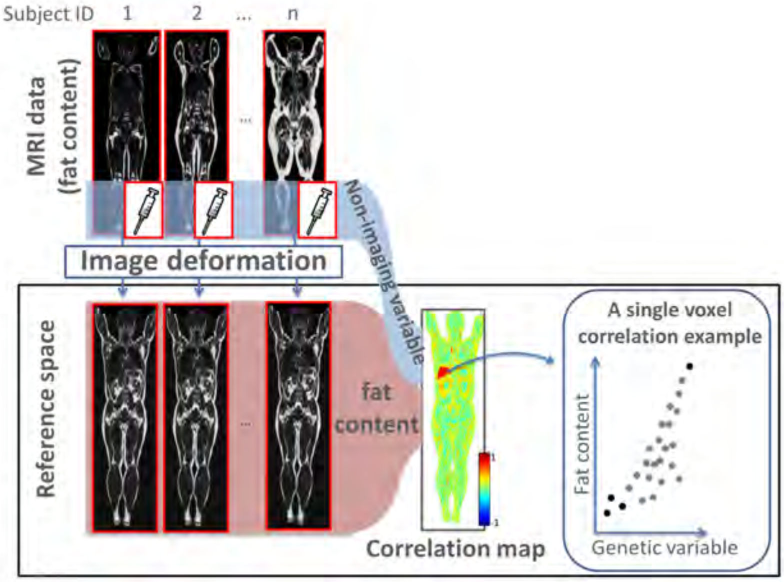

Figure 39: Imiomics - Large-Scale Analysis of Medical Volume Images

40. **Interactive Deep Learning Segmentation for Decision Support in Neuroradiology**
Ashis Kumar Dhara, Robin Strand, Filip Malmberg
Partner: Johan Wikström and Elna-Marie Larsson, Dept. of Surgical Sciences, Radiology, UU
Funding: Swedish Research Council
Period: 20150501–
Abstract: Many brain diseases can damage brain cells (nerve cells), which can lead to loss of nerve cells and, secondarily, loss of brain volume. Technical imaging advancements allow detection and quantification of very small tissue volumes in magnetic resonance (MR) neuroimaging. Due to the enormous amount of information in a typical MR brain volume scan, and difficulties such as partial volume effects, noise, artefacts, etc., interactive tools for computer aided analysis are absolutely essential for this task. Available interactive methods are often not suited for this problem. Deep learning by convolution neural networks

has the ability to learn complex structures from training data. However, deep learning is often too slow for interactive processing. We develop, analyze and evaluate interactive deep learning segmentation methods for quantification and treatment response analysis in neuroimaging. Interaction speed is obtained by dividing the segmentation procedure into an offline pre-segmentation step and an on-line interactive loop in which the user adds constraints until satisfactory result is obtained. The overarching aim is to allow detailed correct diagnosis, as well as accurate and precise analysis of treatment response in neuroimaging, in particular in quantification of intracranial aneurysm remnants and brain tumors (Gliomas WHO-grades III and IV) growth. See Figure 40.

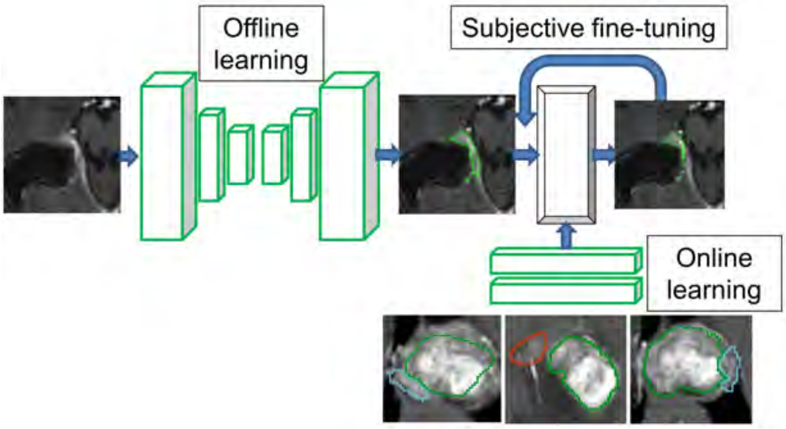

Figure 40: Interactive deep learning segmentation for decision support in neuroradiology

41. **Interactive Segmentation and Analysis of Medical Images**
Filip Malmberg, Robin Strand, Ingela Nyström
Partner: Joel Kullberg, Håkan Ahlström, Dept. of Surgical Sciences, UU
Funding: TN-Faculty, UU
Period: 20110601–20170501
Abstract: Three-dimensional (3D) 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. In this project, we seek to employ these methods for segmentation of medical images, in collaboration with the Dept. of Surgical Sciences at the UU Hospital. A publicly available software for interactive segmentation, emphSmartPaint, can be downloaded from urlhttp://www.cb.uu.se/ filip/SmartPaint/. To date, this software has been downloaded more than 1100 times. During 2017, this software was adapted to fit within a workflow for analysis of very large cohorts. See Figure 41.

42. **Comparison of Articular Osteochondrosis in Domestic Pigs and Wild Boars by Image Processing**
Robin Strand
Partner: Pernille Etterlin, Stina Ekman, Dept. of Biomedical Sciences and Veterinary Public Health, SLU; Kristin Olstad, Dept. of Companion Animal Clinical Sciences, Norwegian University of Life Sciences; Charles Ley, Dept. of Clinical Sciences, SLU
Funding: Gerhard Forsells stipendiestiftelse; TN-Faculty, UU
Period: 20150101–
Abstract: Articular osteochondrosis (OC) often develops in typical locations within joints and the characterization of OC distribution in the pig tarsus is incomplete. Prevalence of OC is high in domestic pigs but is presumed to be low in wild boars. In this project, we develop methods based on image registration for 3D analysis of OC distribution. In 2017, a paper was published in the journal Veterinary Pathology. See Figure 42

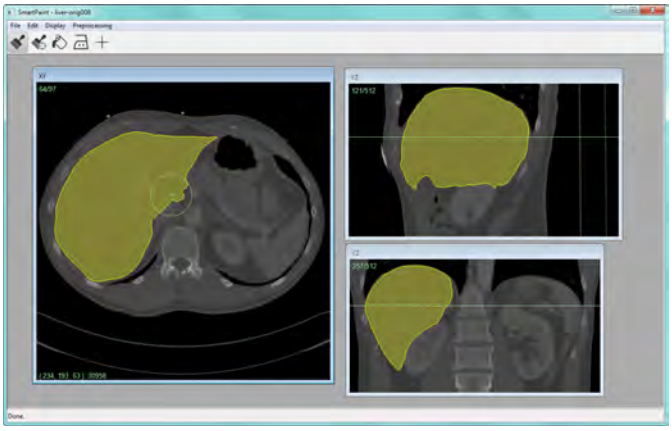

Figure 41: Interactive Segmentation and Analysis of Medical Images

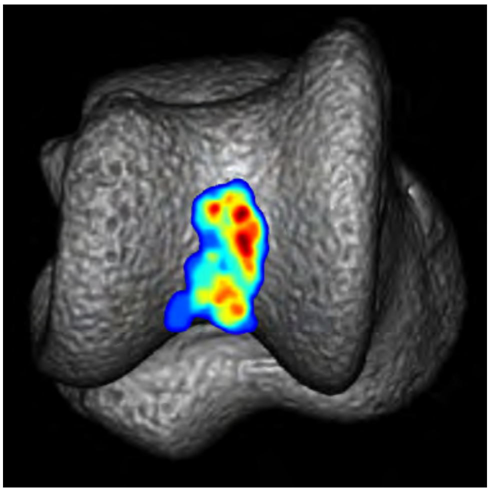

Figure 42: Comparison of Articular Osteochondrosis in Domestic Pigs and Wild Boars by Image Processing

43. **Methods for Combined MR and Radiation Therapy Equipment**
    Robin Strand
    Partner: Anders Ahnesjö, David Tilly, Dept. of Immunology, Genetics and Pathology, UU. Samuel Fransson, Håkan Ahlström, Dept. of Surgical Sciences, Radiology, UU
    Funding: Vinnova; Barncancerfonden; TN-Faculty, UU
    Period: 20160601–
    Abstract: UU and Hospital are current investing in image guided radiotherapy. An important component in the strategy is a combined MR scanner and treatment unit, enabling MR imaging right before and during treatment making it possible to adjust for internal motion. In this project, we develop methods for fast detection and quantification of motion for real-time adjustment of the radiation therapy in the combined MR scanner and treatment unit. See Figure 43.

44. **Computerized Image Analysis for Ophthalmologic Applications**
    Filip Malmberg
    Partner: Camilla Sandberg-Melin and Per Soderberg, Dept. of Neuroscience, UU
    Funding: -
    Period: 20150101–20171001
    Abstract: Ophtalmology is the study of the anatomy, physiology, and diseases of the eye. Optical coherence tomography (OCT) is a non-invasive technique for generating 3D images of the retina of the eye, allowing

ophtalmologists to visualize the different structures of the retina. To complement visual inspection, this project aims to develop image analysis method for accurately measuring geometrical properties of the retina. These measurements help with early detection, diagnosis and treatment guidance for a wide range of retinal diseases and conditions. During 2017, our work within this project was presented at the EVER congress (European Association for Vision and Eye Research).

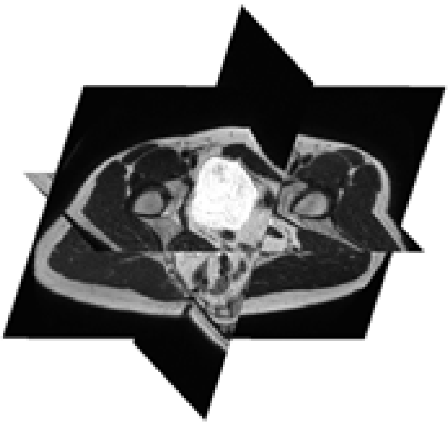

Figure 43: Methods for Combined MR and Radiation Therapy Equipment

45. **Image Processing for Virtual Design of Surgical Guides and Plates**
Fredrik Nysjö, Pontus Olsson, Filip Malmberg, Ingrid Carlbom, Ingela Nyström
Partner: Andreas Thor, Dept. of Surgical Sciences, Oral and Maxillofacial Surgery, UU Hospital; Andres Rodriguez Lorenzo, Dept. of Surgical Sciences, Plastic Surgery, UU Hospital; Daniel Buchbinder, Icahn School of Medicine at Mount Sinai, New York, NY, USA
Funding: -
Period: 20150317–
Abstract: An important part of virtual planning for reconstructive surgery, such as cranio-maxillofacial (CMF) surgery, is the design of customized surgical tools and implants. In this project, we are looking into how distance transforms and constructive solid geometry can be used to generate 3D printable models of surgical guides and plates from segmented computed tomography (CT) images of a patient, and how the accuracy and precision of the modelling can be improved by using grayscale image information in combination with anti-aliased distance transforms. Another part of the project is to develop simple and interactive tools that allow a surgeon to create the models. We have implemented a set of design tools in our existing surgery planning system, HASP, and are currently testing them with surgeons. See Figure 44.

Figure 44: Image Processing for Virtual Design of Surgical Guides and Plates

46. **Skeleton-Based Vascular Segmentation at Interactive Speed**
    Kristína Lidayová, Ewert Bengtsson
    Partner: Hans Frimmel-Division of Scientific Computing, UU; Örjan Smedby and Chunliang Wang-School of Technology and Health, KTH
    Funding: VR grant to Örjan Smedby
    Period: 201207–20170630
    Abstract: Precise segmentation of vascular structures is crucial for studying the effect of stenosis 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 for a segmentation algorithm. The algorithm consists of four levels, of which the first two levels detect healthy arteries of varying sizes, and the remaining two levels specialize in different types of vascular pathology: severe calcification and occlusion. An outline of the proposed algorithm is presented in Figure 45. The algorithm was published in Journal of Medical Imaging 4(2), 2017. During this year, focus has been on replacing the knowledge-based detection of vascular nodes by a convolutional neural network in the centerline tree detection algorithm. The classifier itself yields a precision of 0.81 and recall of 0.83 for medium size vessels, and qualitatively, an enhanced representation of the vascular skeleton could be achieved. The algorithm was presented at the Medical Image Understanding and Analysis (MIUA) 2017 conference.

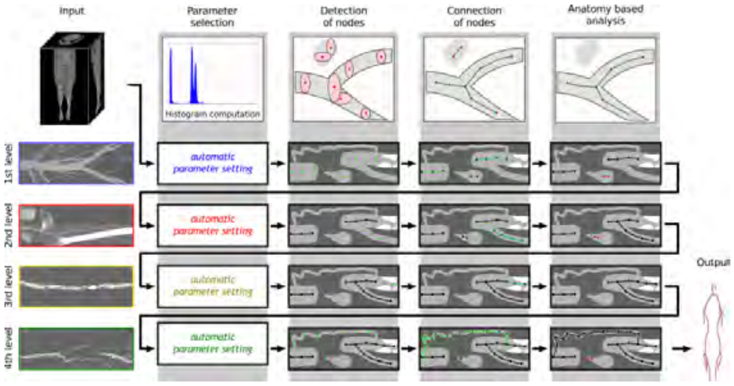

Figure 45: Skeleton-Based Vascular Segmentation at Interactive Speed

47. **Airway Tree Segmentation in Subjects with Acute Respiratory Distress Syndrome**
    Kristína Lidayová, Ewert Bengtsson
    Partner: Hans Frimmel - Dept. of Information Technology, UU; Örjan Smedby-School of Technology and Health, KTH; Marcela Hernández Hoyos-Universidad de Los Andes, Bogotá, Colombia; Maciej Orkisz-University of Lyon, CREATIS, Lyon, France
    Funding: VR grant to Örjan Smedby
    Period: 201512–20170630
    Abstract: Acute Respiratory Distress Syndrome (ARDS) presents a high mortality rate in intensive care units. Fast and accurate analysis of lung aeration on CT images may reduce the mortality rate in ARDS. However, the accuracy of lung aeration analysis is hampered by two factors: the difficulty in delineating the outer boundary of the lungs (due to local lack of contrast), and the inclusion of internal structures not belonging to the parenchyma. To cope with both problems, an airway segmentation can be useful. Our current method detects an approximate airway centerline tree and then applies the obtained intensity and distance information to restrict the region-growing segmentation and prevents it from leaking into the parenchyma. During 2017, the method was evaluated qualitatively on 70 thoractic CT images of subjects with ARDS, acquired at significantly different mechanical ventilation conditions. Quantitative evaluation was performed indirectly showed that the resulting segmentation contained important landmarks. These landmarks improve a registration-based segmentation of the lungs in difficult ARDS cases. The algorithm was presented at the Scandinavian conference on image analysis (SCIA) 2017. See Figure 46

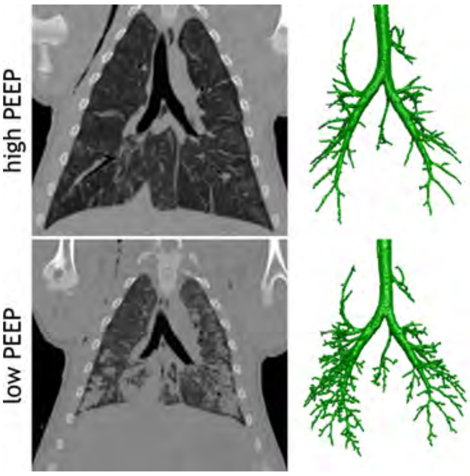

Figure 46: Airway Tree Segmentation in Subjects with Acute Respiratory Distress Syndrome

48. **Coverage Model and its Application to High Precision Medical Image Processing**
Nataša Sladoje, Joakim Lindblad
Partner: Buda Bajić, Slobodan Dražić, Faculty of Technical Sciences, University of Novi Sad, Serbia
Funding: Swedish Governmental Agency for Innovation Systems (VINNOVA); TN-Faculty, UU; Swedish Research Council
Period: 201409–
Abstract: The coverage model, which we have been developing for several years now, provides a framework for representing objects in digital images as spatial fuzzy sets. Membership values indicate to what extent image elements are covered by the imaged components. The model is useful for improving information extraction from digital images and reducing problems originating from limited spatial resolution. We have by now developed methods for estimation of a number of features of coverage representation of shapes and demonstrated their increased precision and accuracy, compared to the crisp representations. Our focus is also on the development of segmentation methods which result in coverage segmentation. During 2017 we have prepared and submitted a journal publication on a coverage segmentation method based on energy minimization, which improves and generalizes our previously published results. The method is applicable to blurred and noisy images, and provides coverage segmentation at increased spatial resolution, while preserving thin fuzzy object boundaries. We have suggested a suitable global optimization scheme to address a challenging non-convex optimization problem. We have evaluated the method on several synthetic and real images, confirming its very good performance. See Figure 47.

Figure 47: Coverage Model and its Application to High Precision Medical Image Processing

49. **HASP: Haptics-Assisted Surgery Planning**
Ingrid Carlbom, Pontus Olsson, Fredrik Nysjö, Johan Nysjö, Ingela Nyström
Partner: Daniel Buchbinder, Icahn School of Medicine at Mount Sinai, New York, NY, USA; Andreas Thor, Johanna Nilsson, Dept. of Surgical Sciences, Oral and Maxillofacial Surgery, UU Hospital; Andres Rodriguez Lorenzo, Dept. of Surgical Sciences, Plastic Surgery, UU Hospital
Funding: BIO-X 1.5M SEK; Thuréus Stiftelsen: 150 K SEK, TN-Faculty, Facultyof Medicine, UU Hospital
Period: 20150101–
Abstract: The goal of HASP, our haptics assisted surgery planning system, is to put the planning process for

complex head and neck surgery into the hands of the surgeon. During 2017, we continued the evaluation of HASP and the BoneSplit segmentation software both at the UU Hospital and at Mount Sinai Beth Israel in NYC. At the UU Hospital, a trauma study using HASP is ongoing and will be completed during 2018. We will evaluate the haptic model in HASP on CT data from a scanned plastic skull and ten retrospective cases. For the plastic skull, we are comparing accuracy and precision between users, whereas for the retrospective cases we are comparing precision only. At Mount Sinai Beth Israel the focus has been validation of the accuracy of HASP with ten retrospective cases. Prospective cases are also in the planning. For each case, we produce a neomandible from resin models generated by a 3D printer of the mandible, cutting guides, fibula, and case-specific plates, that are cut and glued together. We will then compare a CT model of the reconstructed resin neomandible with the HASP neomandible, and verify their correspondence. We expect to complete the study during 2018. See Figure 48.

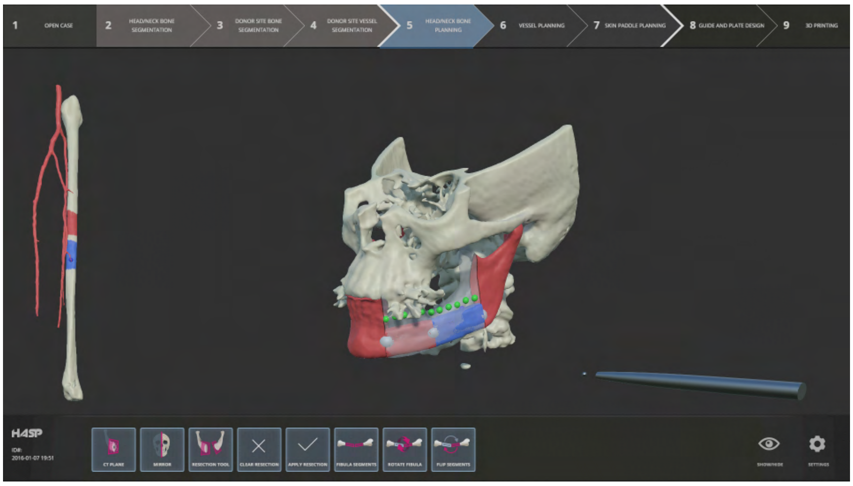

Figure 48: HASP: Haptics-Assisted Surgery Planning

50. **Virtual Surgical Planning for Soft Tissue Resection and Reconstruction**
Ludovic Blache, Filip Malmberg, Fredrik Nysjö, Ingela Nyström, Ingrid Carlbom
Partner: Andres Rodriguez Lorenzo, Dept. of Surgical Sciences, Plastic Surgery, UU Hospital; Andreas Thor, Dept. of Surgical Sciences, Oral and Maxillofacial Surgery, UU Hospital
Funding: TN-Faculty
Period: 20161010–
Abstract: With the increased use of 3D models and CAD technologies in the medical domain, virtual surgical planning is now frequently used. Most current solutions focus on bone surgical operations. However, for head and neck oncologic resection, soft tissue ablation and reconstruction are common operations. When the surgeon removes a tumor, a defect results in the face consisting of different tissue layers. To reconstruct this defect it is usually needed to transplant vascularized tissue from other parts of the body. In collaboration with the Dept. of Surgical Science at the UU Hospital, we aim at providing a virtual planning solution for such surgical operations. We have developed and implemented a modelling method to estimate the shape and dimensions of soft tissue resections. Our approach takes advantage of a simple sketch-based interface, which allows the user to paint the contour of the resection on a patient specific 3D model reconstructed from a CT scan. The volume is then virtually cut and carved following this pattern to provide a 3D model of the resected volume. We then seek to develop a numerical model, based on finite element method, to simulate the non-rigid behavior of the soft tissue flap during the reconstruction process. See Figure 49.

51. **Statistical Considerations in Whole-Body MR Analyses**
Eva Breznik, Robin Strand, Filip Malmberg
Partner: Joel Kullberg, Håkan Ahlström, Dept. of Surgical Sciences, UU
Funding: Centre for Interdisciplinary Mathematics, CIM, UU; TN-Faculty, UU
Period: 201609–
Abstract: In this project, the focus is on testing and developing methods for Imiomics, to facilitate utilization of whole-body MR images for medical purposes. For inference about activated areas, present in the

image, statistical tests are done on series of images at every voxel. This introduces accuracy and reliability problems when drawing conclusions regarding the images or multi-voxel areas as a whole, due to the large number of tests that are considered at the same time. The solution to this problem is a proper multiple testing correction method. Therefore we need to test the existing ones on our specific datasets and explore possibilities of new ones, specifically tailored to our problem. Results have been in part presented at SSBA 2017 in Linköping. See Figure 50.

