5th Eurographics Workshop

Visual Computing for Biology and Medicine

Chester, United Kingdom
September 14th and 15th, 2015
www.vcbm.org
Conference Locations

- Riverside Innovation Centre – Workshop Venue
- Abode Chester – Workshop Dinner
- The Architect Pub – Meet and Greet.
Full address of Workshop Venue:
Riverside Innovation Centre  
University of Chester  
Castle Drive  
Chester  
CH1 1SL  
Tel. +44 (0)1244 515500  
http://www.riversideinnovationcentre.co.uk/  

WIFI
Username: ricuser  
Password: innov8r

Programme at a Glance ...

Sunday, September 13
If you are arriving in Chester on Sunday 13th September then please join us for an informal Meet and Greet session with other VCBM delegates. We will meet at 7pm at The Architect – a classic pub restaurant within Chester’s city walls overlooking the racecourse and within walking distance of the conference venue.

Note that the cost of food and drink is not covered in the delegate fee and you have to purchase your own refreshments.

The Architect  
54 Nicholas Street  
Chester CH1 2NX

Monday, September 14
09:00 – 09:15 Opening  
09:15 – 10:15 Keynote: Denis Noble - What is Life? A systems biology perspective  
10:15 – 10:45 Break  
10:45 – 12:05 Segmentation and Registration (4 papers)

12:05 – 13:30 Lunch

13:30 – 14:50 Molecular Visualization and Visual Analytics (4 papers)  
14:50 – 15:30 Break / Poster Session (9 posters)  
15:30 – 16:50 Volume Visualization (4 papers)

17.30 Museum and City Walls  
19.00 Workshop Dinner (Chester Abode)

Tuesday, September 15
09:00 – 10:20 Visual Computing for Vessel Structures (4 papers)  
10:20 – 10:50 Break / Poster Session  
10:50 – 12:30 Haptics and Interaction (5 papers)

12:30 – 13:40 Lunch


14:40 – 15:10 Closing Ceremonies including NVIDIA Best Paper Prize
Keynote Speakers

What is Life? A systems biology perspective
Monday at 09.15

Professor Denis Noble CBE FRS FRCP is a British biologist who held the Burdon Sanderson Chair of Cardiovascular Physiology at the University of Oxford from 1984 to 2004 and was appointed Professor Emeritus and co-Director of Computational Physiology. He is one of the pioneers of Systems Biology and developed the first viable mathematical model of the working heart in 1960.

Noble’s research focuses on using computer models of biological organs and organ systems to interpret function from the molecular level to the whole organism. Together with international collaborators, his team has used supercomputers to create the first virtual organ, the virtual heart.

As Secretary-General of the International Union of Physiological Sciences 1993-2001, he played a major role in launching the Physiome Project, an international project to use computer simulations to create the quantitative physiological models necessary to interpret the genome, and he was elected President of the IUPS at its world congress in Kyoto in 2009.

Noble is also a philosopher of biology, and his book The Music of Life challenges the foundations of current biological sciences, questions the central dogma, its unidirectional view of information flow, and its imposition of a bottom-up methodology for research in the life sciences.

Numerical simulation in medicine: from training to per-operative guidance.
Tuesday at 13.40

Stephane Cotin joined INRIA in 2007 as Research Director. Since January 2010 he has lead the SHACRA group, a multidisciplinary team of scientists involved in the field on medical simulation. Stephane also manages the development of a Large Scale Initiative on Medical Simulation.

Abstract
The variety, complexity and central role of modern medicine have been a strong motivation for many recent scientific developments. While medical imaging has become an integral part of today’s medicine, new fields are emerging, such as robotics, simulation, augmented reality, or workflow analysis. In this talk I will highlight the increasingly important role of (real-time) numerical simulation in various domains, such as training, but also for planning and in the assistance of complex interventions. I will illustrate the impact of simulation through a series of results in various areas of medicine, such as interventional radiology, ophthalmology, and laparoscopic surgery. Finally I will discuss some of the remaining challenges that still hinder the use of computational anatomy and simulation in medicine.
**Paper Abstracts**

Note that the full version of the papers are available online to all delegates. Access details are in your delegates pack.

