

Università  
della  
Svizzera  
italiana

Faculty  
of Informatics

Institute of  
Computational  
Science  
ICS

# **USI Università della Svizzera italiana** Institute of Computational Science

## Five Year Report 2009-2014



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WHO WE ARE AND  
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## IMPRESSUM

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Prof. Piero Martinoli



## COMPUTATIONAL SCIENCE AT USI

# THREE REASONS BEHIND A FARSIGHTED CHOICE

In 1996 the Università della Svizzera italiana was founded as an assertion of the cultural identity of this region, but it soon became clear that in the mean time USI could not limit itself to indulge in that role only – it had to become a source of human capital and new knowledge, capable of stimulating authentic innovation processes, for the economic and social sustainability of our region.

This was the first assumption we made, five years ago, which led us to found the Institute of Computational Science (ICS). Few fields of research can deliver such a high potential of dialogue between Academia and Economy: from physics to finance, through chemistry, biology, medicine,

pharmacology, climatology, meteorology, engineering, and more. All of these are possible applications for our Canton to build upon – once the financial crisis and the fiscal disputes have been settled – in order to look beyond and find new prospects for economic growth and social development. A few budding entities are already visible, such as the Center for Computational Medicine in Cardiology, a joint USI and Cardiocentro Ticino initiative.

The second inspiration from five years ago was purely scientific: the field of computational science is widely considered one of the most promising areas of contemporary science in terms of possible new discoveries, and

its strong multi and interdisciplinary character can push human knowledge through the barricades of traditional disciplines. The computational speed of new generation supercomputers is not only the key to new discoveries, but also the reason for asking new questions. This is a fascinating and pivotal sector for which USI is beginning to be acknowledged as a solid center of expertise.

The third reason for founding ICS was a practical one – pragmatism, which is a good habit in general and also very pertinent to the academic sector. The Swiss National Supercomputing Centre (CSCS), located right here in Ticino, was, with no doubt, a driving force for the creation of ICS. Likewise, and

thanks to the Institute itself, the Swiss Federal Institute of Technology (ETH, which owns CSCS) was convinced to maintain the Centre in Ticino and clear it from its “white elephant” status, from a scientific perspective, making it instead the “sun” in the middle of a new galaxy of research projects and high-level scientists.

Our vision is very clear: we are investing in avantgarde skills and scientific knowledge, and also in reasonable niche sectors, in an environment of clear relationships between the economy and research centres. I am proud of how ICS fits perfectly in this perspective and I am also extremely grateful to those who have made it happen. I am referring to the

Sergio Mantegazza Foundation for the funding, right from the beginning, of the professorship of Michele Parinello. Thanks to this, our region can be proud of its university and can reach into the future with full confidence.





Prof. Rolf Krause



## COMPUTATIONAL SCIENCE AT USI

# DIRECTOR'S INTRODUCTION

Computational science is virtually everywhere: engineering, natural sciences, economy, social sciences, environmental sciences, logistics and medicine – just to mention a few areas which exploit, heavily, the possibility to analyze, model, and predict complex processes virtually on a computer.

May it be the design of new machine parts, weather prediction, the analysis of big data, climate research, optimization of production processes, or the planning of therapy in clinics – computational science has not only become an indispensable tool for scientific research, it has also found its way into our daily lives.

Naturally, computational science is an interdisciplinary field; located at the intersection of mathematics, informatics, and the respective areas of application. Computational science transfers mathematical insight and algorithmic knowledge into reality. Using modern (super-)computers, for carrying out simulations and data analysis, computational science helps to understand and shape the world we live in.

The Institute of Computational Science (ICS) at USI was found in 2008 as part of the Faculty of Informatics, since then it has grown, in only five years, into a large and central node for computational science in Switzerland. ICS covers a broad range of scientific

areas and consists, currently, of eight working groups in advanced computing, high-performance methods for numerical simulation, medicine and engineering, computational time series analysis, computational shape analysis, multi-scale and multi-physics models in computational biology, computational modeling of cardiac electrophysiology, computational biology, and medicinal chemistry and drug design.

The fascinating and ground breaking potential for turning into the simulation of things such as a virus, global mantle convection, or a beating heart has been driving our work from the very beginning and provides our path to scientific discovery.