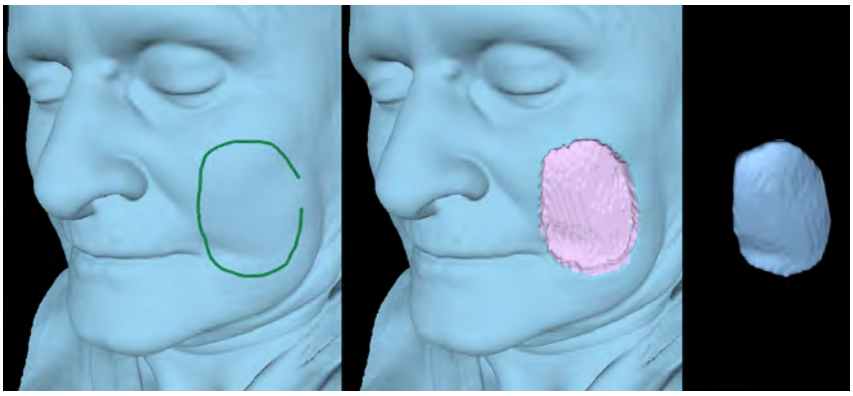

Figure 49: Virtual surgical planning for soft tissue resection and reconstruction

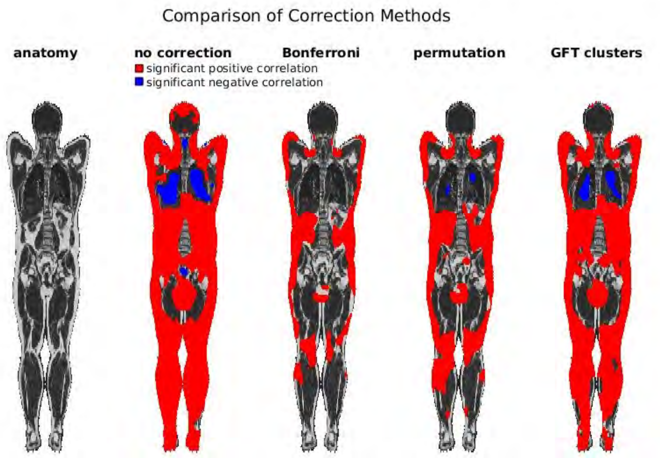

Figure 50: Statistical Considerations in Whole-Body MR Analyses

52. **Abdominal Organ Segmentation**
Eva Breznik, Robin Strand, Filip Malmberg
Partner: Joel Kullberg, Håkan Ahlström, Division of Radiology, Dept. of Surgical Sciences, UU
Funding: Centre for Interdisciplinary Mathematics, CIM, UU; TN-Faculty, UU
Period: 201706–
Abstract: We focus on improving the existing registration method for whole-body scans by including segmentation results as prior knowledge. Segmentation of the organs in the abdomen is a daunting task, as the organs vary a lot in their properties and size. And having a robust method to segment a number of them would not only be useful in clinical setting, but it could also help guide the registration method in those areas, which are most challenging to register. In search for such a method, we apply convolutional neural networks, look at various architectures, better sampling strategies and possibilities of including prior knowledge in the process. Preliminary results on improvements we achieved by integrating anatomical knowledge with a fully convolutional network (deepMedic) were presented at WiML in Long Beach. See Figure 51.

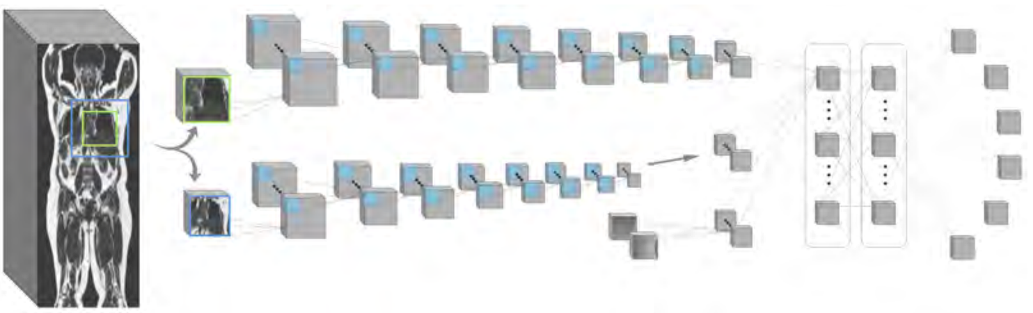

Figure 51: Abdominal organ segmentation

53. **Calving Detection**
    Robin Strand
    Partner: Dorothée Vallot, Rickard Pettersson, Dept. of Earth Sciences, UU. Sigit Adinugroho, MSc student, CBA; Penelope How, Institute of Geography, School of GeoSciences, University of Edinburgh, UK
    Funding: TN-Faculty
    Period: 20150101–
    Abstract: Calving processes are an important unknown in glacier systems terminating in the ocean. Automatic image analysis methods for the analysis of calving fronts of glaciers are monitored by time-lapse cameras are developed in this project. The methods are based on detecting changes in segmented calving fronts of glaciers. The area of the calving event is then computed based on the relative camera position.

5.4 Mathematical and Geometrical Theory

54. **Precise Image-Based Measurements through Irregular Sampling**
Teo Asplund, Robin Strand, Gunilla Borgefors
Partner: Cris Luengo-Flagship Biosciences Inc., Westminster, Colorado, USA, Matthew Thurley-Luleå University of Technology, Luleå
Funding: Swedish Research Council
Period: 20150401–
Abstract: We develop mathematical morphology on irregularly sampled signals. This is beneficial for a number of reasons: 1. Irregularly sampled signals would traditionally have to be resampled onto the regular grid to allow morphology to be applied, however, such resampling can require interpolating data where the original signal contained large holes. This can lead to very poor performance. 2. The morphological operators depend on suprema/infima in the signal. A regularly sampled signal is likely to miss these. 3. The operators produce lines along which the derivative is not continuous, thereby introducing unbounded frequencies and breaking the correspondence between the sampled signal and the continuous bandlimited one. 4. The structuring element is limited by the sampling grid. We have shown that moving to morphology on irregularly sampled signals can yield results that better approximate continuous morphology than the traditional morphological operators, yielding more accurate measurements both in 1D- and 2D grayscale morphology. See Figure 52.

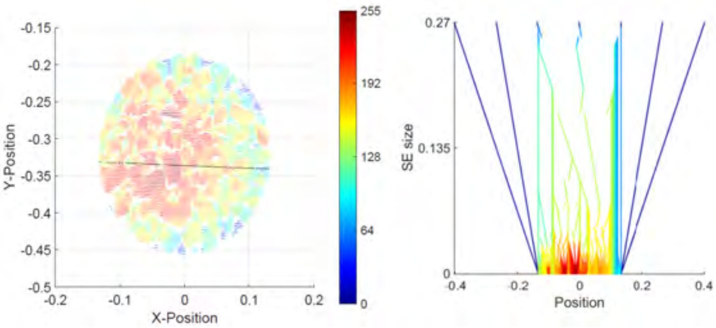

Figure 52: Precise Image-Based Measurements through Irregular Sampling

55. **Complex Convexity**
Christer Kiselman
Funding: Université de Nice 1967-10-01, 1968-09-30; UU 1968-10-01, 2006-04-30;
Period: 19671001–
Abstract: A bounded open set with boundary of class C^1 which is locally weakly lineally convex is weakly lineally convex, but, as shown by Yurii Zelinskii, this is not true for unbounded domains. We construct explicit examples, Hartogs domains, showing this. Their boundary can have regularity $C^{1,1}$ or $C^inf ty$.Obstructions to constructing smoothly bounded domains with certain homogeneity properties are presented. A current activity is a study of one-sided regularity of subsets of R^n or C^n. Preliminary results on this kind of regularity were presented at a conference on September 16, 2015. See Figure 53.

56. **Discrete Convolution Equations**
Christer Kiselman
Funding: Kingdom of Sweden.
Period: 20120111–
Abstract: We study solvability of convolution equations for functions with discrete support in R^n, a special case being functions with support in the integer points. The more general case is of interest for several grids in Euclidean space, like the body-centred and face-centered tesselations of three-space, as well as for the non-periodic grids that appear in the study of quasicrystals. The theorem of existence of fundamental solutions by de Boor, Höllig & Riemenschneider is generalized to general discrete supports, using only elementary methods. We also study the asymptotic growth of sequences and arrays using the Fenchel transformation. Estimates using the Fourier transformation are studied. Now duality of convolution will be investigated. A study of quasicrystals is part of this project.

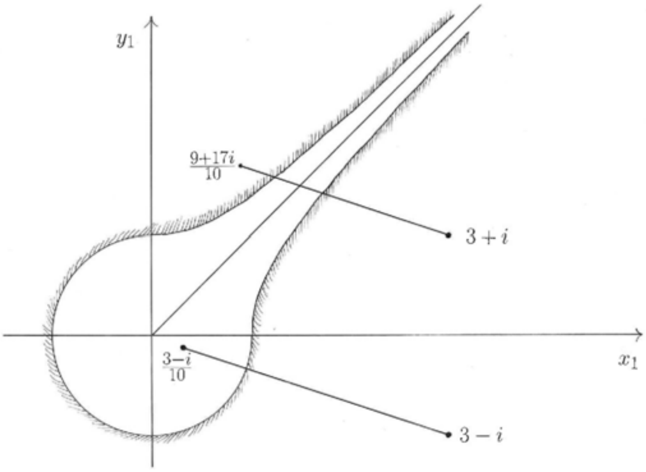

Figure 53: The base in the complex plane of a locally lineally convex set in C^2 which is not lineally convex (courtesy Hania Uscka-Wehlou).

57. **Existence of Continuous Right Inverses to Linear Mappings in Elementary Geometry.**
Christer Kiselman
Partner: Erik Melin, Comsol AB, Stockholm
Funding: Christer: UU 2005 — 2006-04-30; Kingdom of Sweden 2006-05-01 — . Erik: UU 2005–2008.
Period: 20050908–
Abstract: A linear mapping of a compact convex subset of a finite-dimensional vector space always possesses a right inverse, but may lack a continuous right inverse even if the set is smoothly bounded. Examples showing this are given as well as conditions guaranteeing the existence of a continuous right inverse, also for other sets.

58. **Digital Hyperplanes**
Christer Kiselman
Partner: Adama Arouna Kone, Universite des Sciences, des Techniques et des Technologies de Bamako, USTTB, Bamako I
Funding: Christer: Kingdom of Sweden. Adama: International Science Programme (ISP) 2011–2016; Universite des Sciences, des Techniques et des Technologies de Bamako, USTTB, Bamako I 2011 — .
Period: 20100101–
Abstract: Digital planes in all dimensions are studied.The general goal is to generalize to any dimension the results of Kiselman's 2011 paper in Mathematika (11-1).

59. **Mathematical Concepts and their Linguistic Expression in a Multicultural Setting**
Christer Kiselman
Partner: Christer Kiselman, Adama Arouna KonÃ©, Lars Mouwitz, Fanja Rakontondrajao, Amites Rasho, Shiva Samieinia, Xiaoqin Wang; possibly others.
Funding: Hania: Man In The Middle AB (MITM). Christer: Kingdom of Sweden. Adama: UniversitÃ© des Sciences, des Techniques et des Technologies de Bamako. Lars: Kingdom of Sweden. Fanja: UniversitÃ© d'Antananarivo. Shiva: Stockholm University; The Ruth and Nils-Erik
Period: 20161201–
Abstract: To study the relation between mathematical concepts and their expression in several languages. Special attention is devoted to the use of non-native languages.

60. **Digital Distance Functions and Distance Transforms**
Robin Strand, Gunilla Borgefors
Partner: Benedek Nagy - Dept. of Computer Science, Faculty of Informatics, University of Debrecen, Hungary; Nicolas Normand, IRCCyN - University of Nantes, France
Funding: TN-Faculty, UU
Period: 19930901–

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. A manuscript on distance functions based on multiple types of weighted steps combined with neighborhood sequences has been produced in collaboration with Strand, Nagy and Normand. The manuscript holds (mainly theoretical) results on for example metricity and optimal parameters. Figure 54 illustrates the shapes of disks with different number of weights, when the optimization criterion is roundness in the Euclidean sense.

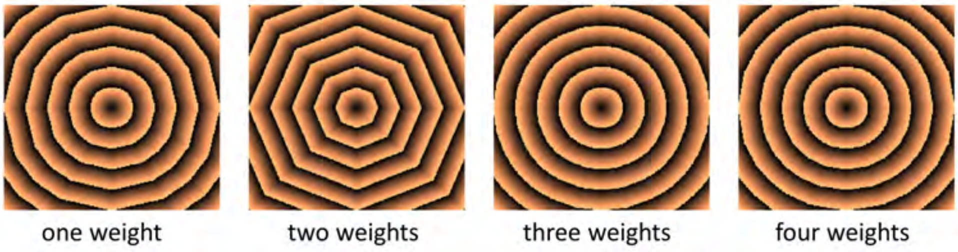

Figure 54: Digital Distance Functions and Distance Transforms

61. **Feature Point Descriptors for Image Stitching**
Anders Hast, Ida-Maria Sintorn, Damian J. Matuszewski, Carolina Wählby
Partner: Vironova AB; Dept. of Electronic Computers RSREU, Ryazan, Russia
Funding: TN-Faculty; UU; Science for Life Laboratory
Period: 20150101–20171130
Abstract: When microscopy images are to be put together to form a larger image than one field of view, images are stitched together based on key point features in the images. Several methods for matching these images exist, but are often general in the sense that they can handle scale and rotation, which are not present in this particular case. Therefore, these methods are like cracking a nut with a sledge hammer, and we have investigated how simpler and therefore more efficient and also faster methods can be developed and applied for solving this task. Several key point descriptors have been investigated that are based on new sampling strategies and also new ways of combining these samples, using for instance elements of the Fourier transform, instead of histograms of gradients etc. A paper describing two versions of fast and simple feature point descriptor with or without rotation invariance was presented at the WSCG conference. This project resulted in the publication: Matuszewski DJ, Hast A, Wählby C, Sintorn I-M (2017) A short feature vector for image matching: The Log-Polar Magnitude feature descriptor. PLoS ONE 12(11): e0188496. See Figure 55

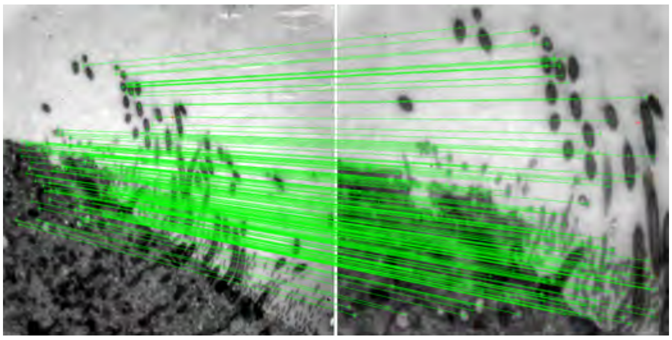

Figure 55: Feature Point Descriptors for Image Stitching

62. Image Enhancement Based on Energy Minimization

Nataša Sladoje, Joakim Lindblad, Amit Suveer, Ida-Maria Sintorn
Partner: Buda Bajić, Faculty of Engineering, University of Novi Sad, Serbia; Anindya Gupta, T. J. Seebeck Dept. of Electronics, Tallinn University of Technology, Estonia
Funding: Swedish Governmental Agency for Innovation Systems (VINNOVA); TN-Faculty, UU; Swedish Research Council
Period: 201409—-

Abstract: A common approach to solve the ill-posed problem of image restoration is to formulate it as an energy minimization problem. A priori knowledge is, typically, included through a regularization component. Total variation is among most popular approaches, due to simplicity and generally good performance. We have studied performance of energy minimization based restoration for enhancing images degraded with blur and different types of noise - Gaussian, Poisson and mixed Poisson-Gaussian. During 2017, our focus was on application of the developed approaches. We have included energy minimization based denoising in a comparative study of performances of different denoising methods on TEM images of Cilia. We have also developed a Deep learning based method for the same task. Results are presented in the publication ”Denoising of Short Exposure Transmission Electron Microscopy Images for Ultrastructural Enhancement”, accepted for the IEEE International Symposium on Biomedical Imaging - ISBI 2018. In addition, we have incorporated deblurring and super-resolution reconstruction in the energy function proposed earlier for coverage segmentation and achieved improved segmentation results. We have suggested an improved global optimization scheme which makes the method applicable to blurred and noisy data. We have prepared and submitted a journal publication. See Figure 56.

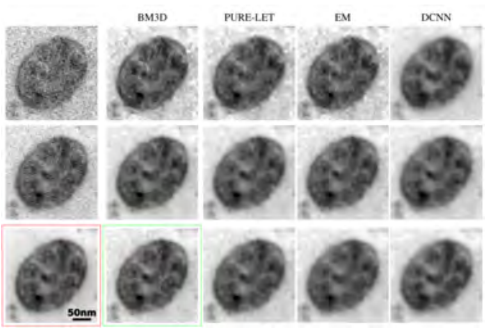

Figure 56: Image Enhancement Based on Energy Minimization

63. Predictive Modelling of Real Time Video of Outdoor Scenes Captured With a Moving Handheld Camera

Nataša Sladoje, Joakim Lindblad
Partner: Joakim Lindblad, Protracer AB, Stockholm
Funding: Swedish Governmental Agency for Innovation Systems (VINNOVA); Protracer AB
Period: 201510–20170931

Abstract: This project is inspired by the growing market demand for real time matchmoving technologies in sports broadcasting. Matchmoving, also referred to as video tracking or camera tracking, is a technique that allows 3D computer graphics to be inserted into a live broadcast to enhance the visual experience for the viewing audience. The major technological and functional limitation of existing real time matchmoving technology is its reliance on cameras installed on stands and on a known background settings. Within this project, we have explored and developed software for robust predictive modelling (statistical analysis) of real time video of outdoor scenes captured with a moving handheld camera. This is a collaborative project with Topgolf Sweden AB (formerly Protracer AB), the world-leading provider of ball tracking technology. The outcomes of this project has part in the very successful expansion of the Toptracer product, including CBS Sports announcing their use of Toptracer on 10 holes for every PGA TOUR event during 2018, particularly the tracking of second and third shots wirelessly from the fairway. See Figure 57

Figure 57: Predictive Modelling of Real Time Video of Outdoor Scenes Captured With a Moving Handheld Camera

64. **Regional Orthogonal Moments for Texture Analysis**
    Ida-Maria Sintorn, Carolina Wählby
    Partner: Vironova AB; Sven Nelander, Dept. of Immunology, Genetics and Pathology, UU
    Funding: Swedish Research Council
    Period: 201501—-
    Abstract: The purpose of this project is to investigate and systematically characterize a novel approach for texture analysis, which we have termed Regional Orthogonal Moments (ROMs). The idea is to combine the descriptive strength and compact information representation of orthogonal moments with the well-established local filtering approach for texture analysis. We will explore ROMs and quantitative texture descriptors derived from the ROM filter responses, and characterize them with special consideration to noise, rotation, contrast, scale robustness, and generalization performance, important factors in applications with natural images. In order to do this we will utilize and expand available image texture datasets and adapt machine learning methods for microscopy image prerequisites. The two main applications for which we will validate the ROM texture analysis framework are viral pathogen detection and identification in MiniTEM images, and glioblastoma phenotyping of patient specific cancer stem cell cultures for disease modeling and personalized treatment. During 2016, a paper comparing and evaluating several ROM filter banks on a number of different texture datasets was submitted and is awaiting the review response.

65. **Distance Measures Between Images Based on Spatial and Intensity Information, with Applications in Biomedical Image Processing**
    Johan Öfverstedt, Nataša Sladoje, Joakim Lindblad
    Partner: Ida-Maria Sintorn, Vironova AB
    Funding: Swedish Governmental Agency for Innovation Systems (VINNOVA), TN-Faculty
    Period: 20170101–
    Abstract: Many approaches to solving fundamental image analysis problems, such as template matching, image registration, classification and image retrieval are based on some numeric measure of distance (or similarity) between images. This project is focused on a family of such distance measures which are based on the combination of intensity and spatial information. We have studied how to extend the measures from scalar-valued representations to information-rich hybrid object representations. This has resulted in a M.Sc. thesis titled ”Similarity of Hybrid Object Representations With Applications in Object Recognition and Classification”, a conference paper ”Distance Between Vector-Valued Fuzzy Sets Based on Intersection Decomposition with Applications in Object Detection” presented at the ISMM conference in Paris, France, in May 2017, and a conference paper ”Distance Between Vector-valued Representations of Objects in Images with Application in Object Detection and Classification” presented at the IWCIA conference in Plovdiv, Bulgaria, in June 2017. A biomedical application on which we evaluate the developed methods is template matching-based detection of cilia in TEM. We have shown promising performance compared to the common pixel-based measures such as normalized cross-correlation. We are extending the approach towards affine image registration. See Figure 58.

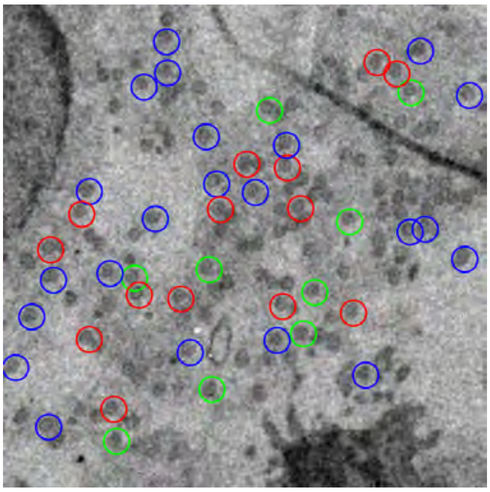

Figure 58: Distance Measures Between Images Based on Spatial and Intensity Information, with Applications in Biomedical Image Processing

66. **The Mimimum Barrier Distance**
Robin Strand, Filip Malmberg
Partner: Punam K. Saha, Dept. of Electrical and Computer Engineering and 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; Stan Sclaroff, Dept. of Computer Science, Boston University, USA; Jianming Zhang, Adobe Research, San Jose, USA
Funding: TN-Faculty, UU
Period: 20110300–
Abstract: This project studies the minimum barrier distance (MBD), given by the difference between the maximum and minimum values that has to be passed to go from one point to another. Theoretical properties as well as efficient computational solutions for the MBD have been developed. During 2017, two papers related to the BMD were presented at the international conference on Discrete Geometry for Computer Imagery in Vienna. The first paper presented a summary and overview of previous research in this area. The second paper introduced a related distance function, the Boolean Map Distance (BMD). During the year, Filip Malmberg also visited Stan Sclaroff in Boston, to collaborate on further development of the BMD. See Figure 59.