### Segmentation and Registration – Monday 10.45

**CoWRadar: Visual Quantification of the Circle of Willis in Stroke Patients. Miao, Haichao; Mistelbauer, Gabriel; Gröller, Eduard**

This paper presents a method for the visual quantification of cerebral arteries, known as the Circle of Willis (CoW). The CoW is an arterial structure that is responsible for the brain’s blood supply. Dysfunctions of this arterial circle can lead to strokes. The diagnosis relies on the radiologist’s expertise and the software tools used. These tools consist of very basic display methods of the volumetric data without support of advanced technologies in medical image processing and visualization. The goal of this paper is to create an automated method for the standardized description of cerebral arteries in stroke patients in order to provide an overview of the CoW’s configuration. This novel display provides visual indications of problematic areas as well as straightforward comparisons between multiple patients. Additionally, we offer a pipeline for extracting the CoW from Time-of-Flight Magnetic Resonance Angiography (TOF-MRA) data sets. An enumeration technique for the labeling of the arterial segments is therefore suggested. We also propose a method for detecting the CoW’s main supplying arteries by analyzing the coronal, sagittal and transverse image planes of the data sets. We evaluated the feasibility of our visual quantification approach in a study of 63 TOF-MRA data sets and compared our findings to those of three radiologists. The obtained results demonstrate that our proposed techniques are effective in detecting the arteries of the CoW.

**Visual Analysis of Medical Image Segmentation Feature Space for Interactive Supervised Classification. Molchanov, Vladimir; Chitiibo, Teodora; Linsen, Lars**

Classification of image regions is a crucial step in many image segmentation algorithms. Assigning a segment to a certain class can be based on various numerical characteristics such as size, intensity statistics, or shape, which build a multi-dimensional feature space describing the segments. It is commonly unclear and not intuitive, however, how much influence or weight should be assigned to the individual features to obtain a best classification. We propose an interactive supervised approach to the classification step based on a feature-space visualization. Our visualization method helps the user to better understand the structure of the feature space and to interactively optimize feature selection and assigned weights. When investigating labeled training data, the user generates optimal descriptors for each target class. The obtained set of descriptors can then be transferred to classify unlabeled data. We show the effectiveness of our approach by embedding our interactive supervised classification method into a medical image segmentation pipeline for two application scenarios: detecting vertebral bodies in sagittal CT image slices, where we improve the overall accuracy, and detecting the pharynx in head MRI data.

**Uncertainty Estimation and Visualization for Multi-modal Image Segmentation. Al-Taie, Ahmed; Hahn, Horst; Linsen, Lars**

Multi-modal imaging allows for the integration of complementary information from multiple medical imaging modalities for an improved analysis. The multiple information channels may lead to a reduction of the uncertainty in the analysis and decision-making process. Recently, efforts have been made to estimate the uncertainty in unimodal image segmentation decisions and visually convey this information to the medical experts that examine the image segmentation results. We propose an approach to extend uncertainty estimation and visualization methods to multi-modal image segmentations. We combine probabilistic unimodal image segmentation results using the concept of ensemble of classifiers. The uncertainty is computed using a measure that is based on the Kullback-Leibler divergence. We apply our approach for an improved segmentation of Multiple Sclerosis (MS) lesions from multiple MR brain imaging modalities. Moreover, we demonstrate how our approach can be used to estimate and visualize the growth of a brain tumor area for imaging data taken at multiple points in time. Both the MS lesion and the area of tumor growth are detected as areas of high uncertainty due to different characteristics in different imaging modalities and changes over time, respectively.

**Image registration methods for patient-specific virtual physiological human models. Oliveira, Julia; Giessler, Paul; Deserno, Thomas**

In this paper, current status of image registration is reviewed with respect to physiological, morphological and anatomical aspects. There are ample choices of recent techniques for image registration which can be used, and a technique suitable for image registration of the pelvis region supporting the femoral nerve block was applied for the development of patient-specific models. Virtual physiological human (VPH) model and magnetic resonance image (MRI) are used for patient-specific image registration. Results are presented in the form of image registration with respect to the skin of the models.