Based on this spirit, the different groups at ICS have been creating local cooperations, e.g. with CSCS in Lugano, IRB in Bellinzona, and Cardiocentro Ticino as well as national cooperations, e.g. with ETHZ, EPFL, University of Basel, and, of course, international cooperations with partners from the EU, US, Asia and Australia.

Since its first days, ICS has been growing at a considerable rate; starting with a single chair five years ago, now more than 60 people are working in computational science at the institute – professors, postdoctoral and doctoral researchers, as well as master students. ICS currently hosts a PhD and a Master programme in computational science,

which are both offered within the Faculty of Informatics.

Moreover, a new center, the Center for Computational Medicine in Cardiology, has been created, so as to directly transfer computational ideas into clinical practice.

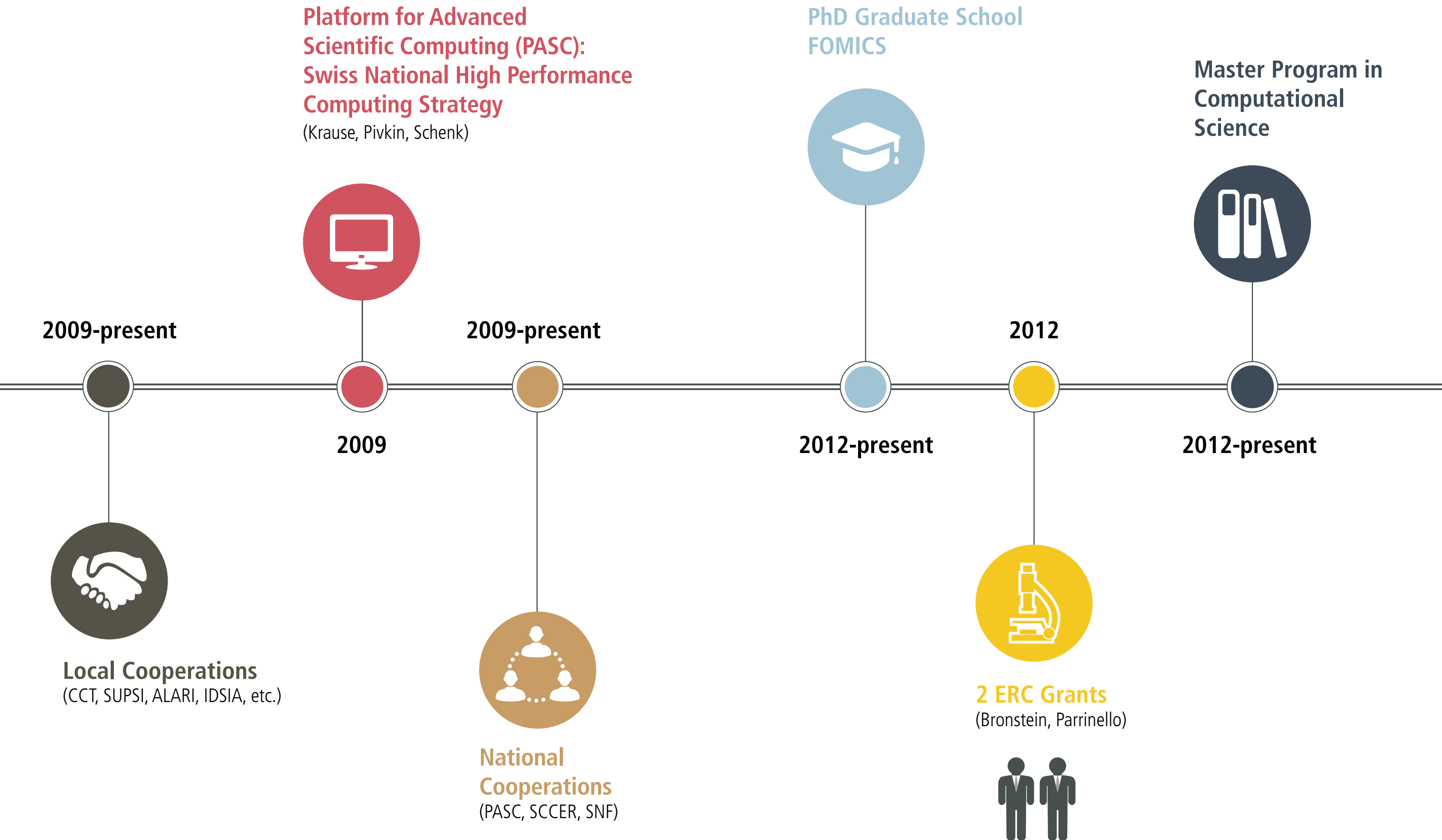
It is this idea of interdisciplinary work of fostering scientific discovery through mathematical modeling and numerical simulation, which forms the core of the Institute of Computational Science. Building on that spirit, ICS looks forward into a bright future, where theory will meet reality in the form of models, simulations, and algorithms.