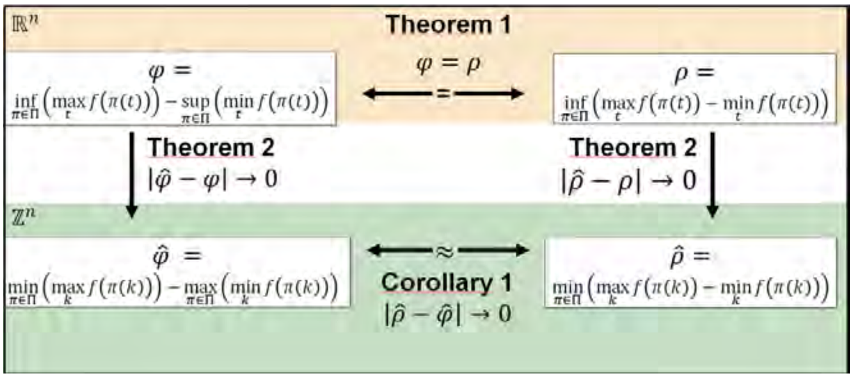

Figure 59: The Mimimum Barrier Distance

67. **Skeletonization**
Gunilla Borgefors
Partner: Punam Saha-Dept. of Electrical and Computer Engineering and Dept. of Radiology, University of Iowa, Iowa City, USA, Gabriella Sanniti di Baja-Institute for high performance computing and networking, CNR, Naples Italy
Funding: UU
Period: 20131001–
Abstract: Skeletonization has been a useful tool for many different image analysis and manipulation tasks since its inception fifty years ago. The purpose of this project is to collect information about the many different skeletonization methods that have been invented and to spread the knowledge about them and their usefulness. In 2016 Saha and Borgefors edited a Special Issue of Pattern Recognition Letters on the current state-of-the-art of skeletonization theory and applications, including a review Chapter. This year the book ´Skeletonization
textendash Theory, Methods, and Applications
prime edited by Saha, Borgefors, and Sanniti di Baja was published by Associated press (see Section 6.1). It includes extended and updated version of the special issue, completely new contributions, and an extended survey chapter. See Figure 60.

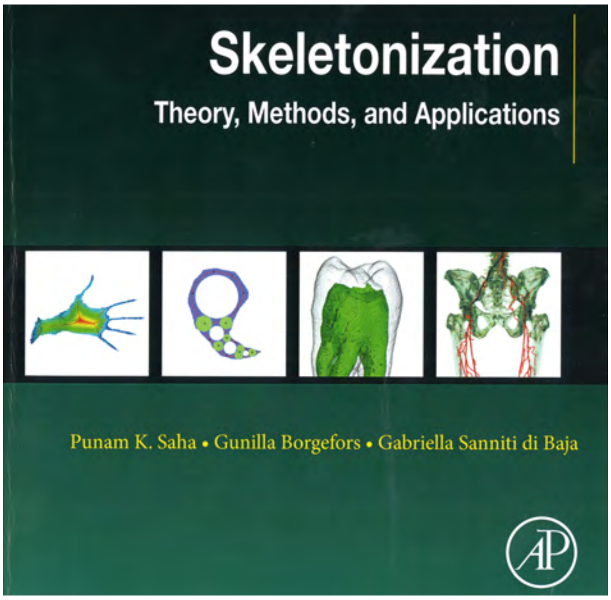

Figure 60: Skeletonization

5.5 Humanities

68. **Zamenhof's Yiddish Grammar**
Christer Kiselman
Funding: Kingdom of Sweden
Period: 20150801–
Abstract: Zamenhof wrote a Yiddish grammar (in Russian) around 1880. It was published in full only in 1982. A study of this grammar is now being undertaken. In particular, a comparison with his language project Universal Language from about the same time is of interest.

69. **Recognition and Datamining for Handwritten Text Collections**
Anders Brun, Ewert Bengtsson, Fredrik Wahlberg, Tomas Wilkinson, Kalyan Ram, Anders Hast, Ekta Vats
Partner: Carl Nettelblad, Dept. of Information Technology, Lasse Mårtensson, Dept. of Business and Economics Studies, Högskolan i Gävle; Mats Dahllöf, Dept. of Linguistics and Philology, UU; Alicia Fornés, Universitat Autonoma de Barcelona, Spain; Jonas Lindström, Dept. of History, UU
Funding: UU; Swedish Research Council; Riksbankens Jubileumsfond; eSSENCE
Period: 20120101–
Abstract: This cross disciplinary initiative takes its point of departure in the analysis of handwritten text manuscripts using computational methods from image analysis and linguistics. It sets out to develop a manuscript analysis technology providing automatic tools for large-scale transcription, linguistic analysis, digital paleography and generic data mining of historical manuscripts. The mission is to develop technology that will push the digital horizon back in time, by enabling digital analysis of handwritten historical materials for both researchers and the public. One postdoc started and several new results were presented. See Figure 61.

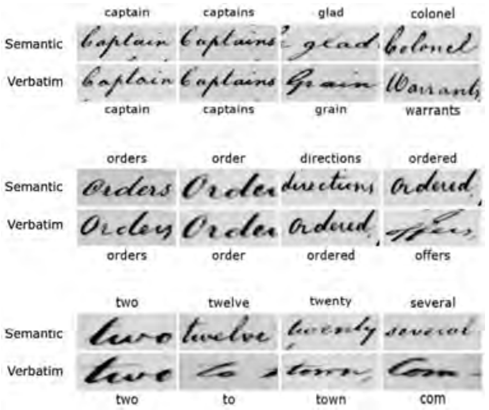

Figure 61: Recognition and Datamining for Handwritten Text Collections

70. **Writer Identification and Dating**
Anders Brun, Fredrik Wahlberg, Anders Hast, Ekta Vats
Partner: Lasse Mårtensson, Dept. of Business and Economics Studies, Högskolan i Gävle; Mats Dahllöf, Dept. of Linguistics and Philology, UU; Alicia Fornés, Universitat Autonoma de Barcelona, Spain
Funding: UU; Swedish Research Council; Riksbankens Jubileumsfond; eSSENCE
Period: 201401—-
Abstract: The problem of identifying the writer of some handwritten text is of great interest in both forensic and historical research. Sadly the magical CSI machine for identifying a scribal hand does not exist. Using image analysis, statistical models of how a scribe used the quill pen on a parchment can be collected. These measurements are treated as a statistical distribution over writing practices. We are using this information to identify single writers and perform style based dating of historical manuscripts. During 2016 we continuted to analyze over 10000 manuscript pages form the collection Svenskt Diplomatarium, from Riksarkivet. Using our newest methods, based on recent trends in deep learning, we are able to estimate the production date of a manuscript in this collection with a median error of less than 12 years. See Figure 62.

Figure 62: Writer Identification and Dating

71. **Image Analysis for Landscape Analysis**
Anders Brun
Partner: Bo Malmberg, Michael Nielsen, Dept. of Human Geography, Stockholm University; Anders Wästfelt, Dept. of Economics, SLU
Funding: SLU; Stockholm University
Period: 200901—-
Abstract: This project is a collaboration with researchers at SU and SLU. It aims to derive information about rural and city landscapes 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. This is an ongoing collaboration, which has so far resulted in one patent and one journal publication on the detection of damaged forest from aerial photographies. See Figure 63.

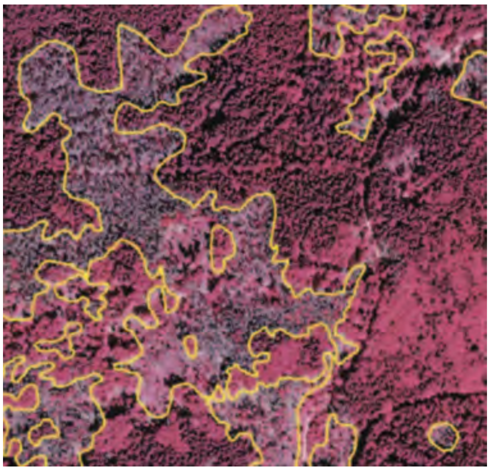

Figure 63: Image Analysis for Landscape Analysis

72. **Color Names**
Gunilla Borgefors
Funding: UU
Period: 20160701–
Abstract: Color is a very important aspect of both image analysis and visualization. Therefore, naming colors is also important. What is cerulean to an artist may be just blue to you and the same color as grass to a Zulu! In fact, there are many languages that do not have a term for blue, while Russian does not

have a single term for blue, but two distinct ones. Recently, there is a trend in machine and deep learning applications to use many different color names for image annotation, retrieval, and training. In this project I investigate results from color semantics and color perception experiments to get a better understanding on how different people understand color names and what the consequences for how you should name colors in various applications. A paper has been accepted for the ICPRAM conference Jan. 2018. See Figure 64.

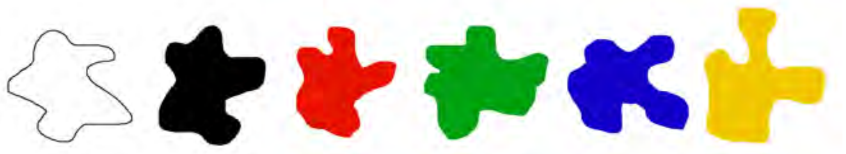

Figure 64: Color names

5.6 Cooperation partners

International

Adobe Research, San Jose, USA

AGH University of Science and Technology, Dept. of Geoinformatics and Applied Computer Science, Cracow, Poland

Antaros Medical, BioVenture Hub, Mölndal, Sweden

Bialystok University of Technology, Faculty of Computer Science, Bialystok, Poland

British Columbia Cancer Research Centre, Canada

Broad Institute of Harvard and MIT, Boston

Centre for Development of Advanced Computing (CDAC), Thiruvananthapuram, Kerala, India

Chan Zuckerberg Biohub, San Francisco, CA, USA

Dept. of Bioengineering and Applied Physics, Stanford University, USA

Dept. of Companion Animal Clinical Sciences, Norwegian University of Life Sciences

Dept. of Computer Science, Boston University, USA

Dept. of Computer Science, Faculty of Informatics, University of Debrecen, Hungary

Dept. of Computer Science, Stanford University, Palo Alto, USA

Dept. of Developmental Biology, Stanford University School of Medicine, USA

Dept. of Electrical and Computer Engineering, University of Iowa, IA, USA

Dept. of Electronic Computers RSREU, Ryazan, Russia

Dept. of Electronics, Tallinn University of Technology, Estonia

Dept. of Mathematics, West Virginia University, Morgantown, WV, USA

Dept. of Mathematics and Theoretical Physics, University of Cambridge, UK

Dept. of Paediatrics, Paracelsus Medical University, Salzburg, Austria

Dept. of Plant Developmental Biology, Institute of Experimental Biology, University of Wrocĺaw, Poland

Dept. of Radiology, MIPG, University of Pennsylvania, PA, USA

Dept. of Radiology, University of Iowa, IA, USA

École Normale d’Enseignement Technique et Professionnel (ENETP), Bamako, Mali

ETH Zürich, Switzerland

Faculty of Computer and Information Science, University of Ljubljana, Slovenia

Faculty of Technical Sciences, University of Novi Sad, Serbia

Flagship Biosciences Inc., Westminster, Colorado, USA

Icahn School of Medicine at Mount Sinai, New York, NY, USA

Imperial College, London

Institute for high performance computing and networking, CNR, Naples Italy

Institute of Biochemistry and Biology, Plant Physiology, University of Potsdam, Germany

Institute of Cellular Therapeutics, Allegheny Health Network, Pittsburgh, USA

Institute of Geography, School of GeoSciences, University of Edinburgh, UK

IRCCyN - University of Nantes, France

Laboratoire Reproduction et Développement des Plantes, Université de Lyon, France

Leeds Teaching Hospitals NHS Trust, UK

Pontificia Universidad Católica del Perú, Lima, PeruObesity Research Unit, Paracelsus

Medical University, Salzburg, Austria

Mathematical Institute, Serbian Academy of Sciences and Arts, Belgrade, Serbia

Oslo University Hospital, Norway

Pomeranian Medical University, Dept. of Ophthalmology, Szczecin, Poland

Regional Cancer Centre, Kerala, India

Sainsbury Laboratory, University of Cambridge, UK

Semmelweis University, Hungarian Academy of Sciences, Budapest, Hungary

Silesian University of Technology, Institute of Informatics, Gliwice, Poland

Sygehus Sønderjylland, Dept. of Ophthalmology, Sønderborg, Denmark

The Donelly Center, University of Toronto, Canada

The Ohio State University, USA

Universidad de Los Andes, Bogotá, Colombia

Universitat Autonoma de Barcelona, Spain

Universite des Sciences, des Techniques et des Technologies de Bamako, USTTB, Bamako, Mali

Université d'Antanarivo, Antanarivo, Madagascar

University of Iceland

University of Leeds, UK

University of Lyon, CREATIS, Lyon, France

University of Ottawa, Canada

National

Dept. of Cell and Molecular Biology, UU

Dept. of Earth Sciences, UU

Dept. of Engineering Sciences, UU

Dept. of History, UU

Dept. of Immunology, Genetics and Pathology, UU

Dept. of Linguistics and Philology, UU

Dept. of Medical Cell Biology, UU

Dept. of Medical Sciences, UU

Dept. of Neurology, UU

Dept. of Neuroscience, UU

Dept. of Organismal Biology, Environmental Toxicology, UU

Dept. of Pharmaceutical Biosciences, UU

Dept. of Surgical Pathology, UU

Dept. of Surgical Sciences, UU

Dept. of Women's and Children's Health, UU

ACCESS Linnaeus Centre, KTH

AstraZeneca AB, Mölndal

Astrego Diagnostics AB, Uppsala

Autoliv Dev AB, Vårgårda, Sweden

Children Obesity Clinic, Uppsala University Hospital

Comsol AB, Stockholm
Computational Biology and Biological Physics, Dept. of Astronomy and Theoretical Physics, Lund University
Dept. of Anatomy, Physiology, and Biochemistry, SLU
Dept. of Applied Physics, KTH
Dept. of Biochemistry and Biophysics, Stockholm University
Dept. of Biomedical Sciences and Veterinary Public Health, SLU
Dept. of Biosciences and Nutrition, Karolinska Institute, Stockholm
Dept. of Business and Economics Studies, Högskolan i Gävle
Dept. of Clinical Sciences, SLU
Dept. of Economics, SLU
Dept. of Forest Genetics and Plant Physiology, Swedish University of Agricultural Sciences, Umeå
Dept. of Human Geography, Stockholm University
Dept. of Industrial Development, IT and Land Management, University of Gävle
Dept. of Laboratory Medicine, Karolinska Institute, Stockholm
Dept. of Medical Biochemistry and Biophysics, Karolinska Institute, Stockholm
Dept. of Medicine, Karolinska Institute, Stockholm
Discovery Sciences, Innovative Medicines, AstraZeneca, Gothenburg, Sweden
Division of Building Materials, KTH, Stockholm
Hok Instrument AB, Västerås, Sweden
Luleå University of Technology, Luleå
Mathematical Sciences, Chalmers, Gothenburg
Medicinsk Tandvård, Folktandvården AB
Medicinsk Tandvård, Södersjukhuset
Protracer AB, Stockholm
SciLifeLab, Stockholm
SP Technical Research Institute of Sweden, Sustainable Built Environment, Stockholm
Vironova AB, Stockholm

6 Publications

Our most important products are our examined students, at all levels. Our second most important products are our publications. This year, we published 27 articles in scientific journals and 18 in fully reviewed proceedings, presenting new results. This is about the same as the previous four years, see Figure 65. Someone from CBA was first author of 17 of the 27 journal articles and for all proceedings articles. Almost all journal articles were in different journals, half of them in journals we had never published in before, whereas most proceedings articles are found in conferences that we revisited. We had as many as six articles in the Scandinavian conference, but we also had three articles in the – for us – new International Conference on Computer Vision (ICCV).

In 2017, three of our seniors were co-editors of two books and one conference proceeding. In addition we wrote two chapters in each of the books. Book chapters are important to present results that are already known to be useful and important to a wider scientific public. Christer Kiselman also wrote three articles to popularize science for the general public.

Note that Authors affiliated with CBA are in bold and as many of us have several affiliations we mark CBA with a star for extra clarity.

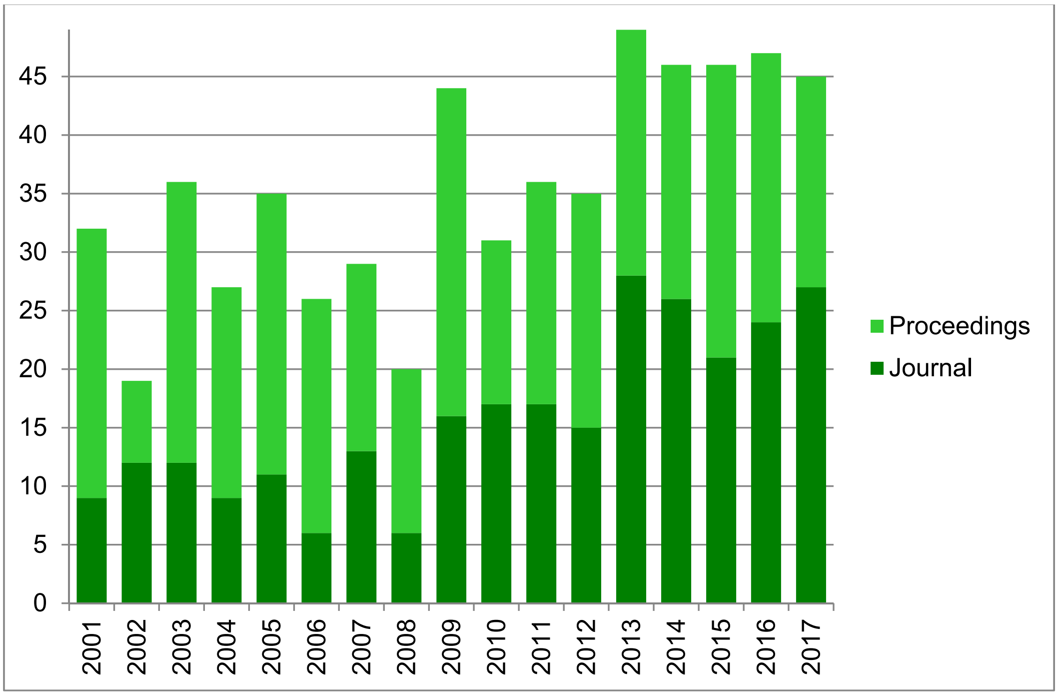

Figure 65: The number of publications from CBA 2001–2017.

6.1 Edited books and proceedings

1. **Analysis Meets Geometry: The Mikael Passare Memorial Volume**
   Editors: Mats Andersson(1), Jan Boman(2), **Christer Kiselman**, Pavel Kurasov(2), Ragnar Sigurdsson(3)
   (1) Chalmers University of Technology, Gothenburg
   (2) Stockholms University
   (3) University of Iceland
   Publisher: Birkhäuser Verlag

Abstract: This book is dedicated to the memory of Mikael Passare, an outstanding Swedish mathematician who devoted his life to developing the theory of analytic functions in several complex variables and exploring geometric ideas first-hand. It includes several papers describing Mikael's life as well as his contributions to mathematics, written by friends of Mikael's who share his attitude and passion for science. A major section of the book presents original research articles that further develop Mikael's ideas and which were written by his former students and co-authors. All these mathematicians work at the interface of analysis and geometry, and Mikael's impact on their research cannot be underestimated. Most of the contributors were invited speakers at the conference organized at Stockholm University in his honor. This book is an attempt to express our gratitude towards this great mathematician, who left us full of energy and new creative mathematical ideas.
Editorial Material: Curriculum Vitae, Mikael Passare, pages 3-4; Mikael Passare's Publications, pages 5-9.

2. **Skeletonization : Theory, Methods, and Applications**
Editors: Punam K. Saha(1), **Gunilla Borgefors**, Gabriella Sanniti di Baja(2)
(1) Dept. of Electrical and Computer Engineering and the Dept. of Radiology, University of Iowa, IA, USA
(2) Institute for high performance computing and networking, CNR, Naples Italy
Publisher: Academic Press
Abstract: Skeletonization: Theory, Methods and Applications is a comprehensive reference on skeletonization, written by the world's leading researchers in the field. The book presents theory, methods, algorithms and their evaluation, together with applications. Skeletonization is used in many image processing and computer vision applications such as shape recognition and analysis, shape decomposition and character recognition, as well as medical imaging for pulmonary, cardiac, mammographic applications.

3. **Progress in Pattern Recognition, Image Analysis, Computer Vision, and Applications, Proceedings from CIARP 2017**
Editors: César Beltrán-Castañón(1), **Ingela Nyström**(*), Fazel Famili(2)
(*) CBA
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6.2 Book chapters

1. **Mikael Passare (1959 – 2011)**
Author: **Christer O. Kiselman**(*)
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Book: Analysis Meets Geometry: The Mikael Passare Memorial Volume, pages 35-57
Editors: Mats Andersson, Jan Boman, **Christer Kiselman**, Pavel Kurasov, Ragnar Sigurdsson
Publisher: Birkhäuser Verlag
Abstract: Mikael Passare was a brilliant mathematician who died much too early. In this chapter, we present a sketch of his work and life.

2. **Convexity of marginal functions in the discrete case**
Authors: **Christer O. Kiselman**(*), Shiva Samieinia(1)
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Book: Analysis Meets Geometry: The Mikael Passare Memorial Volume, pages 287-309
Editors: Mats Andersson, Jan Boman, **Christer Kiselman**, Pavel Kurasov, Ragnar Sigurdsson
Publisher: Birkhäuser Verlag
Abstract: We define, using difference operators, classes of functions defined on the set of points with integer coordinates, which are preserved under the formation of marginal functions. The duality between classes of functions with certain convexity properties and families of second-order difference operators plays an important role and is explained using notions from mathematical morphology.