### Molecular Visualization and Visual Analytics – Monday 13.30

**FoldSynth: Interactive 2D/3D Visualisation Platform for Molecular Strands. Todd, Stephen; Todd, Peter; Fol Leymarie, Frederic; Latham, William; Kelley, Lawrence; Sternberg, Michael; Hugues, Jim; Taylor, Stephen**

FoldSynth is an interactive platform designed to help understand the characteristics and commonly used visual abstractions of molecular strands with an emphasis on proteins and DNA. It uses a simple model of molecular forces to give real time interactive animations of the folding and docking processes. The shape of a molecular strand is shown as a 3D visualisation floating above a 2D triangular matrix representing distance constraints, contact maps or other features of residue pairs. As well as more conventional
Digital visualization is also interactive and can be used to manipulate a molecule, define constraints, control and view the folding dynamically, or even design new molecules. While the 3D visualization is more realistic showing a molecule representation approximating the physical behavior and spatial properties, the 2D visualization offers greater visibility, in that all molecular positions (and pairings) are always in view; the 3D mode may suffer occlusions and create complex views which are typically hard to understand to humans.

Instant visualization of secondary structures of molecular models. Hermosilla, Pedro; Vinacua, Alvar; Vázquez, Pere-Pau

Molecular Dynamics simulations are of key importance in the drug design field. Among all possible representations commonly used to inspect these simulations, ribbons has the advantage of giving the expert a good overview of the conformation of the molecule. Although several techniques have been previously proposed to render ribbons, all of them have limitations in terms of space or calculation time, making them not suitable for real-time interaction with simulation software. In this paper we present a novel adaptive method that generates ribbons in real-time, taking advantage of the tessellation shader. The result is a fast method that requires no precomputation, and that generates high quality shapes and shading.

cellVIEW: A Tool for Illustrative and Multi-scale Rendering of Large Biomolecular Datasets. le Muzic, Mathieu; Autin, Ludovic; Parulek, Julius; Viola, Ivan

In this article we introduce cellVIEW, a new system to interactively visualize large biomolecular datasets on the atomic level. Our tool is unique and has been specifically designed to match the ambitions of our domain experts to model and interactively visualize structures comprised of several billions atom. The cellVIEW system integrates acceleration techniques to allow for real-time graphics performance of 60 Hz display rate on datasets representing large viruses and bacterial organisms. Inspired by the work of scientific illustrators, we propose a level-of-detail scheme which purpose is two-fold: accelerating the rendering and reducing visual clutter. The main part of our datasets is made out of macromolecules, but it also comprises nucleic acids strands which are stored as sets of control points. For that specific case, we extend our rendering method to support the dynamic generation of DNA strands directly on the GPU. It is noteworthy that our tool has been directly implemented inside a game engine. We chose to rely on a third party engine to reduce software development work-load and to make bleeding-edge graphics techniques more accessible to the end-users. To our knowledge cellVIEW is the only suitable solution for interactive visualization of large bimolecular landscapes on the atomic level and is freely available to use and extend.

Discovering Medical Knowledge Using Visual Analytics. Sturm, Werner; Schreck, Tobias; Holzinger, Andreas; Ulrich, Torsten

Due to advanced technologies, the amount of biomedical data has been increasing drastically. Such large data sets might be obtained from hospitals, medical practices or laboratories and can be used to discover unknown knowledge and to find and reflect hypotheses. Based on this fact, knowledge discovery systems can support experts to make further decisions, explore the data or to predict future events. To analyze and communicate such a vast amount of information to the user, advanced techniques such as knowledge discovery and information visualization are necessary. Visual analytics combines these fields and supports users to integrate domain knowledge into the knowledge discovery process. This article gives a state-of-the-art overview on visual analytics research with a focus on the biomedical domain, systems biology and genomics data.