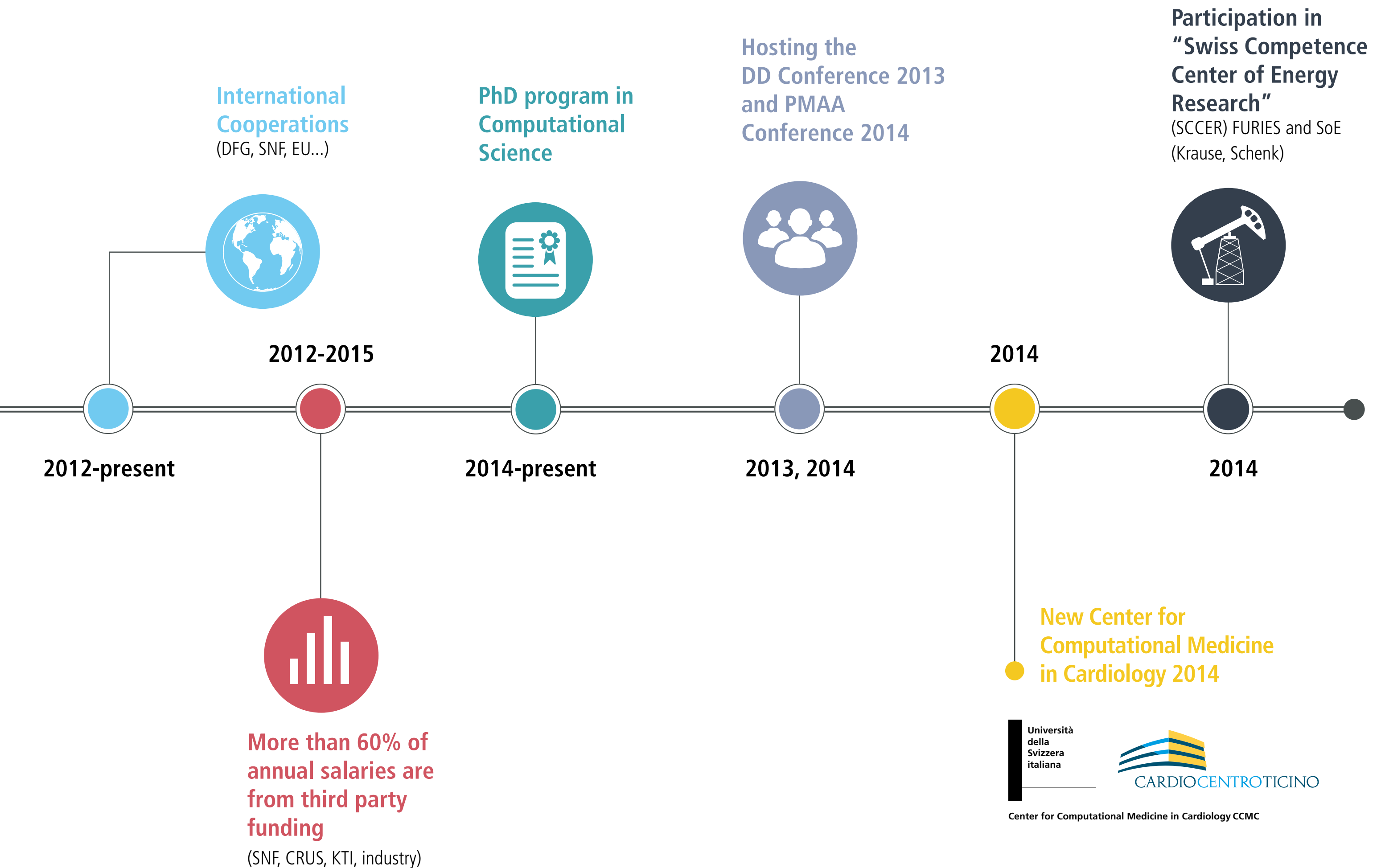
# MILESTONES AND HIGHLIGHTS