3. **Skeleton-based fast, fully automated generation of blood vessel systems**
Authors: **Kristína Lidayová**, Hans Frimmel(1), Chunliang Wang(2), **Ewert Bengtsson**, Örjan Smedby(2)
(1) Dept. of Information Technology, UU
(2) Royal Institute of Technology, Stockholm
Book: Skeletonization : Theory, Methods, and Applications, pages 345-382
Editors: Punam K. Saha, **Gunilla Borgefors**, Gabriella Sanniti di Baja
Publisher: Academic Press
Abstract: This chapter focuses on skeleton detection for clinical evaluation of blood vessel systems. In clinical evaluation, there is a need for fast and accurate segmentation algorithms that can reliably provide vessel measurements and additional information for clinicians to decide the diagnosis. Since blood vessels have a characteristic tubular shape, their segmentation can be accelerated and facilitated by first identifying the rough vessel centerlines, which can be seen as a special case of an image skeleton extraction algorithm. A segmentation algorithm will finally use the resulting skeleton as a seed region during the segmentation. The proposed method takes an unprocessed 3D computed tomography angiography (CTA) scan as an input and generates a connected graph of centrally located arterial voxels. The method works in two levels, where large arteries are captured in the first level, and small arteries are added in the second one. Experimental results show that the method can achieve high overlap rate and acceptable detection rate accuracies. High computational efficiency of the method opens the possibility for an interactive clinical use.

4. **Skeletonization and its applications – a review**
Authors: Punam K. Saha(1), **Gunilla Borgefors**(*), Gabriella Sanniti di Baja(2)
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(1) Dept. of Electrical and Computer Engineering and the Dept. of Radiology, University of Iowa, IA, USA
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Book: Skeletonization : Theory, Methods, and Applications, pages 3-42
Editors: Punam K. Saha, **Gunilla Borgefors**, Gabriella Sanniti di Baja
Publisher: Academic Press
Abstract: Skeletonization provides a compact yet effective representation of 2-D and 3-D objects, which is useful in many low- and high-level image-related tasks including object representation, retrieval, manipulation, matching, registration, tracking, recognition, and compression. Also, it facilitates efficient characterization of topology, geometry, scale, and other related local properties of an object. Despite that the notion of skeletonization is well defined in a continuous space, in the discrete world of image processing and computer vision, it is not, and, therefore, it is more often described using procedural approaches. Several computational approaches are available in the literature for extracting the skeleton of an object, some of which are widely different even at the level of their basic principles. In this chapter, we present a comprehensive and concise survey of different skeletonization principles and algorithms and discuss their properties, challenges, and benefits. Different important aspects of skeletonization, namely, topology preservation, skeleton simplification and pruning, multiscale skeletonization, and parallelization are discussed. Finally, various applications of skeletonization are reviewed, and the fundamental issues related to the analysis of performance of different skeletonization algorithms are debated.

6.3 Journal articles

1. **Automated deep-phenotyping of the vertebrate brain**
   Authors: **Amin Allalou**(*,1), Yuelong Wu(1), Mostafa Ghannad-Rezaie(1,2), Peter M Eimon(1), Mehmet Fatih Yanik(1,2)
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   (1) Massachusetts Institute of Technology, United States
   (2) ETH Zürich, Switzerland
   Journal: eLife, vol. 6:e23379
   Abstract: Here, we describe an automated platform suitable for large-scale deep-phenotyping of zebrafish mutant lines, which uses optical projection tomography to rapidly image brain-specific gene expression patterns in 3D at cellular resolution. Registration algorithms and correlation analysis are then used to compare 3D expression patterns, to automatically detect all statistically significant alterations in mutants, and to map them onto a brain atlas. Automated deep-phenotyping of a mutation in the master transcriptional regulator fezf2 not only detects all known phenotypes but also uncovers important novel neural deficits that were overlooked in previous studies. In the telencephalon, we show for the first time that fezf2 mutant zebrafish have significant patterning deficits, particularly in glutamatergic populations. Our findings reveal unexpected parallels between fezf2 function in zebrafish and mice, where mutations cause deficits in glutamatergic neurons of the telencephalon-derived neocortex.

2. **Mathematical morphology on irregularly sampled data in one dimension**
   Authors: **Teo Asplund(*)**, Cris L. Luengo Hendriks(1), Matthew J. Thurley(2), **Robin Strand(*)**
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   (1) Flagship Biosciences Inc., Westminster, Colorado, USA
   (2) Luleå University of Technology
   Journal: Mathematical Morphology—Theory and Applications, vol. 2, no. 1, pp. 1–24
   Abstract: Mathematical morphology (MM) on grayscale images is commonly performed in the discrete domain on regularly sampled data. However, if the intention is to characterize or quantify continuous-domain objects, then the discrete-domain morphology is affected by discretization errors that may be alleviated by considering the underlying continuous signal. Given a band-limited image, for example, a real image projected through a lens system, which has been correctly sampled, the continuous signal may be reconstructed. Using information from the continuous signal when applying morphology to the discrete samples can then aid in approximating the continuous morphology. Additionally, there are a number of applications where MM would be useful and the data is irregularly sampled. A common way to deal with this is to resample the data onto a regular grid. Often this creates problems where data is interpolated in areas with too few samples. In this paper, an alternative way of thinking about the morphological operators is presented. This leads to a new type of discrete operators that work on irregularly sampled data. These operators are shown to be morphological operators that are consistent with the regular, morphological operators under the same conditions, and yield accurate results under certain conditions where traditional morphology performs poorly.

3. **Quantitative high-content/high-throughput microscopy analysis of lipid droplets in subject-specific adipogenesis models**
   Authors: **Maxime Bombrun**(*,3), Hui Gao(1,2), **Petter Ranefall**(*,3), Niklas Mejhert(2), Peter Arner(2), **Carolina Wählby**(*,3)
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   Journal: Cytometry Part A, Vol. 91, No. 11, pp. 1068-1077
   Abstract: Neutral lipids packed in lipid droplets (LDs) are essential as a source of fuel for organisms, and specialized storing cells, the adipocytes, provide a buffer for energy variations. Many modern-society-disorders are connected with excess accumulation or deficiency of LDs in adipose tissue. Intracellular LD number and size distribution reflect the tissue conditions, while the associated mechanisms and genes rs are still poorly understood. Large-scale genetic screens using human in vitro differentiated primary adipocytes require cell samples donated from many patients. The heterogeneity appearing between donors highlighted the need for high-throughput methods robust to individual variations. Previous image analysis algorithms

failed to handle individual LDs, but focused on averages, hiding population heterogeneity. We present a new high-content analysis (HCA) technique for analysis of fat cell metabolism using data from a large-scale RNAi screen including images of more than 500 k in vitro differentiated adipocytes from three donors. The RNAi-based suppression of Perilipin 1 (PLIN1), a protein involved in the adipocyte lipid metabolism, served as a positive control, while cells treated with randomized RNA served as negative controls. We validate our segmentation by comparing our results to those of previously published methods: We also evaluate the discriminative power of different morphological features describing LD size distribution. Classification of cells as containing few large or many small LDs followed by calculating the percentage of cells in each class proved to discriminate the positive PLIN1-suppressed phenotype from the untreated negative control with an area under the receiver operating characteristic curve of 0.98. The results suggest that this HCA method offers improved segmentation and classification accuracy, and can, thus, be utilized to quantify changes in LD metabolism in response to treatment in many cell models relevant to a variety of diseases

4. **A comprehensive structural, biochemical and biological profiling of the human NUDIX hydrolase family**
   Authors: Jordi Carreras-Puigvert(1,2), Marinka Zitnik(3,4), Ann-Sofie Jemth(1,2) , Megan Carter(5), Judith E Unterlass(1,2) , Björn Hallström(6), Olga Loseva(1,2), Zhir Karem(1,2), José Manuel Calderón-Montaño(1,2), Cecilia Lindskog(7), Per-Henrik Edqvist(7), **Damian J Matuszewski**(*), Hammou Ait Blal(6), Ronnie P A Berntsson(5), Maria Häggblad(5,8), Ulf Martens(5,8), Matthew Studham(5,9), Bo Lundgren(5,8), **Carolina Wählby**(*,10), Erik L L Sonnhammer(5,9), Emma Lundberg(6), Pål Stenmark(5), Blaz Zupan(3,11), Thomas Helleday(1,2)
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   (11) Dept. of Molecular and Human Genetics, Baylor College of Medicine, Houston, USA
   Journal: Nature communications, Vol. 8, no 1, 1541
   Abstract: The NUDIX enzymes are involved in cellular metabolism and homeostasis, as well as mRNA processing. Although highly conserved throughout all organisms, their biological roles and biochemical redundancies remain largely unclear. To address this, we globally resolve their individual properties and inter-relationships. We purify 18 of the human NUDIX proteins and screen 52 substrates, providing a substrate redundancy map. Using crystal structures, we generate sequence alignment analyses revealing four major structural classes. To a certain extent, their substrate preference redundancies correlate with structural classes, thus linking structure and activity relationships. To elucidate interdependence among the NUDIX hydrolases, we pairwise deplete them generating an epistatic interaction map, evaluate cell cycle perturbations upon knockdown in normal and cancer cells, and analyse their protein and mRNA expression in normal and cancer tissues. Using a novel FUSION algorithm, we integrate all data creating a comprehensive NUDIX enzyme profile map, which will prove fundamental to understanding their biological functionality.

5. **Single-cell analysis of human pancreas reveals transcriptional signatures of aging and somatic mutation patterns**
   Authors: Martin Enge(1), H. Efsun Arda(2), **Marco Mignardi**(*,1,3), John Beausang(1), Rita Bottino(4), Seung K. Kim(2), Stephen R. Quake(1,4,5)
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Journal: Cell, Vol. 171, No. 2, pp. 321-330.e14
Abstract: As organisms age, cells accumulate genetic and epigenetic errors that eventually lead to impaired organ function or catastrophic transformation such as cancer. Because aging reflects a stochastic process of increasing disorder, cells in an organ will be individually affected in different ways, thus rendering bulk analyses of postmitotic adult cells difficult to interpret. Here, we directly measure the effects of aging in human tissue by performing single-cell transcriptome analysis of 2,544 human pancreas cells from eight donors spanning six decades of life. We find that islet endocrine cells from older donors display increased levels of transcriptional noise and potential fate drift. By determining the mutational history of individual cells, we uncover a novel mutational signature in healthy aging endocrine cells. Our results demonstrate the feasibility of using single-cell RNA sequencing (RNA-seq) data from primary cells to derive insights into genetic and transcriptional processes that operate on aging human tissue.

6. **Osteochondrosis, Synovial Fossae, and Articular Indentations in the Talus and Distal Tibia of Growing Domestic Pigs and Wild Boars**
Authors: P. E. Etterlin(1), S. Ekman(1), **Robin Strand**(*), K Olstad(2), C. J. Ley(3)
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Journal: Veterinary pathology, Vol. 54, No. 3, pp. 445-456
Abstract: Articular osteochondrosis (OC) often develops in typical locations within joints, and the characterization of OC distribution in the pig tarsus is incomplete. Prevalence of OC is high in domestic pigs but is presumed to be low in wild boars. Postmortem and computed tomography (CT) examinations of the talus and distal tibia from 40 domestic pigs and 39 wild boars were evaluated for the locations and frequencies of OC, synovial fossae, and other articular indentations, and frequency distribution maps were made. All domestic pigs but only 5 wild boars (13%) had OC on the talus. In domestic pigs, OC consistently affected the axial aspect of the medial trochlea tali in 11 (28%) joints and the distomedial talus in 26 (65%) joints. In wild boars, all OC lesions consistently affected the distomedial talus. On the articular surface of the distal tibia, all domestic pigs and 34 wild boars (87%) had synovial fossae and 7 domestic pigs (18%) had superficial cartilage fibrillation opposite an OC lesion (kissing lesion). Other articular indentations occurred in the intertrochlear groove of the talus in all domestic pigs and 13 wild boars (33%) and were less common on the trochlea tali. The prevalence of tarsal OC in wild boars is low. In domestic pigs and wild boars, OC is typically localized to the distomedial talus and in domestic pigs also to the medial trochlea tali. Further investigations into the reasons for the low OC prevalence in wild boars may help in developing strategies to reduce OC incidence in domestic pigs.

7. **New computerized staging method to analyze mink testicular tissue in environmental research**
Authors: **Azadeh Fakhrzadeh** (*), Ellinor Sporndly-Nees(1), Elisabeth Ekstedt(1), Lena Holm(1), **Cris L Luengo Hendriks**(*)
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Journal: Environmental Toxicology and Chemistry, Vol. 36, no 1, 156-164
Abstract: Histopathology of testicular tissue is considered to be the most sensitive tool to detect adverse effects on male reproduction. When assessing tissue damage, seminiferous epithelium needs to be classified into different stages to detect certain cell damages; but stage identification is a demanding task. The authors present a method to identify the 12 stages in mink testicular tissue. The staging system uses Gata-4 immunohistochemistry to visualize acrosome development and proved to be both intraobserver-reproducible and interobserver-reproducible with a substantial agreement of 83.6% (kappa=0.81) and 70.5% (kappa=0.67), respectively. To further advance and objectify this method, they present a computerized staging system that identifies these 12 stages. This program has an agreement of 52.8% (kappa 0.47) with the consensus staging by 2 investigators. The authors propose a pooling of the stages into 5 groups based on morphology, stage transition, and toxicologically important endpoints. The computerized program then reached a substantial agreement of 76.7% (kappa=0.69). The computerized staging tool uses local ternary patterns to describe the texture of the tubules and a support vector machine classifier to learn which textures correspond to which stages. The results have the potential to modernize the tedious staging process required in toxicolog-

ical evaluation of testicular tissue, especially if combined with whole-slide imaging and automated tubular segmentation.

8. **Deep Fish: Deep learning-based classification of zebrafish deformation for high-throughput screening**
Authors: **Omer Ishaq(*,1), Sajith Kecheril Sadanandan(*,1), Carolina Wählby(*,1)**
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Journal: Journal of Biomolecular Screening, Vol. 22, No. 1, pp. 102-107
Abstract: Zebrafish (Danio rerio) is an important vertebrate model organism in biomedical research, especially suitable for morphological screening due to its transparent body during early development. Deep learning has emerged as a dominant paradigm for data analysis and found a number of applications in computer vision and image analysis. Here we demonstrate the potential of a deep learning approach for accurate high-throughput classification of whole-body zebrafish deformations in multifish microwell plates. Deep learning uses the raw image data as an input, without the need of expert knowledge for feature design or optimization of the segmentation parameters. We trained the deep learning classifier on as few as 84 images (before data augmentation) and achieved a classification accuracy of 92.8% on an unseen test data set that is comparable to the previous state of the art (95%) based on user-specified segmentation and deformation metrics. Ablation studies by digitally removing whole fish or parts of the fish from the images revealed that the classifier learned discriminative features from the image foreground, and we observed that the deformations of the head region, rather than the visually apparent bent tail, were more important for good classification performance.

9. **Characterization of interfacial stress transfer ability in acetylation-treated wood fibre composites using X-ray microtomography**
Authors: Thomas Joffre(1), Kristoffer Segerholm(2,3), Cecilia Persson(1), Stig L. Bardage(2), **Cris L. Luengo Hendriks**(*), Per Isaksson(1)
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Journal: Industrial crops and products (Print), vol. 95, pp. 43–49
Abstract: The properties of the fibre/matrix interface contribute to stiffness, strength and fracture behaviour of fibre-reinforced composites. In cellulosic composites, the limited affinity between the hydrophilic fibres and the hydrophobic thermoplastic matrix remains a challenge, and the reinforcing capability ofthe fibres is hence not fully utilized. A direct characterisation of the stress transfer ability through pull-out tests on single fibres is extremely cumbersome due to the small dimension of the wood fibres. Here a novel approach is proposed:the length distribution ofthe fibres sticking out ofthe matrix atthe fracture surface is approximated using X-ray microtomography and is used as an estimate of the adhesion between the fibres and the matrix. When a crack grows in the material, the fibres will either break or be pulled-out of the matrix depending on their adhesion to the matrix: good adhesion between the fibres and the matrix should result in more fibre breakage and less pull-out of the fibres than poor adhesion. The effect of acetylation on the adhesion between the wood fibres and the PLA matrix was evaluated at different moisture contents using the proposed method. By using an acetylation treatment of the fibres it was possible to improve the strength of the composite samples soaked in the water by more than 30%.

10. **Automated training of deep convolutional neural networks for cell segmentation**
Authors: **Sajith Kecheril Sadanandan**(*,1), **Petter Ranefall**(*,1), Sylvie Le Guyader(2), **Carolina Wählby**(*,1)
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Journal: Scientific Reports, vol 7, eid 7860
Abstract: Deep Convolutional Neural Networks (DCNN) have recently emerged as superior for many image segmentation tasks. The DCNN performance is however heavily dependent on the availability of large amounts of problem-specific training samples. Here we show that DCNNs trained on ground truth created automatically using fluorescently labeled cells, perform similar to manual annotations.

11. **Domains of holomorphy for Fourier transforms of solutions to discrete convolution equations**
Author: **Christer O. Kiselman(*)**
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Journal: Science China Mathematics, no. 6, vol. 60, pp. 1005-1018
Abstract: We study solutions to convolution equations for functions with discrete support in Rn, a special case being functions with support in the integer points. The Fourier transform of a solution can be extended to a holomorphic function in some domains in Cn, and we determine possible domains in terms of the properties of the convolution operator.

12. **How to best fold a triangle**
Author: **Christer O. Kiselman**(*)
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Journal: Mathematische Semesterberichte, vol. 64, 25 pages
Abstract: We fold a triangle once along a straight line and study how small the area of the folded figure can be. It can always be as small as the fraction 2 minus the square root of 2 of the area of the original triangle. This is best possible: For every positive number q less than 2 minus the square root of 2 there are triangles that cannot be folded better than the fraction q.

13. **Improved centerline tree detection of diseased peripheral arteries with a cascading algorithm for vascular segmentation**
Authors: **Kristína Lidayová**(*), Hans Frimmel(1), **Ewert Bengtsson**(*), Örjan Smedby(2)
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Journal: Journal of Medical Imaging, Vol. 4, pp. 024004:1-11
Abstract: Vascular segmentation plays an important role in the assessment of peripheral arterial disease. The segmentation is very challenging especially for arteries with severe stenosis or complete occlusion. We present a cascading algorithm for vascular centerline tree detection specializing in detecting centerlines in diseased peripheral arteries. It takes a three-dimensional computed tomography angiography (CTA) volume and returns a vascular centerline tree, which can be used for accelerating and facilitating the vascular segmentation. The algorithm consists of four levels, two of which detect healthy arteries of varying sizes and two that specialize in different types of vascular pathology: severe calcification and occlusion. We perform four main steps at each level: appropriate parameters for each level are selected automatically, a set of centrally located voxels is detected, these voxels are connected together based on the connection criteria, and the resulting centerline tree is corrected from spurious branches. The proposed method was tested on 25 CTA scans of the lower limbs, achieving an average overlap rate of 89% and an average detection rate of 82%. The average execution time using four CPU cores was 70 s, and the technique was successful also in detecting very distal artery branches, e.g., in the foot.

14. **On the precision of third person perspective augmented reality for target designation tasks**
Authors: **Fei Liu**(*,1), **Stefan Seipel**(*,1)
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Journal: Multimedia tools and applications, vol. 76, no. 14, pp. 15279–15296
Abstract: The availability of powerful consumer-level smart devices and off-the-shelf software frameworks has tremendously popularized augmented reality (AR) applications. However, since the built-in cameras typically have rather limited field of view, it is usually preferable to position AR tools built upon these devices at a distance when large objects need to be tracked for augmentation. This arrangement makes it difficult or even impossible to physically interact with the augmented object. One solution is to adopt third person perspective (TPP) with which the smart device shows in real time the object to be interacted with, the AR information and the user herself, all captured by a remote camera. Through mental transformation between the user-centric coordinate space and the coordinate system of the remote camera, the user can directly interact with objects in the real world. To evaluate user performance under this cognitively demanding situation, we developed such an experimental TPP AR system and conducted experiments which required subjects to make markings on a whiteboard according to virtual marks displayed by the AR system. The same markings were also made manually with a ruler. We measured the precision of the markings as well as the time to accomplish the task. Our results show that although the AR approach was on average

around half a centimeter less precise than the manual measurement, it was approximately three times as fast as the manual counterpart. Additionally, we also found that subjects could quickly adapt to the mental transformation between the two coordinate systems.

15. **Passive in-vehicle driver breath alcohol detection using advanced sensor signal acquisition and fusion**
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Journal: Traffic Injury Prevention, vol. 18, p.. S31–S36
Abstract: Objective: The research objective of the present investigation is to demonstrate the present status of passive in-vehicle driver breath alcohol detection and highlight the necessary conditions for large-scale implementation of such a system. Completely passive detection has remained a challenge mainly because of the requirements on signal resolution combined with the constraints of vehicle integration. The work is part of the Driver Alcohol Detection System for Safety (DADSS) program aiming at massive deployment of alcohol sensing systems that could potentially save thousands of American lives annually. Method: The work reported here builds on earlier investigations, in which it has been shown that detection of alcohol vapor in the proximity of a human subject may be traced to that subject by means of simultaneous recording of carbon dioxide (CO2) at the same location. Sensors based on infrared spectroscopy were developed to detect and quantify low concentrations of alcohol and CO2. In the present investigation, alcohol and CO2 were recorded at various locations in a vehicle cabin while human subjects were performing normal in-step procedures and driving preparations. A video camera directed to the driver position was recording images of the driver's upper body parts, including the face, and the images were analyzed with respect to features of significance to the breathing behavior and breath detection, such as mouth opening and head direction. Results: Improvement of the sensor system with respect to signal resolution including algorithm and software development, and fusion of the sensor and camera signals was successfully implemented and tested before starting the human study. In addition, experimental tests and simulations were performed with the purpose of connecting human subject data with repeatable experimental conditions. The results include occurrence statistics of detected breaths by signal peaks of CO2 and alcohol. From the statistical data, the accuracy of breath alcohol estimation and timing related to initial driver routines (door opening, taking a seat, door closure, buckling up, etc.) can be estimated.The investigation confirmed the feasibility of passive driver breath alcohol detection using our present system. Trade-offs between timing and sensor signal resolution requirements will become critical. Further improvement of sensor resolution and system ruggedness is required before the results can be industrialized. Conclusions: It is concluded that a further important step toward completely passive detection of driver breath alcohol has been taken. If required, the sniffer function with alcohol detection capability can be combined with a subsequent highly accurate breath test to confirm the driver's legal status using the same sensor device. The study is relevant to crash avoidance, in particular driver monitoring systems and driver-vehicle interface design.