Volume Visualization – Monday 15.30

Interactive Position-dependent Customization of Transfer Function Classification Parameters in Volume Rendering. Brix, Tobias; Scherzinger, Aaron; Völker, Andreas; Hinrichs, Klaus

In direct volume rendering (DVR) and related techniques a basic operation is the classification of data values by mapping (mostly scalar) intensities to color values using a transfer function. However, in some cases this kind of mapping might not suffice to achieve satisfying rendering results, for instance when intensity homogeneities occur in the volume data due to technical restrictions of the scanner technology. In this case it might be desirable to customize one or more parameters of the visualization depending on the position within the volume. In this paper we propose a novel approach for an interactive position-dependent customization of arbitrary parameters of the transfer function classification. Our method can easily be integrated into existing volume rendering pipelines by incorporating an additional operation during the classification step. It allows the user to interactively modify the rendering result by specifying reference points within the data set and customizing their associated visualization parameters while receiving direct visual feedback. Since the additional memory requirements of our method do not depend on the size of the visualized data our approach is applicable to large data sets, for instance in the field of ultra microscopy.

Motion-moderated 2D Transfer Function for Volume Rendering 4D CMR Data. Walton, Simon; Chen, Min; Holloway, Cameron

Cardiovascular Magnetic Resonance (CMR) produces time-varying volume data by combining conventional MRI techniques with ECG gating. It allows physicians to inspect the dynamics of a beating heart, such as myocardium motion and blood flows. Because the material intensity changes over time in a typical CMR scan, this poses a challenging problem in specifying an effective transfer function for depicting the geometry of a beating heart or other moving objects. In this paper, we propose to moderate the traditional transfer function based on intensity and intensity gradient. This enables us to depict the exterior boundary of a beating heart in a temporally consistent manner. We examine several different ways of moderating an intensity-based transfer function, and evaluate these designs in conjunction with practical CMR data. We present a ray-casting pipeline which includes optional flow estimation and a mechanism to assist temporal coherence in animation.
Illustrative Multi-volume Rendering for PET/CT Scans. Lawonn, Kai; Smit, Noeska; Preim, Bernhard; Vilanova, Anna;
In this paper we present illustrative visualization techniques for PET/CT datasets. PET/CT scanners acquire both PET and CT image data in order to combine functional metabolic information with structural anatomical information. Current visualization techniques mainly rely on 2D image fusion techniques to convey this combined information to physicians. We introduce an illustrative 3D visualization technique, specifically designed for use with PET/CT datasets. This allows the user to easily detect foci in the PET data and to localize these regions by providing anatomical contextual information from the CT data. Furthermore, we provide transfer function specifically designed for PET data that facilitates the investigation of interesting regions. Our technique allows users to get a quick overview of regions of interest and can be used in treatment planning, doctor-patient communication and interdisciplinary communication. We conducted a qualitative evaluation with medical experts to validate the utility of our method in clinical practice.

Fiber Stipples for Crossing Tracts in Probabilistic Tractography. Reichenbach, Andre; Goldau, Mathias; Hlawitschka, Mario
Given diffusion weighted magnetic resonance (dMRI) data, tractography methods may reconstruct estimations of neural connections of the human brain, so called tracts. Probabilistic tractography algorithms generate a scalar value for each point of the brain, which describes the confidence of an existing structural connection to a predefined seed region. Recently presented Fiber-Stippling is a promising tool to effectively visualize such scalar values on axis aligned cutting planes. However, Fiber-Stippling only works with principal diffusion directions and cannot handle complex tract configurations, such as overlapping or crossing tracts, which are very important to neuroscience. In this work we present an illustrative technique for probabilistic tracts in such configurations, which is based on Fiber-Stippling. Our technique supports multiple diffusion directions as given by high angular resolution diffusion images (HARDI) and hence can visualize crossing tracts, while preserving all of the advantages of Fiber-Stippling. We solve this by visually supporting the stiples, while not altering the original visualization metaphor. Our work is an important contribution to adequate visualization of neuroanatomy, as crossing tracts are a frequent phenomena inside of the human brain. Moreover, our technique may be customized to crossing line fields in general.