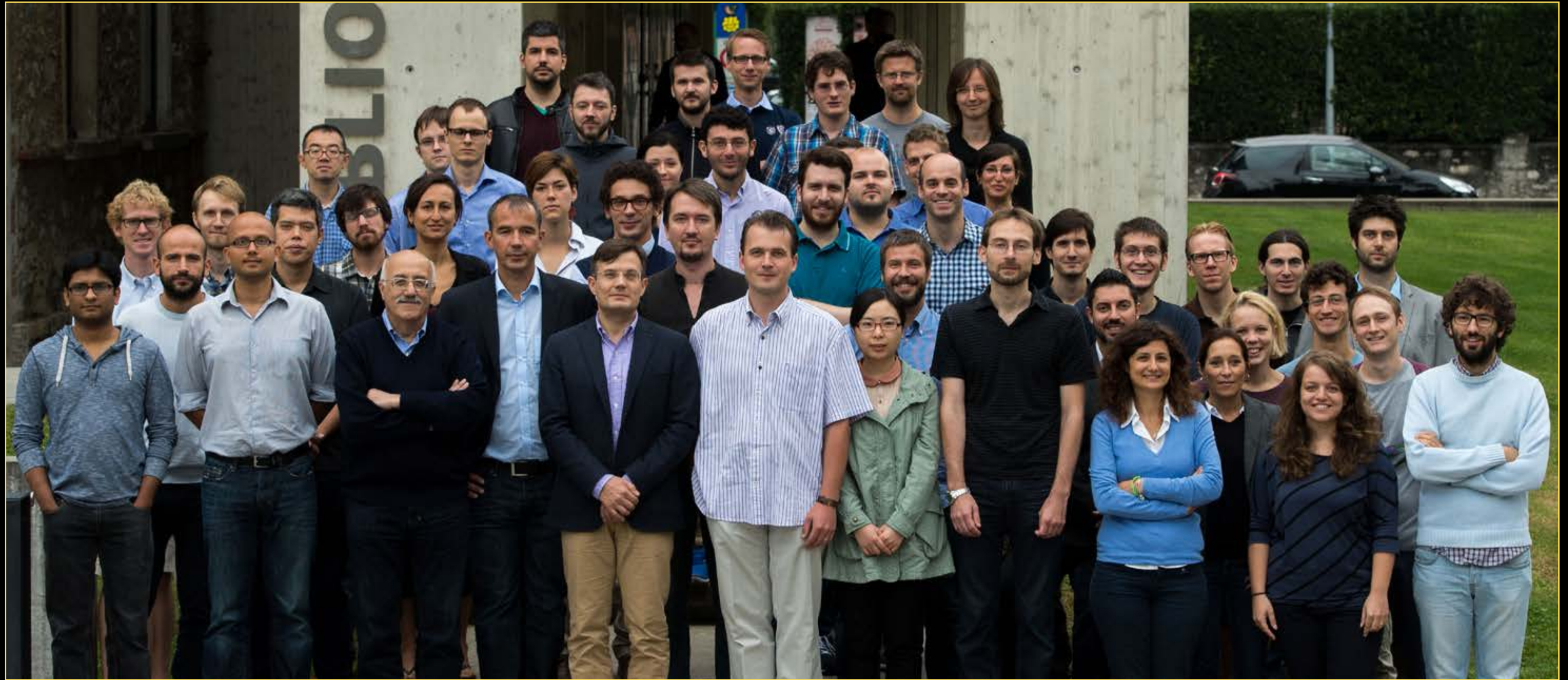
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