16. **Automated segmentation of human cervical-supraclavicular adipose tissue in magnetic resonance images**
Authors: Elin Lundström(1), **Robin Strand**(*,1), Anders Forslund(2,3), Peter Bergsten(4), Daniel Weghuber(5,6), Håkan Ahlström(1,7), Joel Kullberg(1,7)
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Journal: Scientific Reports, Vol. 7, eid 3064
Abstract: Human brown adipose tissue (BAT), with a major site in the cervical-supraclavicular depot, is a promising anti-obesity target. This work presents an automated method for segmenting cervical-supraclavicular adipose tissue for enabling time-efficient and objective measurements in large cohort research studies of BAT. Fat fraction (FF) and R2* maps were reconstructed from water-fat magnetic res-

onance imaging (MRI) of 25 subjects. A multi-atlas approach, based on atlases from nine subjects, was chosen as automated segmentation strategy. A semi-automated reference method was used to validate the automated method in the remaining subjects. Automated segmentations were obtained from a pipeline of preprocessing, affine registration, elastic registration and postprocessing. The automated method was validated with respect to segmentation overlap (Dice similarity coefficient, Dice) and estimations of FF, R2* and segmented volume. Bias in measurement results was also evaluated. Segmentation overlaps of Dice = 0.93 +/- 0.03 (mean +/- standard deviation) and correlation coefficients of r >0.99 (P <; 0.0001) in FF, R2* and volume estimates, between the methods, were observed. Dice and BMI were positively correlated (r = 0.54, P = 0.03) but no other significant bias was obtained (P >= 0.07). The automated method compared well with the reference method and can therefore be suitable for time-efficient and objective measurements in large cohort research studies of BAT.

17. **Mechanochemical polarization of contiguous cell walls shapes plant pavement cells**
    Authors: Mateusz Majda(1), Peter Grones(1), **Ida-Maria Sintorn**(*), Thomas Vain(1), Pascale Milani(2), Pawel Krupinski(3), Beata Zagórska-Marek(4), Corrado Viotti(1,5), Henrik Jönsson(1,6,7), Ewa J. Mellerowicz(1), Olivier Hamant(2), Stéphanie Robert(1)
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    (7) Dept. of Mathematics and Theoretical Physics, University of Cambridge, UK
    Journal: Developmental Cell, vol. 43, no. 3, pp. 290–304, eid e4
    Abstract: The epidermis of aerial plant organs is thought to be limiting for growth, because it acts as a continuous load-bearing layer, resisting tension. Leaf epidermis contains jigsaw puzzle piece-shaped pavement cells whose shape has been proposed to be a result of subcellular variations in expansion rate that induce local buckling events. Paradoxically, such local compressive buckling should not occur given the tensile stresses across the epidermis. Using computational modeling, we show that the simplest scenario to explain pavement cell shapes within an epidermis under tension must involve mechanical wall heterogeneities across and along the anticlinal pavement cell walls between adjacent cells. Combining genetics, atomic force microscopy, and immunolabeling, we demonstrate that contiguous cell walls indeed exhibit hybrid mechanochemical properties. Such biochemical wall heterogeneities precede wall bending. Altogether, this provides a possible mechanism for the generation of complex plant cell shapes.

18. **Exact evaluation of targeted stochastic watershed cuts**
    Authors: **Filip Malmberg**(*),**Chris Luengo Hendriks**(*),**Robin Strand**(*)
    (*) CBA
    Journal: Discrete Applied Mathematics, Vol. 216, No. 2, pp 449-460
    Abstract: Seeded segmentation with minimum spanning forests, also known as segmentation by watershed cuts, is a powerful method for supervised image segmentation. Given that correct segmentation labels are provided for a small set of image elements, called seeds, the watershed cut method completes the labeling for all image elements so that the boundaries between different labels are optimally aligned with salient edges in the image. Here, a randomized version of watershed segmentation, the targeted stochastic watershed, is proposed for performing multi-label targeted image segmentation with stochastic seed input. The input to the algorithm is a set of probability density functions (PDFs), one for each segmentation label, defined over the pixels of the image. For each pixel, we calculate the probability that the pixel is assigned a given segmentation label in seeded watershed segmentation with seeds drawn from the input PDFs. We propose an efficient algorithm (quasi-linear with respect to the number of image elements) for calculating the desired probabilities exactly.

19. **SmartPaint : a tool for interactive segmentation of medical volume images**
Authors: **Filip Malmberg**(*), Richard Nordenskjöld(1), **Robin Strand**(*,1), Joel Kullberg(1)
(*) CBA
(1) Dept. of Radiology, Oncology and Radiation Sciences, UU
Journal: Computer Methods in Biomechanics and Biomedical Engineering - Imaging and Visualization, vol. 5, no. 1, pp. 36–44
Abstract: We present SmartPaint, a general-purpose method and software for interactive segmentation of medical volume images. SmartPaint uses a novel paint-brush interaction paradigm, where the user segments objects in the image by 'sweeping' over them with the mouse cursor. The key feature of SmartPaint is that the painting tools adapt to the image content, selectively sticking to objects of interest while avoiding other structures. This behaviour is achieved by modulating the effect of the tools by both the Euclidean distance and the range distance (difference in image intensity values) from the mouse cursor. We evaluate SmartPaint on three publicly available medical image datasets, covering different image modalities and segmentation targets. The results show that, with a limited user effort, SmartPaint can produce segmentations whose accuracy is comparable to both the state-of-the-art automatic segmentation methods and manual delineations produced by expert users. The SmartPaint software is freely available, and can be downloaded from the authors' web page (http://www.cb.uu.se/similar to filip/SmartPaint/).

20. **A short feature vector for image matching : The Log-Polar Magnitude feature descriptor**
Authors: **Damian J. Matuszewski(*,1), Anders Hast(*), Carolina Wählby(*,1), Ida-Maria Sintorn(*,1,2)**
(*) CBA
(1) SciLifeLab, UU
(2) Vironova AB, Stockholm
Journal: PLoS ONE, vol. 12, no. 11, eid e0188496
Abstract: The choice of an optimal feature detector-descriptor combination for image matching often depends on the application and the image type. In this paper, we propose the Log-Polar Magnitude feature descriptor - a rotation, scale, and illumination invariant descriptor that achieves comparable performance to SIFT on a large variety of image registration problems but with much shorter feature vectors. The descriptor is based on the Log-Polar Transform followed by a Fourier Transform and selection of the magnitude spectrum components. Selecting different frequency components allows optimizing for image patterns specific for a particular application. In addition, by relying only on coordinates of the found features and (optionally) feature sizes our descriptor is completely detector independent. We propose 48- or 56-long feature vectors that potentially can be shortened even further depending on the application. Shorter feature vectors result in better memory usage and faster matching. This combined with the fact that the descriptor does not require a time-consuming feature orientation estimation (the rotation invariance is achieved solely by using the magnitude spectrum of the Log-Polar Transform) makes it particularly attractive to applications with limited hardware capacity. Evaluation is performed on the standard Oxford dataset and two different microscopy datasets; one with fluorescence and one with transmission electron microscopy images. Our method performs better than SURF and comparable to SIFT on the Oxford dataset, and better than SIFT on both microscopy datasets indicating that it is particularly useful in applications with microscopy images.

21. **Bridging histology and bioinformatics : Computational analysis of spatially resolved transcriptomics**
Authors: **Marco Mignardi**(*),**Omer Ishaq**(*,1), Xiaoyan Qian(2), **Carolina Wählby**(*,1)
(*) CBA
(1) SciLifeLab, UU
(2) Dept. of Biochemistry and Biophysics, Science for Life Laboratory, Stockholm University
Journal: Proceedings of the IEEE, Vol. 105, No. 3, pp. 530-541
Abstract: It is well known that cells in tissue display a large heterogeneity in gene expression due to differences in cell lineage origin and variation in the local environment. Traditional methods that analyze gene expression from bulk RNA extracts fail to accurately describe this heterogeneity because of their intrinsic limitation in cellular and spatial resolution. Also, information on histology in the form of tissue architecture and organization is lost in the process. Recently, new transcriptome-wide analysis technologies have enabled the study of RNA molecules directly in tissue samples, thus maintaining spatial resolution and complementing histological information with molecular information important for the understanding of many biological processes and potentially relevant for the clinical management of cancer patients. These new methods generally comprise three levels of analysis. At the first level, biochemical techniques are used to

generate signals that can be imaged by different means of fluorescence microscopy. At the second level, images are subject to digital image processing and analysis in order to detect and identify the aforementioned signals. At the third level, the collected data are analyzed and transformed into interpretable information by statistical methods and visualization techniques relating them to each other, to spatial distribution, and to tissue morphology. In this review, we describe state-of-the-art techniques used at all three levels of analysis. Finally, we discuss future perspective in this fast-growing field of spatially resolved transcriptomics.

22. **Using anti-aliased signed distance fields for generating surgical guides and plates from CT images**
Authors: **Fredrik Nysjö**(*), **Pontus Olsson**(*), **Filip Malmberg**(*), **Ingrid B. Carlbom**(*), **Ingela Nyström**(*)
(*) CBA
Journal: Journal of WSCG, Vol. 25, No. 1, pp. 11-20
Abstract: We present a method for generating shell-like objects such as surgical guides and plates from segmented computed tomography (CT) images, using signed distance fields and constructive solid geometry (CSG). We develop a userfriendly modeling tool which allows a user to quickly design such models with the help of stereo graphics, six degrees-of-freedom input, and haptic feedback, in our existing software for virtual cranio-maxiollofacial surgery planning, HASP. To improve the accuracy and precision of the modeling, we use an anti-aliased distance transform to compute signed distance field values from fuzzy coverage representations of the bone. The models can be generated within a few minutes, with only a few interaction steps, and are 3D printable. The tool has potential to be used by the surgeons themselves, as an alternative to traditional surgery planning services.

23. **Influence of applied corneal endothelium image segmentation techniques on the clinical parameters**
Authors: Adam Piorkowski(1), Karolina Nurzynska(2), Jolanta Gronkowska-Serafin(3,4) , **Bettina Selig**(*), Cezary Boldak(5), Daniel Reska(5)
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(2) Silesian University of Technology, Institute of Informatics, Gliwice, Poland
(3) Pomeranian Medical University, Dept. of Ophthalmology, Szczecin, Poland
(4) Sygehus Sønderjylland, Dept. of Ophthalmology, Sønderborg, Denmark
(5) Bialystok University of Technology, Faculty of Computer Science, Bialystok, Poland
Journal: Computerized Medical Imaging and Graphics, vol. 55, pp. 13–27
Abstract: The corneal endothelium state is verified on the basis of an in vivo specular microscope image from which the shape and density of cells are exploited for data description. Due to the relatively low image quality resulting from a high magnification of the living, non-stained tissue, both manual and automatic analysis of the data is a challenging task. Although, many automatic or semi-automatic solutions have already been introduced, all of them are prone to inaccuracy. This work presents a comparison of four methods (fully-automated or semi-automated) for endothelial cell segmentation, all of which represent a different approach to cell segmentation; fast robust stochastic watershed (FRSW), KH method, active contours solution (SNAKE), and TOPCON ImageNET. Moreover, an improvement framework is introduced which aims to unify precise cell border location in images preprocessed with differing techniques. Finally, the influence of the selected methods on clinical parameters is examined, both with and without the improvement framework application. The experiments revealed that although the image segmentation approaches differ, the measures calculated for clinical parameters are in high accordance when CV (coefficient of variation), and CVSL (coefficient of variation of cell sides length) are considered. Higher variation was noticed for the H (hexagonality) metric. Utilisation of the improvement framework assured better repeatability of precise endothelial cell border location between the methods while diminishing the dispersion of clinical parameter values calculated for such images. Finally, it was proven statistically that the image processing method applied for endothelial cell analysis does not influence the ability to differentiate between the images using medical parameters.

24. **Color map design for visualization in flood risk assessment**
Authors: **Stefan Seipel**(*,1), Nancy J. Lim(1)
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(1) Dept. of Industrial Development, IT and Land Management, University of Gävle
Journal: International Journal of Geographical Information Science, vol. 31, no. 11, pp. 2286–2309
Abstract: Visualizations of flood maps from simulation models are widely used for assessing the likelihood

of flood hazards in spatial planning. The choice of a suitable type of visualization as well as efficient color maps is critical to avoid errors or bias when interpreting the data. Based on a review of previous flood uncertainty visualization techniques, this paper identifies areas of improvements and suggests criteria for the design of a task-specific color scale in flood map visualization. We contribute a novel color map design for visualizing probabilities and uncertainties from flood simulation ensembles. A user study encompassing 83 participants was carried out to evaluate the effects of this new color map on user's decisions in a spatial planning task. We found that the type of visualization makes a difference when it comes to identification of non-hazardous sites in the flood risk map and when accepting risks in more uncertain areas. In comparison with two other existing visualization techniques, we observed that the new design was superior both in terms of task compliance and efficiency. In regions with uncertain flood statuses, users were biased toward accepting less risky locations with our new color map design.

25. **A concept for holistic whole body MRI data analysis, Imiomics**
Authors: **Robin Strand**(*,1), **Filip Malmberg**(*), Lars Johansson(1,2), Lars Lind(3), Magnus Sundbom(1), Håkan Ahlström(1,2), Joel Kullberg(1,2)
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Journal: PLoS ONE, Vol. 12, No. 2, eid e0169966
Abstract: Purpose: To present and evaluate a whole-body image analysis concept, Imiomics (imaging omics) and an image registration method that enables Imiomics analyses by deforming all image data to a common coordinate system, so that the information in each voxel can be compared between persons or within a person over time and integrated with non-imaging data. Methods: The presented image registration method utilizes relative elasticity constraints of different tissue obtained from whole-body water-fat MRI. The registration method is evaluated by inverse consistency and Dice coefficients and the Imiomics concept is evaluated by example analyses of importance for metabolic research using non-imaging parameters where we know what to expect. The example analyses include whole body imaging atlas creation, anomaly detection, and cross-sectional and longitudinal analysis. Results: The image registration method evaluation on 128 subjects shows low inverse consistency errors and high Dice coefficients. Also, the statistical atlas with fat content intensity values shows low standard deviation values, indicating successful deformations to the common coordinate system. The example analyses show expected associations and correlations which agree with explicit measurements, and thereby illustrate the usefulness of the proposed Imiomics concept. Conclusions: The registration method is well-suited for Imiomics analyses, which enable analyses of relationships to non-imaging data, e.g. clinical data, in new types of holistic targeted and untargeted big-data analysis.

26. **Objective automated quantification of fluorescence signal in histological sections of rat lens**
Authors: Nooshin Talebizadeh(1), **Nanna Zhou Hagström(2)**, Zhaohua Yu(1), Martin Kronschläger(1), Per Söderberg(1), **Carolina Wählby**(*,2)
(*) CBA
(1) Gullstrand lab of Ophthalmology, Dept. of Neuroscience, UU
(2) SciLifeLab, UU
Journal: Cytometry Part A, Vol. 91,No. 8, pp. 815-821
Abstract: Visual quantification and classification of fluorescent signals is the gold standard in microscopy. The purpose of this study was to develop an automated method to delineate cells and to quantify expression of fluorescent signal of biomarkers in each nucleus and cytoplasm of lens epithelial cells in a histological section. A region of interest representing the lens epithelium was manually demarcated in each input image. Thereafter, individual cell nuclei within the region of interest were automatically delineated based on watershed segmentation and thresholding with an algorithm developed in Matlab. Fluorescence signal was quantified within nuclei, cytoplasms and juxtaposed backgrounds. The classification of cells as labelled or not labelled was based on comparison of the fluorescence signal within cells with local background. The classification rule was thereafter optimized as compared with visual classification of a limited dataset. The performance of the automated classification was evaluated by asking 11 independent blinded observers to classify all cells (n=395) in one lens image. Time consumed by the automatic algorithm and visual classification of cells was recorded. On an average, 77% of the cells were correctly classified as compared with the majority vote of the visual observers. The average agreement among visual observers was 83%. However,

variation among visual observers was high, and agreement between two visual observers was as low as 71% in the worst case. Automated classification was on average 10 times faster than visual scoring. The presented method enables objective and fast detection of lens epithelial cells and quantification of expression of fluorescent signal with an accuracy comparable with the variability among visual observers.

27. **Quantitative image analysis of protein expression and colocalisation in skin sections**
Authors: Hanqian Zhang(1), Maja Ericsson(1), Marie Virtanen(1), Simone Weström(1), **Carolina Wählby**(*,2), Anders Vahlquist (1), Hans Törmä(1)
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(1) Dept. of Medical Sciences, Dermatology and Venereology, UU
(2) SciLifeLab, UU
Journal: Experimental dermatology, Vol. 27, month 11
Abstract: Immunofluorescence (IF) and in situ proximity ligation assay (isPLA) are techniques that are used for in situ protein expression and colocalization analysis, respectively. However, an efficient quantitative method to analyze both IF and isPLA staining on skin sections is lacking. Therefore, we developed a new method for semi-automatic quantitative layer-by-layer measurement of protein expression and colocalization in skin sections using the free open-source software CellProfiler. As a proof of principle, IF and isPLA of ichthyosis-related proteins TGm-1 and SDR9C7 were examined. The results indicate that this new method can be used for protein expression and colocalization analysis in skin sections.

6.4 Refereed conference proceedings

1. **Historical document binarization combining semantic labeling and graph cuts**
   Authors: **Kalyam Ram Ayyalasomayajula**(*), **Anders Brun**(*)
   (*) CBA
   In Proceedings: Image Analysis. SCIA 2017, Lecture Notes in Computer Science, vol. 10269, pp. 386–396
   Abstract: Most data mining applications on collections of historical documents require binarization of the digitized images as a pre-processing step. Historical documents are often subjected to degradations such as parchment aging, smudges and bleed through from the other side. The text is sometimes printed, but more often handwritten. Mathematical modeling of appearance of the text, background and all kinds of degradations, is challenging. In the current work we try to tackle binarization as pixel classification problem. We first apply semantic segmentation, using fully convolutional neural networks. In order to improve the sharpness of the result, we then apply a graph cut algorithm. The labels from the semantic segmentation are used as approximate estimates of the text and background, with the probability map of background used for pruning the edges in the graph cut. The results obtained show significant improvement over the state of the art approach.

2. **Image processing and its hardware support analysis vs synthesis - Historical trends**
   Author: **Ewert Bengtsson**(*)
   (*) CBA
   In Proceedings: Image Analysis. SCIA 2017, Lecture Notes in Computer Science, vol. 10269, pp. 3–14
   Abstract: Computers can be used to handle images in two fundamentally different ways. They can be used to analyse images to obtain quantitative data or some image understanding. And they can be used to create images that can be displayed through computer graphics and visualization. For both of these purposes it is of interest to develop efficient ways of representing, compressing and storing the images. While SCIA, the Scandinavia Conference of Image Analysis, according to its name is mainly concerned with the former aspect of images, it is interesting to note that image analysis throughout its history has been strongly influenced also by developments on the visualization side. When the conference series now has reached its 20th milestone it may be worth reflecting on what factors have been important in forming the development of the field. To understand where you are it is good to know where you come from and it may even help you understand where you are going.

3. **Decoding gene expression in 2D and 3D**
   Authors: **Maxime Bombrun(*,1), Petter Ranefall(*,1), Joakim Lindblad(*,1), Amin Allalou(*,1), Gabriele Partel(*,1), Leslie Solorzano(*,1)**, Xiaoyan Qian(2), Mats Nilsson(2), **Carolina Wählby**(*,1)
   (*) CBA
   (1) SciLifeLab, UU
   (2) Science for Life Laboratory, Dept. of Biochemistry and Biophysics, Stockholm University, Solna
   In Proceedings: Image Analysis. SCIA 2017. Lecture Notes in Computer Science, vol. 10270, pp. 257–268
   Abstract: Image-based sequencing of RNA molecules directly in tissue samples provides a unique way of relating spatially varying gene expression to tissue morphology. Despite the fact that tissue samples are typically cut in micrometer thin sections, modern molecular detection methods result in signals so densely packed that optical “slicing” by imaging at multiple focal planes becomes necessary to image all signals. Chromatic aberration, signal crosstalk and low signal to noise ratio further complicates the analysis of multiple sequences in parallel. Here a previous 2D analysis approach for image-based gene decoding was used to show how signal count as well as signal precision is increased when analyzing the data in 3D instead. We corrected the extracted signal measurements for signal crosstalk, and improved the results of both 2D and 3D analysis. We applied our methodologies on a tissue sample imaged in six fluorescent channels during five cycles and seven focal planes, resulting in 210 images. Our methods are able to detect more than 5000 signals representing 140 different expressed genes analyzed and decoded in parallel.

4. **Convolutional neural networks for false positive reduction of automatically detected cilia in low magnification TEM images**
   Authors: **Anindya Gupta(*,1)**, **Amit Suveer**(*), **Joakim Lindblad**(*,2), Anca Dragomir(3), **Ida-Maria Sintorn**(*,4), **Nataša Sladoje**(*,2)
   (*) CBA
   (1) T.J. Seebeck Dept. of Electronics, Tallinn University of Technology Estonia

(2) Mathematical Institute, Serbian Academy of Sciences and Arts, Belgrade, Serbia
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(4) Vironova AB, Stockholm
In Proceedings: Image Analysis. SCIA 2017. Lecture Notes in Computer Science, vol. 10269, pp. 407–418
Abstract: Automated detection of cilia in low magnification transmission electron microscopy images is a central task in the quest to relieve the pathologists in the manual, time consuming and subjective diagnostic procedure. However, automation of the process, specifically in low magnification, is challenging due to the similar characteristics of non-cilia candidates. In this paper, a convolutional neural network classifier is proposed to further reduce the false positives detected by a previously presented template matching method. Adding the proposed convolutional neural network increases the area under Precision-Recall curve from 0.42 to 0.71, and significantly reduces the number of false positive objects.

5. **An efficient descriptor based on radial line integration for fast non invariant matching and registration of microscopy images**
   Authors: **Anders Hast**(*), Gustaf Kylberg(1), **Ida-Maria Sintorn**(*,1)
   (*) CBA
   (1) Vironova AB, Stockholm
   In Proceedings: Advanced Concepts for Intelligent Vision Systems. ACIVS 2017. Lecture Notes in Computer Science, vol. 10617, pp. 723–734
   Abstract: Descriptors such as SURF and SIFT contain a framework for handling rotation and scale invariance, which generally is not needed when registration and stitching of images in microscopy is the focus. Instead speed and efficiency are more important factors. We propose a descriptor that performs very well for these criteria, which is based on the idea of radial line integration. The result is a descriptor that outperforms both SURF and SIFT when it comes to speed and the number of inliers, even for rather short descriptors.