Visual Computing for Vessel Structures – Tuesday 09.00
Automated Slice-Based Artery Identification in Various Field-of-View CTA Scans. Major, David; Novikov, Alexey; Wimmer, Maria; Hladíčka, Jiri; Bühler, Katja
Automated identification of main arteries in Computed Tomography Angiography (CTA) scans plays a key role in the initialization of vessel tracking algorithms. Automated vessel tracking tools support physicians in vessel analysis and make their workflow time-efficient. We present a fully-automated framework for identification of five main arteries of three different body regions in various field-of-view CTA scans. Our method detects the two common iliac arteries, the aorta and the two common carotid arteries and delivers seed positions in them. After the field-of-view of a CTA scan is identified, artery candidate positions are regressed slice-wise and the best candidates are selected by Naive Bayes classification. Final artery seed positions are detected by picking the most optimal path over the artery classification results from slice to slice. Our method was evaluated on 20 CTA scans with various field-of-views. The high detection performance on different arteries shows its generality and future applicability for automated vessel analysis systems.

A Two-Level Cascade Classification Algorithm for Real-Time Bifurcation Detection in CTA Images of Blood Vessels. Novikov, Alexey; Wimmer, Maria; Major, David; Bühler, Katja
We introduce a cascade classification algorithm for bifurcation detection in Computed Tomography Angiography (CTA) scans of blood vessels. The proposed algorithm analyzes the vessel surrounding by a trained classifier first, followed by an accurate segmentation of the vessel outer wall by Morphological Active Contour Without Edges and finally extracts the boundary features of the segmented object and classifies its shape by Approximate K-nearest Neighbour classifier. The algorithm shows encouraging and competitive results for blood vessels from various parts of a human body including head, neck and legs.

A Survey of Cardiac 4D PC-MRI Data Processing. Köhler, Benjamin; Born, Silvia; van Pelt, Ray; Preim, Uta; Preim, Bernhard
Cardiac 4D PC-MRI acquisitions gained increasing clinical interest in recent years. They allow to non-invasively obtain extensive information about patient-specific hemodynamics and thus have a great potential to improve the diagnosis of cardiovascular diseases. A dataset contains time-resolved, three-dimensional blood flow directions and strengths, facilitating comprehensive qualitative and quantitative data analysis. The quantification of measures such as stroke volumes helps to assess the cardiac function and monitor disease progression. Qualitative analysis allows to investigate abnormal flow characteristics, such as vortices, that are correlated to different pathologies. Processing the data comprises complex image processing methods as well as flow analysis and visualization. In this work, we mainly focus on the aorta. We provide an overview from data measurement and preprocessing to current visualization and quantification methods so that other researchers can quickly catch up with the topic and take on new challenges to further investigate the potential of 4D PC-MRI.
Histology-Based Evaluation of Optical Coherence Tomographic Characteristics of the Cerebral Artery Wall via Virtual Inflating. Glasser, Sylvia; Hoffmann, Thomas; Boese, Axel; Voß, Samuel; Kalinski, Thomas; Skalej, Martin; Preim, Bernhard
With an increased rate of cerebrovascular diseases, the need for an advanced vessel wall analysis increases as well. In this work, we provide new information of cerebral artery walls extracted with optical coherence tomography (OCT) ex vivo. We present first results of cerebral vessel wall characteristics combined with histological image data. As a prerequisite for this combination, a new image processing method called virtual inflation was developed. This method accounts for the missing blood pressure causing collapsing of the vessels as well as geometrical shape deformations due to catheter probing and histological imaging. We sample the vessel wall thickness locally based on the (deflated) vessel-lumen border instead of the vessel’s centerline. The virtual inflation allows for co-aligning of the different image modalities. It is embedded in a multiple coordinated view framework where correspondences between the data can be highlighted via brushing and linking. In combination with histlogic image data, we provide OCT signal characteristics of the human cerebral artery wall.

Haptics and Interaction – Tuesday 10.50
Haptics-based Modelling of Pigmented Skin Lesions. Granados, Alejandro; Bryan, James; Osborne, Genevieve; Bello, Fernando
Dermatology is under-represented in medical undergraduate education with newly graduated doctors not being able to identify common and important skin conditions. In order to become competent in diagnosing skin lesions, it is important to encounter multiple examples of a condition, as they vary between individuals. Three popular lesions have been identified due to their importance, including nodular melanoma, seborrhoeic keratosis and cherry haemangioma. In this paper we propose a haptics-enabled learning tool for pigmented skin lesions based on haptic texturing. Geometrical modelling, skin deformation and haptics modelling are described. Results of the implementation are presented along with an initial validation study comparing the haptics-based simulator with other methods, including temporary tattoos and silicon made models.