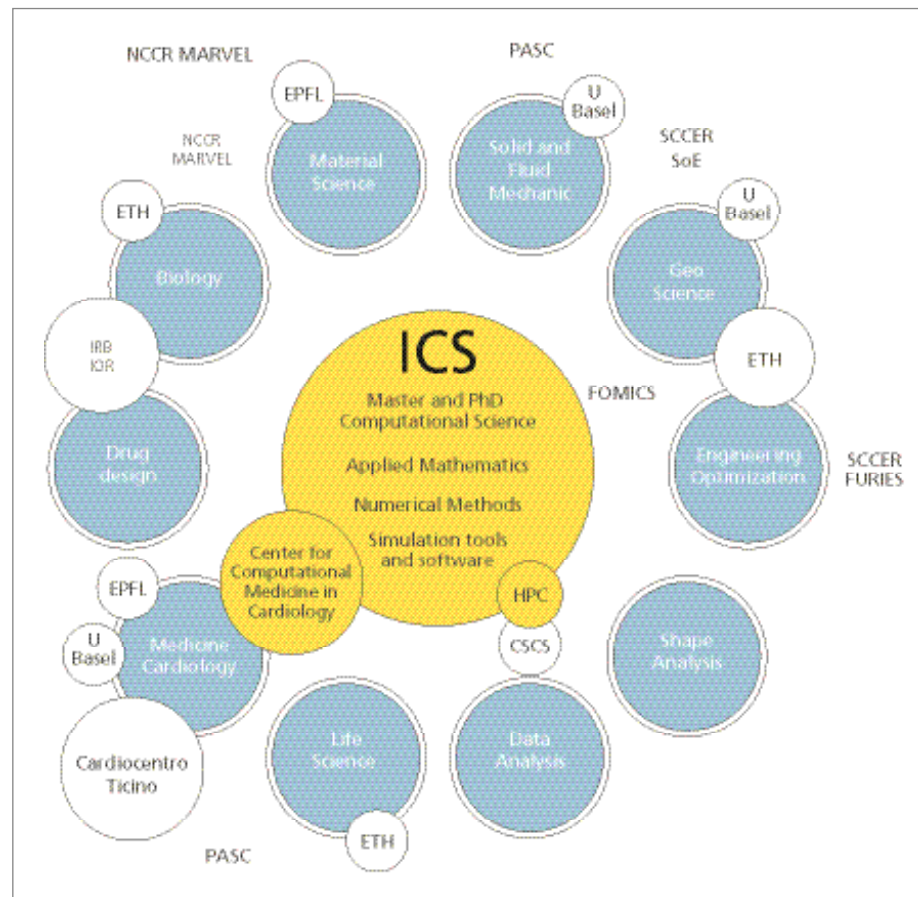