6. **Spheroid segmentation using multiscale deep adversarial networks**
   Authors: **Sajith Kecheril Sadanandan**(*,1), Johan Karlsson(2), **Carolina Wählby**(*,1)
   (*) CBA
   (1) SciLifeLab, UU
   (2) Discovery Sciences, Innovative Medicines, AstraZeneca, Gothenburg, Sweden
   In Proceedings: IEEE International Conference on Computer Vision (ICCV), 2017, pp. 36-41
   Abstract: In this work, we segment spheroids with different sizes, shapes, and illumination conditions from bright-field microscopy images. To segment the spheroids we create a novel multiscale deep adversarial network with different deep feature extraction layers at different scales. We show that linearly increasing the adversarial loss contribution results in a stable segmentation algorithm for our dataset. We qualitatively and quantitatively compare the performance of our deep adversarial network with two other networks without adversarial losses. We show that our deep adversarial network performs better than the other two networks at segmenting the spheroids from our 2D bright-field microscopy images.

7. **Classification of cross-sections for vascular skeleton extraction using convolutional neural networks**
   Authors: **Kristína Lidayová**(*), **Anindya Gupta**(*,1), Hans Frimmel(2), **Ida-Maria Sintorn**(*), **Ewert Bengtsson**(*), Örjan Smedby(3)
   (*) CBA
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   (2) Division of Scientific Computing, Dept. of IT, UU
   (3) School of Technology and Health, KTH Royal Institute of Technology, Stockholm
   In Proceedings: Medical Image Understanding and Analysis MIUA 2017. Communications in Computer and Information Science, vol. 723, pp. 182-194
   Abstract: Recent advances in Computed Tomography Angiography provide high-resolution 3D images of the vessels. However, there is an inevitable requisite for automated and fast methods to process the increased amount of generated data. In this work, we propose a fast method for vascular skeleton extraction which can be combined with a segmentation algorithm to accelerate the vessel delineation. The algorithm detects central voxels - nodes - of potential vessel regions in the orthogonal CT slices and uses a convolutional neural network (CNN) to identify the true vessel nodes. The nodes are gradually linked together to generate an approximate vascular skeleton. The CNN classifier yields a precision of 0.81 and recall of 0.83 for the medium size vessels and produces a qualitatively evaluated enhanced representation of vascular skeletons.

8. **Airway-tree segmentation in subjects with acute respiratory distress syndrome**
Authors: **Kristína Lidayová**(*), Duván Alberto Betancur Gómez(1), Hans Frimmel(2), Marcela Hernández Hoyos(1), Maciej Orkisz(3), Örjan Smedby(4)
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(4) School of Technology and Health, KTH Royal Institute of Technology, Stockholm
In Proceedings: Image Analysis. SCIA 2017. Lecture Notes in Computer Science, vol 10270, pp. 76–87
Abstract: Acute respiratory distress syndrome (ARDS) is associated with a high mortality rate in intensive care units. To lower the number of fatal cases, it is necessary to customize the mechanical ventilator parameters according to the patient's clinical condition. For this, lung segmentation is required to assess aeration and alveolar recruitment. Airway segmentation may be used to reach a more accurate lung segmentation. In this paper, we seek to improve lung segmentation results by proposing a novel automatic airway-tree segmentation that is able to address the heterogeneity of ARDS pathology by handling various lung intensities differently. The method detects a simplified airway skeleton, thereby obtains a set of seed points together with an approximate radius and intensity range related to each of the points. These seeds are the input for an onion-kernel region-growing segmentation algorithm where knowledge about radius and intensity range restricts the possible leakage in the parenchyma. The method was evaluated qualitatively on 70 thoracic Computed Tomography volumes of subjects with ARDS, acquired at significantly different mechanical ventilation conditions. It found a large proportion of airway branches including tiny poorly-aerated bronchi. Quantitative evaluation was performed indirectly and showed that the resulting airway segmentation provides important anatomic landmarks. Their correspondences are needed to help a registration-based segmentation of the lungs in difficult ARDS cases where the lung boundary contrast is completely missing. The proposed method takes an average time of 43 s to process a thoracic volume which is valuable for the clinical use.

9. **The boolean map distance: Theory and efficient computation**
Authors: **Filip Malmberg**(*), **Robin Strand**(*), Jianming Zhang(1), Stan Sclaroff(2)
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(1) Adobe Research, San Jose, USA
(2) Dept. of Computer Science, Boston University, USA
In Proceedings: International Conference on Discrete Geometry for Computer Imagery, Lecture notes in computer science 10502
Abstract: We propose a novel distance function, the boolean map distance (BMD), that defines the distance between two elements in an image based on the probability that they belong to different components after thresholding the image by a randomly selected threshold value. This concept has been explored in a number of recent publications, and has been proposed as an approximation of another distance function, the minimum barrier distance (MBD). The purpose of this paper is to introduce the BMD as a useful distance function in its own right. As such it shares many of the favorable properties of the MBD, while offering some additional advantages such as more efficient distance transform computation and straightforward extension to multi-channel images.

10. **BoneSplit –A 3D painting tool for interactive bone segmentation in CT images**
Authors: **Ingela Nyström**(*), **Johan Nysjö**(*), Andreas Thor(1), **Filip Malmberg**(*)
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(1) Dept. of Surgical Sciences, Uppsala University Hospital
In Proceedings: Pattern Recognition and Information Processing. PRIP 2016. Communications in Computer and Information Science, vol 673, pp. 3–13
Abstract: We present an efficient interactive tool for segmenting individual bones and bone fragments in 3D computed tomography (CT) images. The tool, which is primarily intended for virtual cranio-maxillofacial (CMF) surgery planning, combines direct volume rendering with interactive 3D texture painting to enable quick identification and marking of bone structures. The user can paint markers (seeds) directly on the rendered bone surfaces as well as on individual CT slices. Separation of the marked bones is then achieved

through the random walks algorithm, which is applied on a graph constructed from the thresholded bones. The segmentation runs on the GPU and can achieve close to real-time update rates for volumes as large as 512 x 512 x 512 voxels. The user can perform segmentation editing to correct the result. An evaluation reports segmentation results comparable with manual segmentations, but obtained within a few minutes. In the invited PRIP talk, BoneSplit is presented and how the tool fits into our haptics-assisted surgery-planning system.

11. **Distance between vector-valued representations of objects in images with application in object detection and classification**
Authors: **Nataša Sladoje**(*,1), **Joakim Lindblad**(*,1)
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(1) Mathematical Institute of Serbian Academy of Sciences and Arts, Belgrade, Serbia
In Proceedings: 18th International Workshop on Combinatorial Image Analysis. IWCIA 2017. Lecture Notes in Computer Science, vol. 10256, pp. 243-255
Abstract: We present a novel approach to measuring distances between objects in images, suitable for information-rich object representations which simultaneously capture several properties in each image pixel. Multiple spatial fuzzy sets on the image domain, unified in a vector-valued fuzzy set, are used to model such representations. Distance between such sets is based on a novel point-to-set distance suitable for vector-valued fuzzy representations. The proposed set distance may be applied in, e.g., template matching and object classification, with an advantage that a number of object features are simultaneously considered. The distance measure is of linear time complexity w.r.t. the number of pixels in the image. We evaluate the performance of the proposed measure in template matching in presence of noise, as well as in object detection and classification in low resolution Transmission Electron Microscopy images.

12. **The Minimum Barrier Distance: A summary of recent advances**
Authors: **Robin Strand**(*), Ciesielski (1,2), **Filip Malmberg**(*), Punam K. Saha(3)
(*) CBA
(1) Dept. of Mathematics, West Virginia University, Morgantown, USA
(2) Dept. of Radiology, MIPG, University of Pennsylvania, Philadelphia, USA
(3) Dept. of Electrical and Computer Engineering and Dept. of Radiology, University of Iowa, Iowa City, USA
In Proceedings: Discrete Geometry for Computer Imagery. DGCI 2017. Lecture Notes in Computer Science, vol. 10502, pp. 57-68
Abstract: In this paper we present an overview and summary of recent results of the minimum barrier distance (MBD), a distance operator that is a promising tool in several image processing applications. The theory constitutes of the continuous MBD in R^n its discrete formulation in Z^n (in two different natural formulations), and of the discussion of convergence of discrete MBDs to their continuous counterpart. We describe two algorithms that compute MBD, one very fast but returning only approximate MBD, the other a bit slower, but returning the exact MBD. Finally, some image processing applications of MBD are presented and the directions of potential future research in this area are indicated.

13. **Enhancement of cilia sub-structures by multiple instance registration and super-resolution reconstruction**
Authors: **Amit Suveer**(*), **Nataša Sladoje**(*,1), **Joakim Lindblad**(*,1), Anca Dragomir(2), **Ida-Maria Sintorn**(*,3)
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(1) Mathematical Institute, Serbian Academy of Sciences and Arts, Belgrade, Serbia
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In Proceedings: Image Analysis. SCIA 2017. Lecture Notes in Computer Science, vol. 10270, pp. 362–374
Abstract: Ultrastructural analysis of cilia cross-sectional images using transmission electron microscopy (TEM) assists the pathologists to diagnose Primary Ciliary Dyskinesia, a genetic disease. The current diagnostic procedure is manual and difficult because of poor signal-to-noise ratio in TEM images. In this paper, we propose an automated multi-step registration approach to register many cilia cross-sectional instances. The novelty of the work is in the utilization of customized weight masks at each registration step to achieve good alignment of the specific cilium regions. Registration is followed by super-resolution reconstruction to

enhance the substructural information. Landmarks matching based evaluation of registration results in pixel alignment error of 2.35±1.82 pixels, and the subjective analysis of super-resolution reconstructed cilium shows a clear improvement in the visibility of the substructures such as dynein arms, radial spokes, and central pair.

14. **On-the-fly historical handwritten text annotation**
Authors: **Ekta Vats**(*), **Anders Hast**(*)
(*) CBA
In Proceedings: 14th IAPR International Conference on Document Analysis and Recognition (ICDAR), vol. 8, pp. 10–14
Abstract: The performance of information retrieval algorithms depends upon the availability of ground truth labels annotated by experts. This is an important prerequisite, and difficulties arise when the annotated ground truth labels are incorrect or incomplete due to high levels of degradation. To address this problem, this paper presents a simple method to perform on-the-fly annotation of degraded historical handwritten text in ancient manuscripts. The proposed method aims at quick generation of ground truth and correction of inaccurate annotations such that the bounding box perfectly encapsulates the word, and contains no added noise from the background or surroundings. This method will potentially be of help to historians and researchers in generating and correcting word labels in a document dynamically. The effectiveness of the annotation method is empirically evaluated on an archival manuscript collection from well-known publicly available datasets.

15. **Automatic document image binarization using Bayesian optimization**
Authors: **Ekta Vats**(*), **Anders Hast**(*), Prashant Singh(1)
(*) CBA
(1) Dept. of Information Technology, UU
In Proceedings: 4th International Workshop on Historical Document Imaging and Processing (HIP2017). pp. 89–94
Abstract: Document image binarization is often a challenging task due to various forms of degradation. Although there exist several binarization techniques in literature, the binarized image is typically sensitive to control parameter settings of the employed technique. This paper presents an automatic document image binarization algorithm to segment the text from heavily degraded document images. The proposed technique uses a two band-pass filtering approach for background noise removal, and Bayesian optimization for automatic hyperparameter selection for optimal results. The effectiveness of the proposed binarization technique is empirically demonstrated on the Document Image Binarization Competition (DIBCO) and the Handwritten Document Image Binarization Competition (H-DIBCO) datasets.

16. **Deep convolutional neural networks for detecting cellular changes due to malignancy**
Authors: **Håkan Wieslander**(*), **Gustav Forslid**(*), **Ewert Bengtsson**(*), **Carolina Wählby**(*), Jan-Michaél Hirsch(1), Christina Runow Stark, **Sajith Kecheril Sadanandan**(*)
(*) CBA
(1) Dept. of Surgical Sciences, UU
(2) Swedish Dental Service Medical Dental Care, Södersjukhuset
In Proceedings: IEEE International Conference on Computer Vision (ICCV), 2017, pp. 82-89
Abstract: Discovering cancer at an early stage is an effective way to increase the chance of survival. However, since most screening processes are done manually it is time inefficient and thus a costly process. One way of automizing the screening process could be to classify cells using Convolutional Neural Networks. Convolutional Neural Networks have been proven to be accurate for image classification tasks. Two datasets containing oral cells and two datasets containing cervical cells were used. For the cervical cancer dataset the cells were classified by medical experts as normal or abnormal. For the oral cell dataset we only used the diagnosis of the patient. All cells obtained from a patient with malignancy were thus considered malignant even though most of them looked normal. The performance was evaluated for two different network architectures, ResNet and VGG. For the oral datasets the accuracy varied between 78-82% correctly classified cells depending on the dataset and network. For the cervical datasets the accuracy varied between 84-86% correctly classified cells depending on the dataset and network. The results indicate a high potential for detecting abnormalities in oral cavity and in uterine cervix. ResNet was shown to be the preferable network, with a higher accuracy and a smaller standard deviation.

17. **Neural Ctrl-F : Segmentation-free query-by-string word spotting in handwritten manuscript collections**
    Authors: **Tomas Wilkinson**(*), Jonas Lindström(1), **Anders Brun**(*)
    (*) CBA
    (1) Dept. of History, UU
    In Proceedings: IEEE International Conference on Computer Vision (ICCV), 2017, pp. 4433-4442
    Abstract: In this paper, we approach the problem of segmentation-free query-by-string word spotting for handwritten documents. In other words, we use methods inspired from computer vision and machine learning to search for words in large collections of digitized manuscripts. In particular, we are interested in historical handwritten texts, which are often far more challenging than modern printed documents. This task is important, as it provides people with a way to quickly find what they are looking for in large collections that are tedious and difficult to read manually. To this end, we introduce an end-to-end trainable model based on deep neural networks that we call Ctrl-F-Net. Given a full manuscript page, the model simultaneously generates region proposals, and embeds these into a distributed word embedding space, where searches are performed. We evaluate the model on common benchmarks for handwritten word spotting, outperforming the previous state-of-the-art segmentation-free approaches by a large margin, and in some cases even segmentation-based approaches. One interesting real-life application of our approach is to help historians to find and count specific words in court records that are related to women's sustenance activities and division of labor. We provide promising preliminary experiments that validate our method on this task.

18. **Distance between vector-valued fuzzy sets based on intersection decomposition with applications in object detection**
    Authors: **Johan Öfverstedt**(*), **Nataša Sladoje**(*,1), **Joakim Lindblad**(*,1)
    (*) CBA
    (1) Mathematical Institute of Serbian Academy of Sciences and Arts, Belgrade, Serbia
    In Proceedings: Mathematical Morphology and its Applications to Signal and Image Processing. ISMM 2017. Lecture Notes in Computer Science, vol. 10225, pp. 395–407
    Abstract: We present a novel approach to measuring distance between multi-channel images, suitably represented by vector-valued fuzzy sets. We first apply the intersection decomposition transformation, based on fuzzy set operations, to vector-valued fuzzy representations to enable preservation of joint multi-channel properties represented in each pixel of the original image. Distance between two vector-valued fuzzy sets is then expressed as a (weighted) sum of distances between scalar-valued fuzzy components of the transformation. Applications to object detection and classification on multi-channel images and heterogeneous object representations are discussed and evaluated subject to several important performance metrics. It is confirmed that the proposed approach outperforms several alternative single- and multi-channel distance measures between information-rich image/object representations.

6.5 Other

Authors affiliated with CBA are in bold.

1. **Computer-aided diagnostics in digital pathology**
   Authors: **Ewert Bengtsson**(*), Håvard Danielsen(1), Darren Treanor(2,3,4), Metin N. Gurcan(5), Calum MacAulay(6), Béla Molnár(7)
   (*) CBA
   (1) Oslo University Hospital, Norway
   (2) University of Leeds, UK
   (3) Linköping University
   (4) Leeds Teaching Hospitals NHS Trust, UK
   (5) The Ohio State University, USA
   (6) British Columbia Cancer Research Centre, Canada
   (7) Semmelweis University, Hungarian Academy of Sciences, Budapest, Hungary
   Journal: Cytometry Part A, vol. 91, no 6, p. 551-554
   Comment: Special invitation, editorial material

2. **Discrete convolution operators, the Fourier transformation, and its tropical counterpart: the Fenchel transformation**
   Author: **Christer O. Kiselman**(*)
   (*) CBA
   In Proceedings: 3rd EAUMP Conference: Advances in Mathematics and its Applications, Kampala, Uganda: Makerere University, p. 7-28

3. **Lars Hörmander - some early memories (Chinese)**
   Author: **Christer O. Kiselman**(*)
   (*) CBA
   In Proceedings: Mathematical Advances in Translation, Vol. 36, no 2, p. 120-121
   Comment: Translation into Chinese of the English original translated in 2015

4. **Watching solar eclipses 1945 - 2017**
   Author: **Christer O. Kiselman**(*)
   (*) CBA
   Journal: Bulletin of the Swedish Mathematical Society, no October, p. 17-21
   Comment: Science popularization

5. **Bråk och språk – vad som är förnuftigt och logiskt**
   Authors: **Christer O. Kiselman**(*), Hania Uscka- Wehlou(1)
   (*) CBA
   (1) Dept. of Mathematics, UU
   Journal: Nämnaren : tidskrift för matematikundervisning, no 1, p. 45-49
   Comment: Science popularization

6. **Falska vänner, vassa vrår och språkliga fällor**
   Authors: **Christer O. Kiselman**(*), Hania Uscka-Wehlou(1)
   (*) CBA
   Dept. of Mathematics, UU
   Journal: Nämnaren : tidskrift för matematikundervisning, no 2, p. 43-51
   Comment: Science popularization

7. **CBA Annual Report 2016**
   Editors: Marine Astruc, Gunilla Borgefors, Filip Malmberg, Lena Nordström, Ingela Nyström, Leslie Solorzano, **Robin Strand**
   Publisher: Centre for Image Analysis, 110 pages

7 Activities

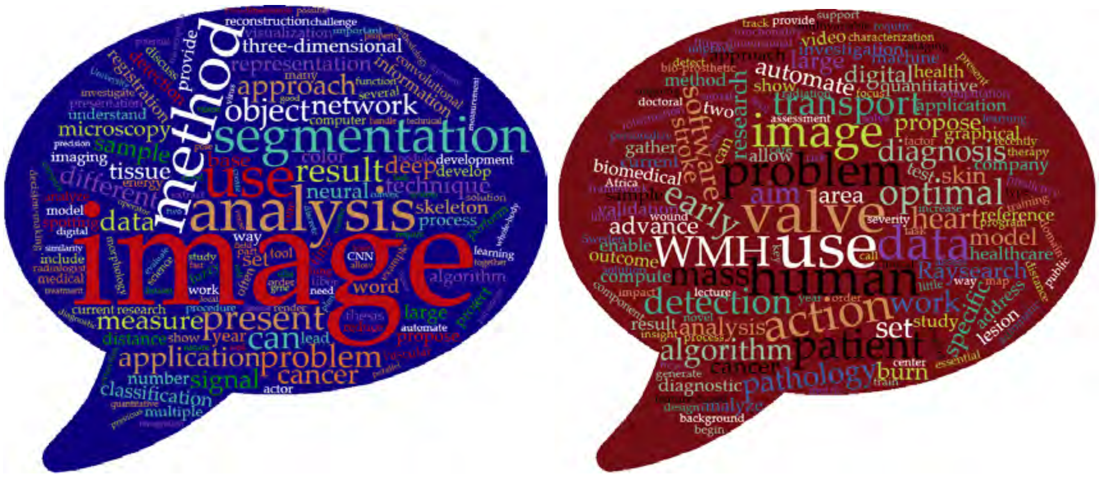
This year, we were part of organising the first Swedish Symposium on Deep Learning, a Summer school for PhD students in Novi Sad, Serbia, and a Workshop together with a Korean Company. The Symposium was very well attended, as this is a very “hot” subject at present.

We are often invited to give seminars outside CBA, this year in Uppsala, Denmark, Russia, Serbia, Canada, and USA. Something we are really proud of is our own longstanding internal seminar series, with one or two 30–45 minute seminars every Monday afternoon. This year, we had 39 seminars, nine of which were given by guests. The average number of attendants was 23, significantly higher than the previous years.

As usual, we attended many national and international meetings, where we presented our work as invited speaker or giving oral or poster presentations of reviewed papers. We also gave presentations at non-reviewed meetings. Attending national and international meetings is inspiring and necessary to be part of the scientific community.

We had an unusual number of visiting scientists, staying for longer periods. Professor Heung-Kook Choi from Inje University Korea stayed for a full sabbatical year. This was a revisit, as he was a PhD student at CBA 1990–96 supervised by Ewert Bengtsson. Another distinguished guest was Professor Douglas Hofstadter from Indiana University, USA who stayed for three months. Other visitors came from Finland, Estonia, Serbia, and Canada.

Other ways of being part of the international scientific community is working for professional organisations, being Editors of scientific journals, serving in programme committees for international and national conferences, reviewing for international journals (which often goes undocumented), being members of dissertation committees, and functioning as evaluators of projects and positions.



(a) (b)

Figure 66: Wordcloud of the titles and abstracts of the internal (a) and external (b) seminars.

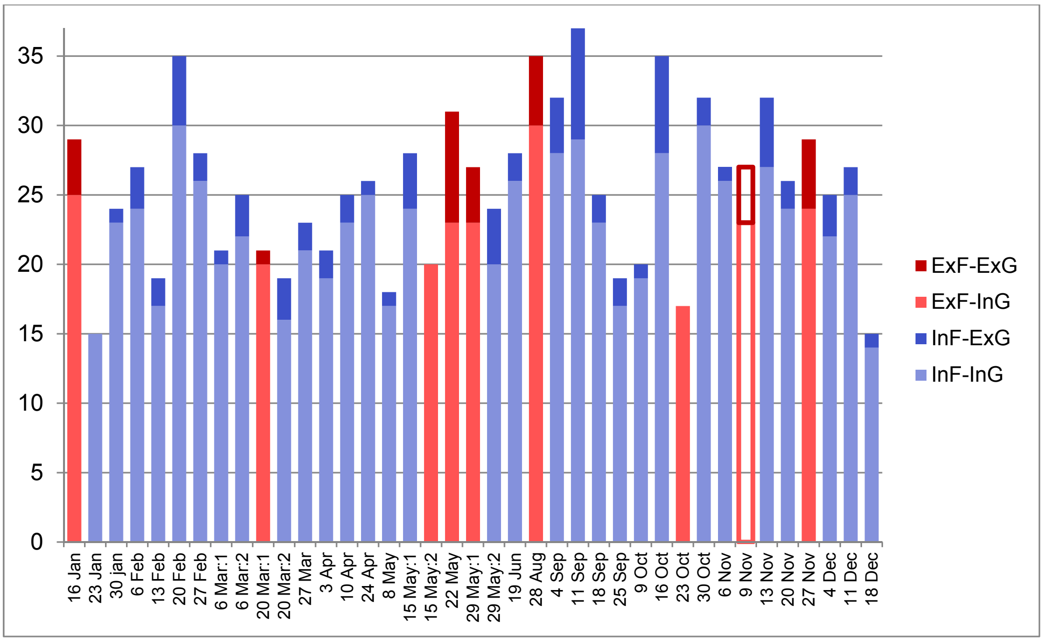


Figure 67: Our own seminar series. Blue represents seminars given by CBA people, while red represents guest lecturers. The saturated part on the bars represents guest attendants. For one seminar data is missing, this is shown as a blank bar and is represented by the median value (in its category).