Simulation-based Ultrasound Training Supported by Annotations, Haptics and Linked Multimodal Views. Law, Yuen; Knott, Thomas; Pick, Sebastian; Weyers, Benjamin; Kuhlen, Torsten
When learning ultrasound (US) imaging, trainees must learn how to recognize structures, interpret textures and shapes, and simultaneously register the 2D ultrasound images to their 3D anatomical mental models. Alleviating the cognitive load imposed by these tasks should free the cognitive resources and thereby improve the learning process. We argue that the amount of cognitive load that is required to mentally rotate the models to match the images to them is too large and therefore negatively impacts the learning process. We present a 3D visualization tool that allows the user to naturally move a 2D slice and navigate around a 3D anatomical model. The slice is displayed in-place to facilitate the registration of the 2D slice in its 3D context. Two duplicates are also shown externally to the model; the first is a simple rendered image showing the outlines of the structures and the second is a simulated ultrasound image. Haptic cues are also provided to the users to help them manoeuvre around the 3D model in the virtual space. With the additional display of annotations and information of the most important structures, the tool is expected to complement the available didactic material used in the training of ultrasound procedures.

Exploration of 3D Medical Image Data for Interventional Radiology using Myoelectric Gesture Control. Hettig, Julian; Mewes, André; Riabikin, Oleksandr; Skalej, Martin; Preim, Bernhard; Hansen, Christian
Human-computer interaction with medical images in a sterile environment is a challenging task. It is often delegated to an assistant or performed directly by the physician with an interaction device wrapped in a sterile plastic sheath. This process is time-consuming and inefficient. To address this challenge, we introduce a gesture-based interface for a medical image viewer that is completely touchlessly controlled by the Myo Gesture Control Armband (Thalmic Labs). Based on a clinical requirement analysis, we propose a minimal gesture set to support basic interaction tasks with radiological images and 3D models. We conducted two user studies and a clinical test to evaluate the interaction device and our new gesture control interface. The evaluation results prove the applicability of our approach and provide an important foundation for future research in physician-machine interaction.

QuantiScale: A Study in Redesigning Interactions for Multi-Touch. Ritter, Felix; Al Issawi, Jumana; Benten, Simon
We investigate the performance of QuantiScale, a new multi-touch interaction technique for the quantification of distances in medical images and discuss the benefits and prospects of redesigning interactions with multi-touch devices. Taking advantage of the multi-touch capabilities, QuantiScale behaves like a tape measure, but automatically adjusts the view onto the measured object to improve precision and speed. The technique has been studied in a real-world scenario measuring the diameter of structures for the diagnostic reading of medical images and provides hints for the replacement of traditional mouse-based interaction with gestural interaction. Results of the quantitative evaluation indicate a high measurement precision particularly for small objects. Participants experienced QuantiScale as being more fun, natural, and intuitive in comparison to mouse-based interaction even though the subjective preference for speed and precision was still in favor of the mouse.
Schematic Electrode Map for Navigation in Neuro Data Sets. Schulte zu Berge, Christian; Weiss, Jakob; Navab, Nassir

Neuro resection surgery is one of the last resorts when treating epilepsy patients where conservative treatment shows no effect on seizure reduction. However, due to the severity of the surgery, the resection planning has to be as precise as possible in order to avoid harming any critical anatomy. The tight time constraints in clinical routine demand for a highly optimized workflow. In this work, we therefore introduce a novel visualization in order to simplify the navigation in the complex multi-modal neuro data sets and support the clinician with the planning procedure. We propose a schematic electrode map based on a force-directed graph model providing an intuitive overview over the topology of the implanted depth electrode configuration. To further facilitate the planning workflow, our carefully designed electrode glyph supports different scalar, nominal and binary annotations augmenting the view with additional information. Brushing and linking techniques allow for easy mapping of the EEG data to the corresponding anatomy, as well as for straight-forward navigation within the visualization of the anatomical and functional imaging modalities in order to identify the origin and spread of the seizure. Our results show that the proposed graph layouting method successfully removes occlusions of the projected electrodes while maintaining the original topology of the depth electrode configuration. Initial discussions with clinicians and the application to clinical data further show the effectiveness of our methods.