WHO WE ARE AND  
WHAT WE DO



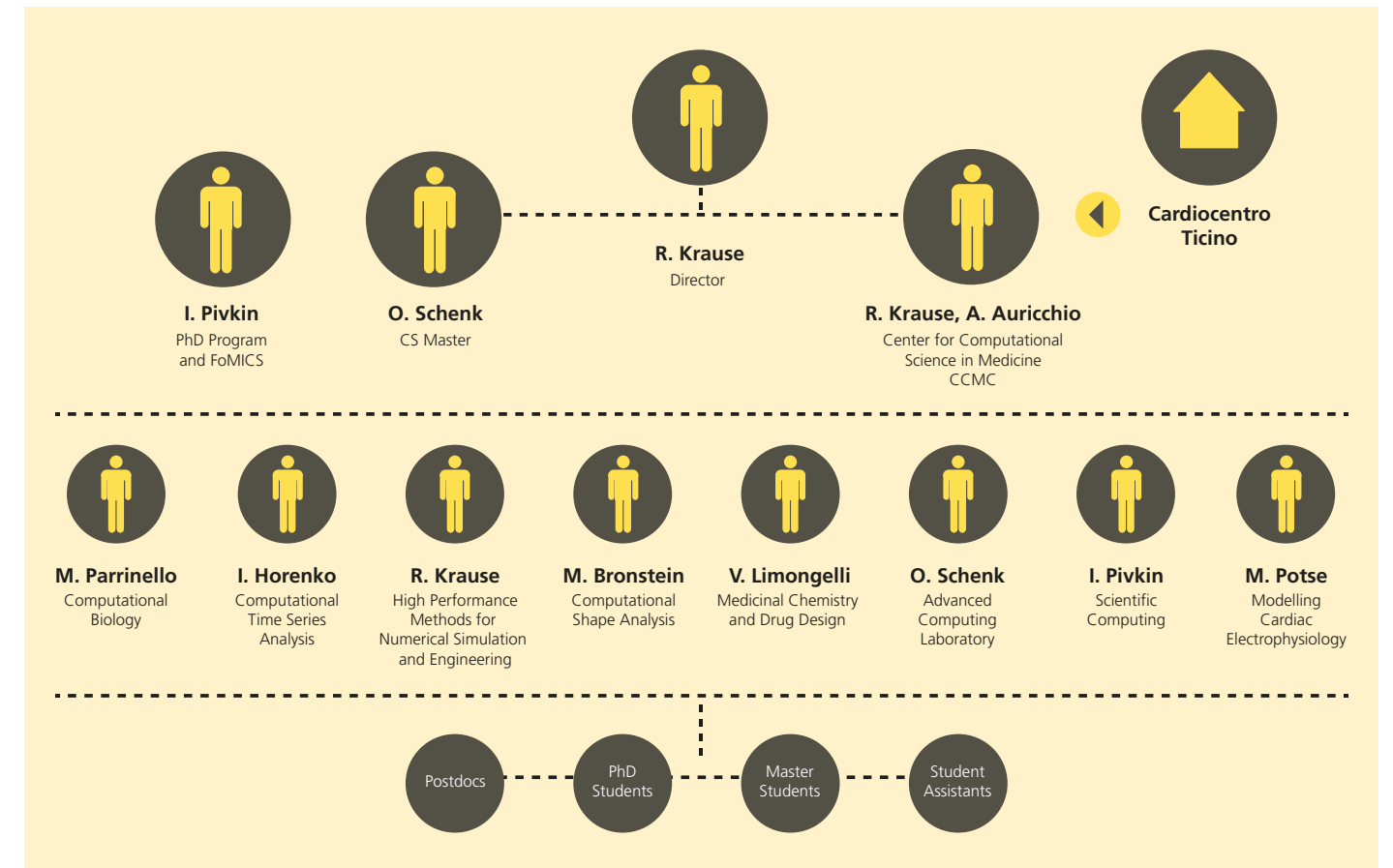


Yellow: Models and Methods, White: Swiss Partners, Blue: Applications

Founded in 2009, for the purpose of realizing the Università della Svizzera italiana's (USI) aim at becoming the next scientific and educational node for computational science in Switzerland, the Institute of Computational Science (ICS) has swiftly established itself in Switzerland and beyond. Five years later, it is now one of the largest institutes in Switzerland, devoted to computational science, deeply embedded into a dense network of renowned national and international cooperation partners. Starting with one professorship in 2009, today at ICS we have seven ordinary professorships, one endowed professorship, and in total a research staff consisting of more than 60 master students, PhD candidates, postdoctoral researchers,

and professors spread amongst eight working groups. At ICS we cover a wide range of state-of-the-art domains in computational science: ranging from advanced computing in computational science, high-performance methods for numerical simulation in science, medicine and engineering, computational time series analysis, computational shape analysis, over multi-scale and multi-physics models in computational biology, computational modeling of cardiac electrophysiology, the simulation of biological and physical systems to our latest addendum, drug design. The core of the scientific work at ICS lies in mathematical modeling, simulation methods, and the creation of scientific software. Exploiting these

core competencies, during the last five years, the different groups at ICS have been conducting transformative research in about 60 different projects. These include projects of national scale such as the Swiss Competence Centers in Energy Research FURIES (EPFL) and SoE (ETH), the NCCR Marvel on Material Science, or the national initiatives for scientific and high-performance computing HP2C and PASC. On the international level, ICS has received two ERC grants (one starting, one advanced), participated in three Priority Programs ('SPP') and Research Units ('Forschergruppe') in Germany and established cooperations with, e.g., Austria, the Czech Republic, Slovakia, the Netherlands, and the United States. These cooperations cover



ICS Organizational Chart (2014 Oct)