7.1 Conference organization

1. **The First Swedish Symposium on Deep Learning**
Organisers: SSBA
Address: Royal Institute of Technology, Stockholm
Brinellvägen 64, Stockholm.
Date: 20170620–20170621
Comment: Anders Brun was in the organizing committee and also one of the founders of this symposium series.

2. **Summer School on Image Processing (SSIP) 2017**
Organisers: Faculty of Technical Sciences, University of Novi Sad, Serbia
Address: Faculty of Technical Sciences, University of Novi Sad, Serbia
Date: 20170713–20170722
Comment: Joakim Lindblad was head of the Program Committee

3. **CBA and JLK Inspection (Korea Company) Joint Workshop**
Organisers: Ewert Bengtsson, Carolina Wählby, Myeong-Jae Lee
Address: CBA
Date: 20171107–20171107

7.2 Seminars held outside CBA

1. **Petter Ranefall**
Date: 20170310
Address: Department of Electrical Engineering, Technical University of Denmark, Lyngby, Denmark
Title: Quantitative Microscopy – Applications and Algorithms

2. **Filip Malmberg**
   Date: 20170316
   Address: Uppsala University
   Title: Minimal Graph Cuts – a Powerful Tool for Solving Optimization Problems in Computerized Image Analysis
   Comment: Docent lecture.
3. **Carolina Wählby and Petter Ranefall**
   Date: 20170331
   Address: Farmbio, BMC, Uppsala
   Title: from Microscopy Images to Quantitative Data
4. **Tomas Wilkinson**
   Date: 20170412
   Address: Dept. of Information Technology, UU
   Title: Machine Learning Journal Club on Deep learning
   Comment: Joint seminar with Niklas Wahlström and Carl Andersson from syscon
5. **Ingela Nyström**
   Date: 20170425
   Address: Federal Research Center "Computer Science and Control" of the Russian Academy of Sciences, Moscow, Russian Federation
   Title: Interactive 3D Image Segmentation and Visualisation – for Cranio-Maxillofacial Surgery Planning and Orthopedic Application
   Comment: A talk in the NCPRIA seminar series with approximately 80 participants.
6. **Petter Ranefall**
   Date: 20170503
   Address: SciLifeLab Science Summit, Uppsala Konsert och Kongress
   Title: BioImage Informatics Facility
7. **Anders Hast**
   Date: 20170504
   Address: Ghent University, Belgium
   Title: Statistical Tools and Methods and their applications in Image Processing, Computer Vision and HTR
8. **Petter Ranefall**
   Date: 20170608
   Address: SciLifeLab PhD student day, Uppsala Biomedical Centre, UU
   Title: Bioimageinformatics: from Microscopy Images to Quantitative Data
9. **Amit Suveer**
   Date: 20170721
   Address: Novi Sad, Serbia
   Title: Image Denoising for Electron Microscopy
   Comment: Summer School in Image Processing (SSIP 2017)
10. *Conference:* NEUBIAS Training School for Facility Staffs: Göteborg
    Joakim Lindblad
    Date: 20170911–20170914
    Address: Centre for Cellular Imaging, Sahlgrenska Academy, at the University of Gothenburg
    Title: Introduction to Matlab
    Comment: Training School is organized within NEUBIAS - A new Network of European BioImage Analysts to advance life science imaging
11. *Conference:* "Big Data Training School for Life Sciences"
    Nataša Sladoje
    Date: 20170921–20170922
    Address: Uppsala
    Title: Neubias: Bioimage Analysis – Current Trends and Future Directions

12. **Filip Malmberg**
Date: 20171018
Address: Department of Computer Science, Boston University, USA
Title: Medical Image Analysis Projects at Uppsala University
13. **Ingela Nyström**
Date: 20171031
Address: Dept. of Electrical and Computer Engineering, University of Victoria, Canada
Title: Interactive 3D Image Segmentation and Visualisation - for Cranio-Maxillofacial Surgery Planning and Orthopedic Applications
Comment: Guest speaker at the IEEE Victoria Section Annual General Meeting
14. **Ingela Nyström**
Date: 20171101
Address: Dept. of Electrical and Computer Engineering, University of Victoria, Canada
Title: Gender Diversity at Work – the Case at Centre for Image Analysis at Uppsala University
Comment: Guest speaker at the IEEE Victoria Section Women in Engineering

7.3 Seminars at CBA

1. **Erik Vidholm, RaySearch Laboratories**
Date: 20170116
Title: Fighting Cancer with Code
2. **Ludovic Blache**
Date: 20170123
Title: Dynamic Representation of Actors' Models from Multi-View Reconstructions
3. **Gunilla Borgefors**
Date: 20160130
Title: Math and Science in the Newspaper – Possibilities and Limitations
4. **Nataša Sladoje**
Date: 201170206
Title: Distance Between Vector-Valued Fuzzy Representations with Application in Object Detection and Classification
5. **Teo Asplund**
Date: 20170213
Title: Mathematical Morphology on Irregularly Sampled Signals
6. **Gunilla Borgefors**
Date: 20170220
Title: What Do You Call That Colour? - an Engineer Reads Linguistics
7. **Tomas Wilkinson**
Date: 20170227
Title: A Deep Learning Method for Word Spotting in Manuscripts
8. **Fredrik Nysjö**
Date: 20170306
Title: Point-based Rendering for Medical Visualization and Digital Sculpting
9. **Johan Öfverstedt**
Date: 20170306
Title: Similarity of Hybrid Object Representations With Applications in Object Recognition and Classification
10. **Ekta Vats**
Date: 20170320
Title: A Fuzzy Approach for Early Human Action Detection

11. **Ewert Bengtsson**
    Date: 20170320
    Title: Image Processing and Its Hardware Support. Analysis vs Synthesis – Historical Trends
12. **Joakim Lindblad**
    Date: 20170327
    Title: on Segmentation by Energy Minimization
13. **Amit Suveer**
    Date: 20170403
    Title: Cilia Substructure Enhancement for TEM Images
14. **Maxime Bombrun**
    Date: 20170410
    Title: Decoding Gene Expression in 2d and 3d
15. **Damian Matuszewski**
    Date: 20170424
    Title: Investigating Deep Segmentation for Viruses in Tem Images
16. **Robin Strand**
    Date: 20170508
    Title: The Current Status of a Large-Scale Whole-Body Mr Image Analysis Project, Imiomics
17. **Kristina Lidayova**
    Date: 20170515
    Title: Fast Methods for Vascular Segmentation Based on Approximate Skeleton Detection
18. **Alexandra Branzan-Albu**
    Date: 20170515
    Title: Fast and Accurate Tracking of Highly Deformable Prosthetic Heart Valves
19. **Prof Alejandro F. Frangi**
    Date: 20170522
    Title: Image-based Cerebrovascular Modeling for Advanced Diagnosis and Interventional Planning
20. **Kimmo Kartasalo**
    Date: 20170529
    Title: Feature-Based Characterization and Detection for 2d and 3d Digital Pathology
21. **Gustav Forslid, Håkan Wieslander, David Ramnerö, Nils Bäckström**
    Date: 20170529
    Title: Master's Thesis Project Presentations: Cnn:S in Computer Vision
22. **Kalyan Ram Ayyalasomayajula**
    Date: 20170619
    Title: Introduction to Proximal Operator for Solving Energy Functionals in Image Processing
23. **Jian Fransén**
    Date: 20170828
    Title: Machine Learning and Computer Vision in Diagnostics: Applications to Burn Wounds and Skin Lesions Assessment
24. **Ingela Nyström**
    Date: 20170924
    Title: A Summary of 25 Years of Research – One Selected Image per Year
25. **Eva Breznik**
    Date: 20170911
    Title: The Deepmedic Network – Segmentation of Abdominal Organs in Mri
26. **Ida-Maria Sintorn**
    Date: 20170918
    Title: Cell culture pattern recognition – getting to know the data and first tests using filter banks

27. **Gabriele Partel**
    Date: 20170925
    Title: Decoding Gene Expression in 'In-Situ' Sequencing: A Graph-Based Approach.
28. **Leslie Solorzano**
    Date: 20171009
    Title: Image Analysis for WSI, a Gastric Cancer Application
29. **Carolina Wählby**
    Date: 20171016
    Title: Quantitative Microscopy: from Hierarchical Approaches to Analysis of Cells, Model Organisms and Tissue
30. **Heung-Kook Choi**
    Date: 20171013
    Title: Stroke Outcomes Are Worse with Larger Leukoaraiosis Volumes
31. **Anders Hast**
    Date: 20171030
    Title: Challenges of Semi-Automatic Transcription of Medieval Manuscripts
32. **Sajith Kecheril Sadanandan**
    Date: 20171106
    Title: Deep Neural Networks and Image Analysis for Quantitative Microscopy
33. **Jeroen van der Laak**
    Date: 20171109
    Title: Deep Learning for Breast Cancer Histopathology
34. **Christer Oscar Kiselman**
    Date: 20171113
    Title: Thoughts on Discretization and Tropicalization
35. **Stefan Seipel**
    Date: 20171120
    Title: Multi-Criteria Decision Making based on Multilayer Raster Images
36. **Axel Ringh**
    Date: 20171127
    Title: Optimal Mass Transport as a Distance Measure Between Images
37. **Ashis Kumar Dhara**
    Date: 20171204
    Title: Self-Learning Tool for Radiologists Using Content-Based Image Retrieval Technique
38. **Johan Öfverstedt**
    Date: 20171211
    Title: A Symmetric Similarity Measure for Gradient-Based Affine Image Registration
39. **Elisabeth Wetzer**
    Date: 20171218
    Title: Evaluating a Novel Approach for Fiber Analysis in Forensic Applications

7.4 Conference participation

7.4.1 Special invited speaker

1. *Conference:* The 1st NEUBIAS 2020 Conference
   Nataša Sladoje, Joakim Lindblad
   Date: 20170212–20170217
   Address: Oeiras-Lisbon, Portugal
   Title: Detection and Enhancement of Objects in Low Resolution Transmission Electron Microscopy Images for Multi-Scale Imaging and Structural Analysis
   Comment: Sladoje and Lindblad co-authored the invited contribution presented by Lindblad.

2. *Conference:* 17th Congress of the European Light Microscopy Initiative (ELMI2017)
   Carolina Wählby
   Date: 20170423–20170526
   Address: Dubrovnik, Croatia
   Title: Digital image analysis in microscopy; hierarchical approaches for sparse data of cells, model organisms and tissue

3. *Conference:* 20th SCIA 2017
   Ewert Bengtsson
   Date: 20170611–20170614
   Address: Tromsö
   Title: Image Processing and Its Hardware Support. Analysis vs Syntesis – Historical Treds.

4. *Conference:* The First Swedish Symposium on Deep Learning (SSDL2017)
   Carolina Wählby
   Date: 20170620–20170621
   Address: Dubrovnik, Croatia
   Title: Deep learning in life science and microscopy - challenges and possibilities

5. *Conference:* 21st Medical Image Understanding and Analysis (MIUA 2017)
   Ingela Nyström
   Date: 20170711–20170713
   Address: University of Edinburgh, UK
   Title: Interactive Image Segmentation and Visualisation for Cranio-Maxillofacial Surgery Planning and Orthopedic Applications
   Comment: Nyström also chaired a session on ”Cardiovascular Imaging”.

6. *Conference:* BioImage Informatics Conference 2017
   Carolina Wählby *Date:* 20170919–20170921
   Address: Banff, Canada
   Title: Deep learning for drug screening; hierarchical approaches for sparse image data of cells, model organisms and tissue

7. *Conference:* International Conference on Computer Vision, ICCV2017, BioImage Computing workshop
   Nataša Sladoje, Joakim Lindblad
   Date: 20171022–20171029
   Address: Venice, Italy
   Title: Tackling a Major Bottleneck in the Bioimage Computing Community – Network of European Bioimage Analysts (Neubias)
   Comment: Sladoje was an invited speaker at the BioImage Computing Workshop

8. *Conference:* XXII IberoAmerican Congress on Pattern Recognition (CIARP 2017)
   Ingela Nyström
   Date: 20171107–20171110
   Address: Universidad Técnica Federico Santa María, Valparaiso, Chile
   Title: Interactive Image Segmentation and Visualization for Cranio-Maxillofacial Surgery Planning and Orthopedic Applications

Comment: Nyström opened and closed the conference on behalf of the IAPR Executive Committee as well as handed the Best Prizes to recipients. Nyström was chairing three sessions: invited speaker José Ruiz-Shulcloper, University of Havana, Cuba; invited speaker Aaron Courville, University of Montreal; and the session on Image Processing. Nyström attended the CIARP Steering Committee meeting as IAPR representative.

7.4.2 Oral presentations – refereed conferences

1. *Conference:* 7th Strategic Conference of Zebrafish Investigators
   Amin Allalou
   Date: 20170114–20170118
   Address: Asilomar Conference Grounds, Pacific Grove, California, USA
   Title: Hyperdimensional in Vivo Phenotyping with Vertebrate Automated Screening Technologies (VASTs)

2. *Conference:* 13th International Symposium on Mathematical Morphology
   Johan Öfverstedt
   Date: 20170515–20170517
   Address: Fontainebleau, France
   Title: Distance Between Vector-Valued Fuzzy Sets Based on Intersection Decomposition with Applications in Object Detection

3. *Conference:* WSCG 2017
   Fredrik Nysjö
   Date: 20170528–20170601
   Address: Plzen, Czech Republic
   Title: Using Anti-Aliased Signed Distance Fields for Generating Surgical Guides and Plates from CT Images

4. *Conference:* 18th International Workshop on Combinatorial Image Analysis, IWCIA2017
   Nataša Sladoje, Joakim Lindblad
   Date: 20170619–20170621
   Address: Plovdiv, Bulgaria
   Title: Distance Between Vector-valued Representations of Objects in Images with Application in Object Detection and Classification
   Comment: N.Sladoje and J. Lindblad co-authored the paper presented by Sladoje

5. *Conference:* 21st Medical Image Understanding and Analysis (MIUA 2017)
   Kristina Lidayova
   Date: 20170711–20170713
   Address: University of Edinburgh, UK
   Title: Classifications of Cross-sections for Vascular Skeleton Extraction Using Convolutional Neural Networks

6. *Conference:* Nordic Zebrafish meeting 2017
   Amin Allalou
   Date: 20170914–20170915
   Address: Evolutionary Biology Center (EBC), UU
   Title: High-Throughput Analysis of Zebrafish Gene Expression Pattern

7. *Conference:* Discrete Geometry for Computer Imagery (DGCI)
   Filip Malmberg
   Date: 20170919–20170921
   Address: Vienna
   Title: The Boolean Map Distance: Theory and Efficient Computation

8. *Conference:* TheIIER International Conference
   Heung Kook Choi
   Date: 20171008–20171009

Address: Nas Hotel, Saint-Petersburg, Russia
Title: Automatic Image Registration Based Control Points and Evaluation

9. *Conference:* Franco-Swedish Workshop
Joakim Lindblad
Date: 20171108–20171108
Address: Institute Pascal laboratory, Campus Le-Puy-en-Velay, France
Title: Coverage Segmentation Based on Energy Minimization
10. *Conference:* Franco-Swedish Workshop
Nataša Sladoje
Date: 20171108–20171108
Address: Institute Pascal laboratory, Campus Le-Puy-en-Velay, France
Title: Distance Between Vector-Valued Representations with Application in Object Detection and Classification
11. *Conference:* Franco-Swedish Workshop
Nataša Sladoje
Date: 20171108–20171108
Address: Institute Pascal laboratory, Campus Le-Puy-en-Velay, France
Title: Automatic Detection of Lung Emboli in CTPA Examinations – Initial Study
12. *Conference:* TheIIER International Conference
Heung Kook Choi
Date: 20171124–20171125
Address: Paris, France
Title: Color Mapping 3D Shape Visualization for Brain Hippocampus Images
Comment: The IIER Excellent Paper Award

7.4.3 Poster presentations – refereed conferences

1. *Conference:* 7th Strategic Conference of Zebrafish Investigators
Amin Allalou
Date: 20170114–20170118
Address: Asilomar Conference Grounds, Pacific Grove, California, USA
Title: Automated Deep-Phenotyping of the Zebrafish Brain
2. *Conference:* Scandinavian Conference on Image Analysis
Amit Suveer, Nataša Sladoje, Joakim Lindblad, Anca Dragomir and Ida-Maria Sintorn
Date: 20170611–20170614
Address: Tromsø, Norway
Title: Enhancement of Cilia Sub-structures by Multiple Instance Registration and Super-resolution Reconstruction
3. *Conference:* Scandinavian Conference on Image Analysis
Anindya Gupta, Amit Suveer, Joakim Lindblad, Anca Dragomir, Ida-Maria Sintorn and Nataša Sladoje
Date: 20170611–20170614
Address: Tromsø, Norway
Title: Convolutional Neural Networks for False Positive Reduction of Automatically Detected Cilia in Low Magnification TEM Images
4. *Conference:* 20th Scandinavian Conference on Image Analysis, SCIA 2017
Max Bombrun
Date: 20170612–20170614
Address: Tromsø, Norway
Title: Decoding Gene Expression in 2D and 3D

5. *Conference:* International Conference on Computer Vision, ICCV 2017
   Tomas Wilkinson
   Date: 20171022–20171029
   Address: Venice, Italy
   Title: Neural Ctrl-F: Segmentation-free Query-by-String Word Spotting in Handwritten Manuscript Collections

6. *Conference:* International Conference on Computer Vision, ICCV 2017
   Sajith Kecheril Sadanandan
   Date: 20171022–20171029
   Address: Venice, Italy
   Title: Spheroid segmentation using multiscale deep adversarial networks

7.4.4 Oral presentations – non-refereed conferences

1. *Conference:* Network of European Bioimage Analysis Conference (NEUBIAS 2017)
   Joakim Lindblad, Ida-Maria Sintorn, Amit Suveer, Anindya Gupta, Anca Dragomir, and Nataša Sladoje
   Date: 20170212–20170217
   Address: Lisbon, Portugal
   Title: Detection and Enhancement of Objects in Low-resolution Transmission Electron Microscopy Images for Multi-scale Imaging and Structural Analysis

2. *Conference:* Sida Conference
   Christer Kiselman
   Date: 20170307–20170308
   Address: Headquaters of the Swedish International Development Cooperation Agency (Sida), Stockholm
   Title: Discretization and Tropicalization: How Are They Related?

3. *Conference:* Swedish Symposium on Image Analysis (SSBA 2017)
   Kalyan Ram Ayyalasomayajula
   Date: 20170313–20170315
   Address: Linköping
   Title: Document Binarization Combining with Graph Cuts and Deep Neural Networks

4. *Conference:* Swedish Symposium on Image Analysis (SSBA 2017)
   Amit Suveer, Nataša Sladoje, Joakim Lindblad, Anca Dragomir and Ida-Maria Sintorn
   Date: 20170313–20170315
   Address: Linköping
   Title: Cilia Ultrastructural Visibility Enhancement by Multiple Instance Registration and Super-resolution Reconstruction

5. *Conference:* Swedish Symposium on Image Analysis (SSBA 2017)
   Anindya Gupta
   Date: 20170313–20170315
   Address: Linköping
   Title: False positive Reduction of Cilia Detected in Low-resolution TEM Images using a Convolutional Neural Network

6. *Conference:* Swedish Symposium on Image Analysis (SSBA 2017)
   Teo Asplund
   Date: 20170313–20170315
   Address: Linköping
   Title: Approximating Continuous One-Dimensional Morphology by Irregular Sampling

7. *Conference:* Swedish Symposium on Image Analysis (SSBA 2017)
   Robin Strand
   Date: 20170313–20170315

Address: Linköping
Title: A Distance Function Defined by a Barrier Cost

8. *Conference:* Swedish Syposium on Image Analysis (SSBA 2017)
   Eva Breznik
   Date: 20170313–20170315
   Address: Linköping
   Title: Permutation-Based Corrections for Multiple Comparisons on Whole-Body Mr Images
9. *Conference:* NordConsNet Workshop 2017
   Robin Strand
   Date: 20170522–20170522
   Address: ITC, Uppsala
   Title: Discrete Optimisation in Image Processing
10. *Conference:* Material for Sustainable Product Development
    Robin Strand
    Date: 20170531–20170531
    Address: Ångström Laboratory
    Title: Material Analysis with Computerized Image Processing
    Comment: The workshop was in Swedish: Material för hållbar produktutveckling. Swedish presentation title: Materialanalys med datoriserad bildbehandling
11. *Conference:* 20th Scandinavian Conference on Image Analysis (SCIA 2017)
    Ingela Nyström
    Date: 20170612–20170614
    Address: University of Tromsœ, Norway
    Title: Opening Ceremony of SCIA 2017 from the International Association for Pattern Recognition
    Comment: Nyström was also chairing the session of special invited speaker Professor Ewert Bengtsson and the session on Pattern Detection and Recognition.
12. *Conference:* Inauguration of MedTech Science and Innovation
    Robin Strand
    Date: 20170614–20170614
    Address: Akademiska Hospital
    Title: Advanced Image Processing as a Tool in Surgery
    Comment: The presentation was in Swedish: Avancerad bildanalys som ett verktyg inom kirurgi
13. *Conference:* International Academy of Sciences, Warsaw
    Christer Kiselman
    Date: 20170910–20170915
    Address: Warsaw Management School, Graduate and Postgraduate School.
    Title: Digital Geometry, Mathematical Morphology, and Discrete Optimization
    Comment: The lectures were given in Esperanto.
14. *Conference:* Workshop on current Biomed-IT projects in Uppsala
    Andreas Thor, Ingela Nyström
    Date: 20171017
    Address: Dept. of Information Technology, UU
    Title: Haptics-Assisted Cranio-Maxillofacial Surgery Planning using Interactive 3D Image Segmentation and Visualisation
    Comment: Robin Strand organised this workshop
15. *Conference:* SME-day in Medical Engineering
    Robin Strand
    Date: 20171129
    Address: Ångström Laboratory
    Title: Presentation of the Arena BioMedical Information Technology
    Comment: An SME-day organized by UU Innovation.