Posters

- Accuracy Assessment of Free Hand Grasping Interaction in Mixed Reality. Maadh Al Kalbani and Ian Williams
- SWiFT Seeing the Wood From the Trees: helping people make sense of their health data. Dan Brown, David Duce, Rachel Franklin, Rachel Harrison, Clare Martin, Marion Waite
- Visualisation of PET data in the Fly Algorithm. Zainab Ali Abbood, Jean-Marie Rocchisani and Franck P. Vidal
- Simulated Motion Artefact in Computed Tomography. Franck P. Vidal and Pierre-Frédéric Villard
- A Statistical Method for Surface Detection. Samuel Smith and Ian Williams
- Automatic real-time annotation of important landmarks in ultrasound-guided femoral nerve blocks. Frank Lindseth, Linda Leidig and Erik Smistad
- Parametric-based reconstruction of 3D mesh models; towards the generation of a parametric human foot biomodel. Alexander Agathos and Philip Azariadis
**Social Event**
**Monday 14th September**

You will have the chance to visit the *Riverside Museum* to explore a collection of curiosities from the world of medicine, nursing, midwifery and social work.

A guided walk around Chester’s famous city walls will also be arranged.

The workshop dinner will take place at the nearby Chester *Abode* Hotel. Famous British chef Michael Caines MBE has created one of the best dining experiences in Chester at the Abode. They provide “great local produce, prepared with passion and skill by our talented team of chefs, served with impeccable Michael Caines style. Simply delicious”. A menu with a British twist has been selected for VCBM delegates, but it is not what you will be expecting!

17.30 – 18.30  Riverside Museum is open for you to explore.
   It is in the basement of the building next door to the Workshop Venue.

18.30  Guided tour of City Walls (optional)

19.00-19.30  Meet at the Abode Hotel. We are using the Tattersalls Room for the workshop dinner. A glass of Pimms will be waiting for you on your arrival.
Programme Chairs:

- Katja Bühler, VRVis Vienna
- Lars Linsen, Jacobs University, Germany
- Nigel W. John, University of Chester, UK

Local Organisers:

- Nick Avis, University of Chester, UK
- Franck Vidal, Bangor University, UK

International Programme Committee:

- Jan Aerts, KU Leuven, Belgium
- Fernando Bello, Imperial College London
- Stefan Bruckner, University of Bergen, Norway
- Stephane Cotin, Inria, France
- Thomas Deserno (RWTH Aachen, Germany)
- Nils Gehlenborg Harvard Medical School, USA
- Carsten Görg University of Colorado, USA
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- Vincent Luboz, Laboratoire TIMC-IMAG, France
- Claes Lundström, Linköping University, Sweden
- Dorit Merhof, RWTH Aachen University, Germany
- Miriah Meyer (University of Utah, USA)
- Klaus Mueller, Stony Brook University, USA
- Vijay Natarajan Indian Institute of Science, Bangalore, India
- Bernhard Preim, University of Magdeburg, Germany
- Timo Ropinski Linköping University, Sweden
- Jos Roerdink University of Groningen, Netherlands
- Falk Schreiber, University Halle-Wittenberg, Germany
- Heidrun Schumann, University of Rostock, Germany
- Alexei Sourin, Nanyang Technological University, Singapore
- Marc Streit, Johannes Kepler University Linz, Austria
- Franck Vidal, Bangor University, Wales, UK
- Pierre-Frederic Villard, University of Lorraine, France
- Ivan Viola, Vienna University of Technology, Austria
- Wolfgang Wein, Technische Universität, München, Germany
- Stefan Wesarg Fraunhofer IGD Darmstadt, Germany
- Michel Westenberg, TU Eindhoven, The Netherlands
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