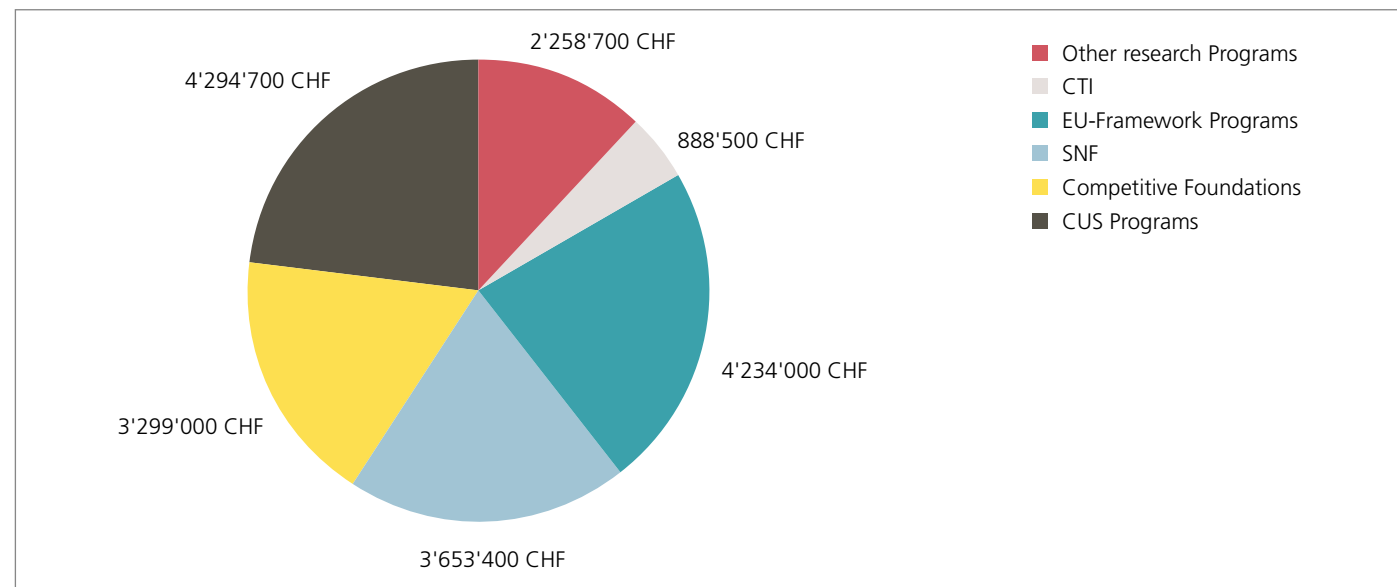
a broad range of science domains, including medicine, life sciences, geo-sciences, engineering, and data and image analysis. With more than 18 Mio CHF of external funding being raised within the last five years from SNF, CUS, private foundations, industry, EU, and CTI, ICS has achieved wide acclaim and recognition and has become an international household name. Additionally, at ICS we have successfully built tight connections to other research institutions and industry in Ticino. Joint projects with the University of Applied Sciences and Arts of Southern Switzerland (SUPSI) and local companies have been established. Moreover, together with the Fondazione Cardiocentro Ticino and the sup-

port of different local foundations, we have been able to create the Center for Computational Medicine in Cardiology (CCMC), which, in a unique way, aims at using computational science as a driving force for creating advances in clinical cardiology - and vice versa. At ICS we provide education, of the highest quality education, in computational science. A well balanced curriculum for the Master Program in Computational Science offered by ICS combines the most relevant topics of Applied Mathematics, Informatics, and High Performance Computing with key elements and concepts from different application areas. Special emphasis is put on the understanding of mathematical and methodo-