16. *Conference:* SME-day in Medical Engineering
    Filip Malmberg
    Date: 20171129
    Address: Ångström Laboratory
    Title: Medical Image Analysis at the Division of Radiology, Uppsala University
    Comment: An SME-day organized by UU Innovation.
17. *Conference:* SME-day in Medical Engineering
    Ingela Nyström
    Date: 20171129
    Address: Ångström Laboratory
    Title: Interactive 3D Image Segmentation and Visualisation for Orthopedic Applications
    Comment: An SME-day organized by UU Innovation.

7.4.5 Poster presentations – non-refereed conferences

1. *Conference:* SciLifeLab Science Summit
   Amit Suveer, Anindya Gupta, Nataša Sladoje, Joakim Lindblad, Anca Dragomir and Ida-Maria Sintorn
   Date: 20170503–20170503
   Address: SciLifeLab, Uppsala
   Title: Automated Workflow for Enhancement of Biological Nanostructures in Transmission Electron Microscopy
2. *Conference:* SciLifeLab Science Summit
   Petter Ranefall
   Date: 20170503
   Address: Uppsala Koncert och Kongress
   Title: BioImage Informatics Facility
3. *Conference:* SciLife Lab PhD Students Summit
   Amit Suveer, Nataša Sladoje, Joakim Lindblad, Anca Dragomir and Ida-Maria Sintorn
   Date: 20170608–20170608
   Address: Uppsala Biomedical Centre, UU
   Title: Automated Transmission Electron Microscopy for Biological Nanostructures Enhancement
4. *Conference:* SSDL2017
   Petter Ranefall
   Date: 20170620–20170621
   Address: Royal Institute of Technology, Stockholm
   Title: Semi-Automatic Training Data Generation for Cell Segmentation CNN:s
5. *Conference:* SSDL2017
   Kalyan Ram Ayyalasomayajula, Anders Brun
   Date: 20170620–20170621
   Address: Royal Institute of Technology, Stockholm
   Title: Semantic Labeling using Convolutional Networks coupled with Graph-Cuts for Document binarization
6. *Conference:* SSDL2017
   Tomas Wilkinson
   Date: 20170620–20170621
   Address: Royal Institute of Technology, Stockholm
   Title: Neural Ctrl-F: Segmentation-free Query-by-String Word Spotting in Handwritten Manuscript Collections

7. *Conference:* SciLifeLab Science Facility Forum
   Petter Ranefall
   Date: 20171003–20171003
   Address: Uppsala University main building
   Title: SciLifeLab BioImage Informatics Facility

8. *Conference:* Swedish e-Science Academy, eSSENCE event
   Ekta Vats
   Date: 20171011–20171012
   Address: Umeå
   Title: Historical Handwritten Text Recognition
   Comment: Poster presentation at Swedish e-Science Academy's annual event

9. *Conference:* Women in Machine Learning, WiML
   Eva Breznik
   Date: 20171203–20171207
   Address: Long Beach, California, US
   Title: Abdominal Organ Segmentation in whole-body MRI

7.4.6 Attended conferences

1. *Conference:* NetDeliver - Network on numerical modeling and simulation of anticancer drug delivery in liver - workshop
   Nataša Sladoje, Joakim Lindblad
   Date: 20170116–20170116
   Address: Paris, France
   Comment: N.Sladoje and J. Lindblad are NetDeliver network members

2. *Conference:* NeuBIAS
   Petter Ranefall
   Date: 20170215–20170217
   Address: Lisbon

3. *Conference:* Swedish Symposium on Image Analysis, SSBA 2017
   Teo Asplund, Ewert Bengtsson, Maxime Bombrun, Gunilla Borgefors, Eva Breznik, Anders Brun, Heung Kook Choi, Anindya Gupta, Joakim Lindblad, Filip Malmberg, Damian Matuszewski, Fredrik Nysjö, Ingela Nyström, Gabriele Partell,Kalyan Ram Ayyalasomayajula, Petter Ranefall, Sajith Kecheril Sadanandan, Ida-Maria Sintorn, Nataša Sladoje, Amit Suveer, Robin Strand, Carolina Wählby
   Date: 20170313–20170315
   Address: Linköping

4. *Conference:* International Symposium on Mathematical Morphology, ISMM 2017
   Teo Asplund, Christer Kiselman
   Date: 20170515–20170517
   Address: Fontainebleau, France
   Comment: Kiselman was a member of the Program Committee, appointed in November 2016.

5. *Conference:* Scandinavian Conference on Image Analysis
   Gunilla Borgefors, Johan Öfverstedt
   Date: 20170611–20170614
   Address: Tromsö, Norway
   Comment: Borgefors presented the ”Best Scandinavian Thesis” Award.

6. *Conference:* SSBA Education Workshop
   Robin Strand
   Date: 20170619
   Address: Royal Institute of Technology, Stockholm

7. *Conference:* Swedish Symposium on Deep Learning
   Eva Breznik, Amit Suveer, Ekta Vats
   Date: 20170620–20170621
   Address: Royal Institute of Technology, Stockholm
8. *Conference:* SIGGRAD 2017
   Fredrik Nysjö
   Date: 20170816–20170818
   Address: Norrköping
9. *Conference:* Royal Socitety of Sciences in Uppsala Day
   Gunilla Borgefors
   Date: 20170829–20170829
   Address: Gustavianum, Uppsala
10. *Conference:* Summer School for Advanced Methods in Biomedical Image Analysis
    Johan Öfverstedt
    Date: 20170903–20170909
    Address: Centre for Biomedical Image Analysis, Faculty of Informatics, Masaryk University, Brno, Czech Republic
11. *Conference:* MICCAI 2017
    Ludovic Blache
    Date: 20170910–20170914
    Address: Quebec City, Quebec, Canada
12. *Conference:* 3rd NEUBIAS workshop
    Nataša Sladoje
    Date: 20170911–20170914
    Address: Gothenburg
13. *Conference:* Discrete Geometry for Computer Images (DGCI)
    Gunilla Borgefors, Christer Kiselman
    Date: 20170919–20170921
    Address: Wienna, Austria
    Comment: Borgefors was Session Chair
14. *Conference:* Digital pathology
    Ewert Bengtsson
    Date: 20171109–20171109
    Address: Uppsala
15. *Conference:* Conference on Zamenhof's life, ideas, and work
    Christer Kiselman
    Date: 20171126–20171126
    Address: Stockholm
16. *Conference:* Neural Information Processing Systems, NIPS
    Eva Breznik
    Date: 20171204–20171209
    Address: Long Beach, California, US

7.5 Visiting scientists

1. **Kimmo Kartasalo**
   Address: BioMediTech Institute and Faculty of Biomedical Sciences and Engineering, Tampere University of Technology, Tampere, Finland
   Host: Carolina Wählby
   Date: 20170106–20170831
   Topic: Analysis of tissue samples

2. **Anindya Gupta**
   Address: Tallinn University of Technology, Estonia
   Host: Ida-Maria Sintorn, Amit Suveer
   Date: 20170201–20170531
   Topic: Automatic Detection and Classification of Structures in Transmission Electron Microscopy using Deep Learning Techniques
   Comments: Visiting researcher and Swedish-Estonian collaboration

3. **Heung Kook Choi**
   Address: Department of Computer Engineering, Inje University, Republic of Korea
   Host: Carlina Wählby, Ingela Nyström, Ewert Bengtsson
   Date: 20170201–20180131
   Topic: Guest Professor

4. **Alexandra Branzan-Albu**
   Address: University of Victoria, Canada
   Host: Ingela Nyström
   Date: 20170512–20170609
   Topic: Sabbatical visit to build network for joint future projects on image analysis

5. **Buda Bajić**
   Address: Faculty of Technical Sciences, University of Novi Sad, Serbia
   Host: Nataša Sladoje, Joakim Lindblad
   Date: 20170815–20171028
   Topic: Image restoration and segmentation by energy minimization, PhD project and a conference paper preparation

6. **Douglas Hofstadter**
   Address: Center for Research on Concepts and Cognition, Indiana University, Bloomington, Indiana, USA
   Hosts: Gunilla Borgefors, Lars-Henrik Eriksson Dept. IT, UU, Ulf Danielsson Dept. Physics and Astronomy, UU
   Date: 20171201–20180223
   Topic: Sabbatical

7.6 Committees

Teo Asplund, Kristína Lidayová, Fredrik Nysjö and Tomas Wilkinson

- Editors, SSBAktuellt, the newsletter of the Swedish Society for Automated Image Analysis

Ewert Bengtsson
International:

- Lifetime Fellow of the Institute of Electrical and Electronics Engineers (IEEE), 20150101–
  Comment: Member since 1974.
- Member of the IEEE Computer Society Fellows Evaluation Committee. 2017–
- Member of the International Society for Optical Engineering (SPIE), 2004–
- Member of the International Society for Analytical Cytology (ISAC), 2000–
- Guest editor of special issue on "Computer-aided Diagnostics in Digital Pathology" in the June 2017 issue of the journal Cytometry A *Comment:* Published by Wiley
- Editorial Board member of *Computer Methods and Programs in Biomedicine,* 1995–
  Comment: Published by Elsevier.
- Editorial Board member of *Machine Graphics & Vision,* 1994–
  Comment: Published by the Polish Academy of Sciences.
- Editorial Board Member of *Journal of Multimedia Information System*, 2014–
  Comment: Published by Korea Multimedia Society.
- Editorial Board Member of *Cytometry A*, 2017–
  Comment: Published by Wiley.
- Programme committee, International Conference of Mass Data Analysis of Images and Signals (MDA).
- Examiner/committee member for the PhD thesis "Prognostic value of large scale genomic instability by image cytometry in selected malignancies and a premalignant condition" by Tarjei Sveinsgjerd Hveem of Department of Informatics, University of Oslo, Norway.
  Comment: The dissertation took place on February 7
- Examiner/committee member for the PhD thesis "Automatic detection of aberrant chromatin structure predicts prognosis in several cancer types" by Andreas Kleppe of Department of Informatics, University of Oslo, Norway.
  Comment: The dissertation took place September 19
- Evaluator of research proposals for the Dutch funding agency "KWF Kankerbestrijding"
- Expert member of the Convergences jury for the ANR French Research Council. *Comment:* Jury meetings in Paris March 28-30

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).
- Scientific board of Swedish Association for Medical Engineering and Physics, "Svensk förening för medicinsk teknik och fysik" 2013-
- Scientific board of Hillevi Fries Research Scholarship Foundation, 2006–
  Comment: A Swedish foundation that accepts applications and gives out research grants for urology research.
- Chair of UU steering group for the ALLVIS project implementing centralized storage of research data for Uppsala University

- Dissertation committee for Tobias Palmér, Dept of Mathematics, Lunds University, March 8. *Comment:* Title:"Computer Vision Based Analysis of Animal Behaviour".
- Expert for evaluating application for docent position at Blekinge Technical University College by Addas Cheddad.
- Assesment committee member for a position as guest professor in digital pathology at Linköping University
- Assesment committee member for a position as assistant lecturer at Blekinge Technical University College

Gunilla Borgefors

International:

- Fellow of the International Association for Pattern Recognition (IAPR), 1998–
  Comment: 1st Vice President 1994–96, Secretary 1990–94, etc., etc.
- Chair of the Fellow committee of the International Association for Pattern Recognition (IAPR), 2016-2018
  Comment: Member 2014-2016.
- Member of the King Sun Fu Prize committee of the International Association for Pattern Recognition (IAPR), 2016-2018
- Fellow of the Institute of Electrical and Electronics Engineers, Inc. (IEEE), 2007-2017
  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–
- DGCI Liaison and Advisory and Programme committee, 13th International Symposium of Mathemathical Morphology (ISMM 2017), Fontainebleau, France, 2017-05-15–17
- Technical committee, 21th Medical Image Understanding and Analysis (MIUA 2017), Edinburgh, Scotland, 2017-07-11–13
- ISMM Liaison and Advisory, 20th International Conference on Discrete Geometry for Computer Imagery (DGCI 2017), Vienna, Austria, 2017-09-19–21
- Programme committee, 22nd Iberoamerican Congress on Pattern Recognition (CIARP 2017), Valparaíso, Chile, 2017-11-07–10
- Advisory committee, 9th International Conference on Advances in Pattern Recognition (ICAPR 2017), Bangalore, India, 2017-12-27–30

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.
- Member of the Board/Steering Committee for Onsala Space Observatory, 2011–
- Member of the Celsius-Linné committee, TN-faculty, UU, 2007-2017
  Comment: Chair 2013-2016. The committee selects the speakers for the annual Celsius and Linné lectures and organizes the following Symposium.
- Member of the Docent committee of the Faculty of Science and Technology, UU, 2014-2017
- Dissertation committee back-up for Alexey Vovobyev, Dept. of Engineering Sciences, UU, 2016-03-31
  Comment: Title: Static and time-dependent mechanical behaviour of preserved archaeological wood: Case studies of the seventeenth century warship Vasa.
- Dissertation committee for Kristina Lidayová, Dept. of Information Technology, UU, 2017-05-22
  Comment: Title: Fast Methods for Vascular Segmentation Based on Approximate Skeleton Detection.

Anders Brun
National:

- Board member, Swedish Society for Automated Image Analysis, 2014–
- Board member, Centre for Image Analysis
- Organizing committee member of The First Swedish Symposium on Deep Learning 2017

Christer Kiselman
International:

- American Mathematical Society (life member)
- Société Mathématique de France
- International Academy of Sciences, San Marino
- Internacia Scienca Akademio Comenius
- Academy of Esperanto (1989 – 20151215)
- European Mathematical Society
- Polska Akademia Umiejetności (Polish Academy of Arts and Sciences)
- Associate Member, Scandinavian Society for Iranian Studies
- Program committee, International Symposium on Mathematical Morphology (ISMM)
- Program committee, International Conference on Discrete Geometry for Computer Imagery (DGCI)
- Reference Group for Mathematics, International Science Programme (ISP) 2002–2017

National:

- Royal Academy of Arts and Sciences, Uppsala, 1983– .
- Royal Society of Sciences, Uppsala, 1984– .
- Royal Swedish Academy of Sciences, 1990– .
- Member of the Royal Society of Sciences in Uppsala (Kungliga Vetenskaps-Societeten)
- Swedish Astronomical Society (life member)
- Swedish Mathematical Society (life member)

Joakim Lindblad
International:

- Management committe member substitute, NEUBIAS – A new Network of European BioImage Analysts to advance life science imaging, 20160503–20200502
Comment: EU COST Action CA 15124
- Program committee, IWCIA 2017 : International Workshop on Combinatorial Image Analysis, Plovdiv, Bulgaria, 2017, 20170619–20170621
- Technical committee, Medical Image Understanding and Analysis Conference (MIUA 2017), Edinburgh, Scotland, July 2017.
- PhD Dissertation committe, Tatjana Jakšic Krüger, Faculty of Technical Sciences, University of Novi Sad, Serbia, 20170627
Comment: Title: Development, implementation and theoretical analysis of the bee colony optimization meta-heuristic method
- Examination committee, Summer School on Image Processing SSIP 2017, Novi Sad Serbia, July 2017.
- Technical program committee, 10th International Symposium on Image and Signal Processing and Analysis (ISPA), Ljubljana, Slovenia, September 2017.

Filip Malmberg
International:

- Deputy editor of *Pattern Recognition Letters,* 2015–
Comment: Published by Elsevier. PRL is an official journal of the International Association of Pattern Recognition.
- Program committee, 22nd Iberoamerican Conference on Pattern Recognition (CIARP 2017), Valparaiso, Chile, November 2017.
- Program committee, Medical Image Understanding and Analysis Conference (MIUA 2017), Edinburgh, Scotland, July 2017.

National

- Ph.D. thesis committee for Benedikt Daurer, 20171215–20171215
Comment: Thesis title: ”Algorithms for Coherent Diffractive Imaging with X-ray Lasers”

Ingela Nyström
International:

- Member of the Executive Committee of the International Association for Pattern Recognition (IAPR) 2008–2018
Comment: 2nd Vice President 2008–2010, Secretary 2010–2014, President 2014–2016, Past President 2016–2018
- Program Committee, 20th Scandinavian Conference on Image Analysis (SCIA 2017), Tromsoe, Norway, June 2017

National:

- Member of the Royal Society of Arts and Sciences of Uppsala (Kungliga Vetenskapssamhället i Uppsala), 2012–
Comment: Board member 2016–
- Member of the Council for Research Infrastructure (RFI), the Swedish Research Council, 2014–
Comment: Vice-Chair 2015–
- Dissertation committee of Olivier Cros, Department of Biomedical Engineering, Linköping University, 20170608
Comment: Title: Structural properties of the mastoid using image analysis and visualization
- Dissertation committee of Himangshu Saikia, Department of Computational Science and Technology, KTH, 20171115
Comment: Title: Comparison and Tracking Methods for Interactive Visualization of Topological Structures in Scalar Fields

- Member of the Board to Elect a new Vice-Chancellor (”Hörandeförsamlingen”) of UU, 2017
- Deputy Member of the Board for Investigation of Misconduct in Research (”Nämnden för utredning av oredlighet i forskning”) at UU, 2017–

Stefan Seipel
International:

- Board of UpGIS, the network of Geographical Information Systems at UU, 2013–

National:

- Board of the Swedish Computer Graphics Association (SIGRAD), 2015

Ida-Maria Sintorn
National:

- Vice Chair of the Swedish Society for Automated Image Analysis (SSBA), 2016–
  Comment: Board member 2008–
- Vi2 division representative in the Collaborations Group at Dept. IT, UU, 2015–
- PhD thesis evaluation committee, 20171020
  Comment: Tobias Pahlberg, Dept. Engineering Sciences and Mathematics, Luleå University of Technology, title: Wood Fingerprint Recognition and Detection of Thin Cracks

Nataša Sladoje
International:

- Associate Editor for Pattern Recognition Letters
  Comment: Published by Elsevier. PRL is an official journal of the International Association of Pattern Recognition.
- Management committe member, NEUBIAS – A new Network of European BioImage Analysts to advance life science imaging, 20160503–20200502
  Comment: COST Action CA 15124
- Programme committe Intern. Conference on Bioimaging, BIOIMAGING 2017, Porto, Portugal, 20170221–20170223
- Program committee, International Symposium on Mathematical Morphology (ISMM2017), Fontainebleau, France, May 2017.
- Technical committee, Medical Image Understanding and Analysis Conference (MIUA 2017), Edinburgh, Scotland, July 2017.
- Examination committee, Summer School on Image Processing SSIP 2017, Novi Sad Serbia, July 2017.

National:

- PhD Dissertation committe, Donglei Chen, Evolutionary Biology Center, Uppsala University, 20170331
  Comment: Title: Three-Dimensional Synchrotron Histology Visualizes the Dental Development of Silurian Stem Osteichthyans
- PhD Dissertation committe, Olga Dyakova, Department of Neuroscience, Uppsala University, 20170929
  Comment: Title: The processing of natural images in the visual system

Robin Strand
International:

- Editor, Frontiers topic: Spread Evaluation and Comparison of Image Analysis Algorithms (SPECIAL), 2016–
- Program Committee, 20th International Conference on Discrete Geometry for Computer Imagery (DGCI 2017), Vienna, Austria

- Program Committee, Medical Image Understanding and Analysis (MIUA 2017), Edinburgh, UK
- Program Committee, 13th International Symposium on Mathematical Morphology (ISMM 2017) Fontainebleau, France
- Technical Committee/reviewer, International Symposium on Biomedical Imaging (ISBI 2017) Melbourne, Australia

National:

- Member and reviewer of the review panel NT-19 (Biomedical Engineering) at the Swedish Research Council, 2017
- Steering committee deputy board member, Analytic Imaging Diagnostic Arena, AIDA, 2017–
- Member of the board for Centre for Image Analysis, Uppsala University, 2017–
- Licentiate thesis opponent of Jennifer Alvén, Chalmers University of Technology, Göteborg, 20170928
  Improving Multi-Atlas Segmentation Methods for Medical Images
- Grading committee, half-time control of PhD thesis of Jonny Nordström, Dept. of Surgical Sciences, UU, 20171130
  Quantitative multi-parameter Position Emission Tomography in Cardiology
- Grading committee, half-time control of PhD thesis of Johanna Nilsson, Dept. of Surgical Sciences, UU, 20170120
  On Virtual Planning in Cranio-Maxillofacial Surgery
- Election committee, Dept. of IT. Deputy member
- Coordinator of biomedical information technology (biomed-IT) at the Dept. of IT

Carolina Wählby
International:

- Management Committee for NEUBIAS, 20160101-20200502
  Comment: A Network of European BioImage Analysts to advance life science imaging (NEUBIAS), fully funded by COST, a European cooperation in Science and Technology.
- Scientific Advisory Board of France BioImaging, 20161201
  Comment: France BioImaging is a French national research infrastructure for biological imaging.
- Thesis opponent, 20171004
  Comment: Virginie Uhlmann, École polytechnique fédérale de Lausanne (EPFL), Lausanne, Switzerland, title: Landmark Active Contours for Bioimage Analysis: A Tale of Point and Curves

National:

- Board of National Microscopy Infrastructure
  Comment: A Swedish infrastructure for advanced microscopy.
- Board of Swedish Bioimaging
  Comment: A Swedish network for research infrastructures in biomedical imaging and image analysis.
- Board of Upptech, 20160906
  Comment: Upptech (Uppsala University School of Technology) has been established by the Faculty of Science and Technology at Uppsala University for raising visibility of, profiling, and enhancing the university's research and teaching within technology.
- Scientific Advisory Board of BioVis, 20160101
  Comment: BioVis is a part of Uppsala University and associated with SciLifeLab, it is a core facility belonging to the Faculty of Medicine.
- Board of Science for Life Laboratory Committee Uppsala, 20160401
  Comment: Science for Life Laboratory, or SciLifeLab, is a national center for molecular biosciences with focus on health and environmental research.

- Board of AIDA, 20170520
  Comment: Analytic Imaging Diagnostics Arena, a Vinnova funded arena for Deep Learning in medical and biomedical image analysis.
- Member of the Docent committee of the Faculty of Science and Technology, UU, 2017–