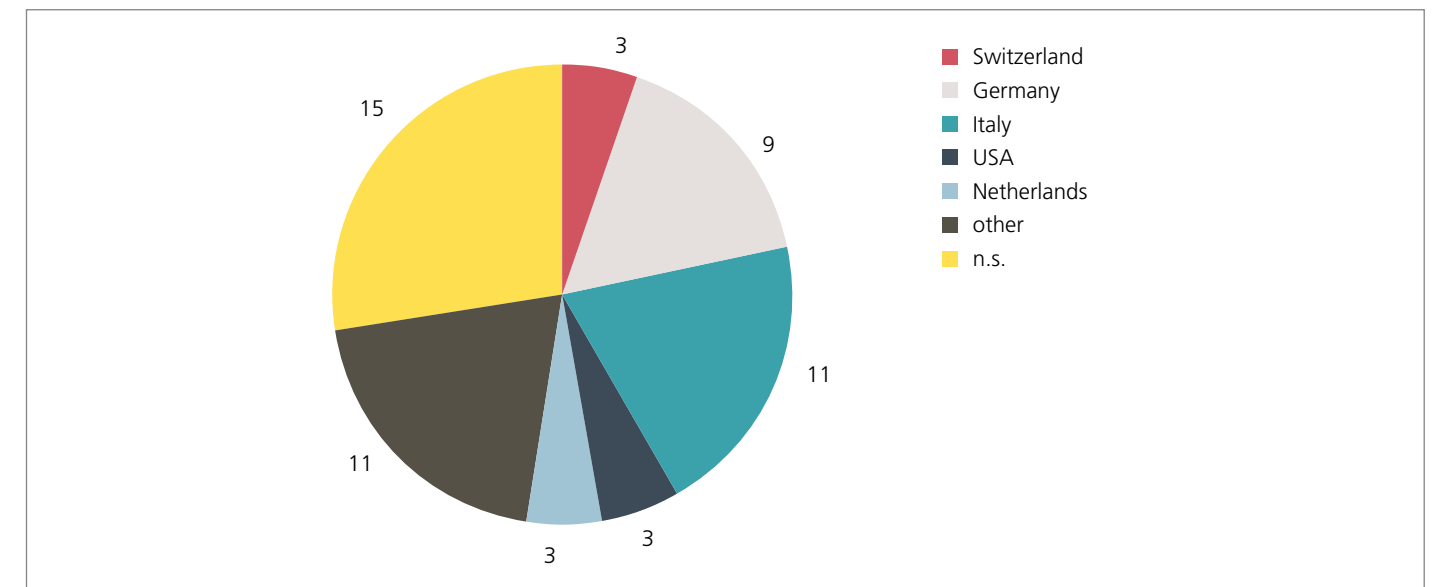
logical concepts as a universal bridge between real world processes, numerical simulation and its realization. After the master studies, students can continue within the PhD Program FOMICS, 'Foundations in Mathematics and Informatics for Computational Science', leading to a PhD in 'Computational Science'. In terms of its clear focus on computational science, this educational offer holds a unique position, not only within Switzerland, but also internationally.

# ICS IN FIGURES

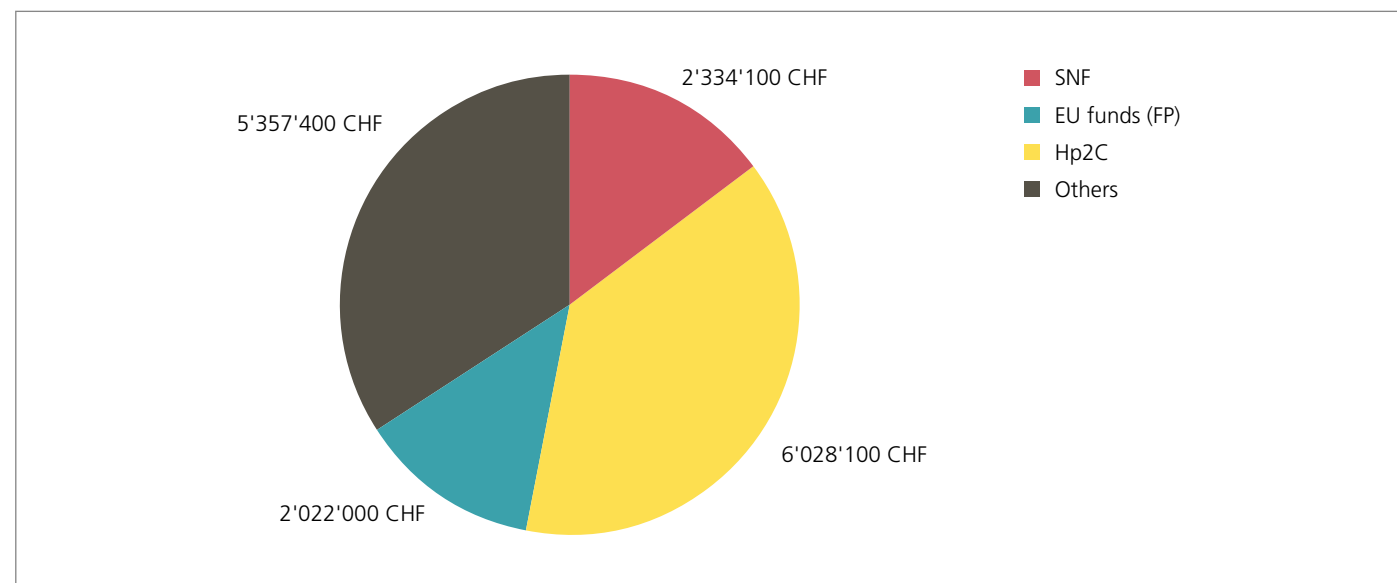
## Research funding 2009-2017



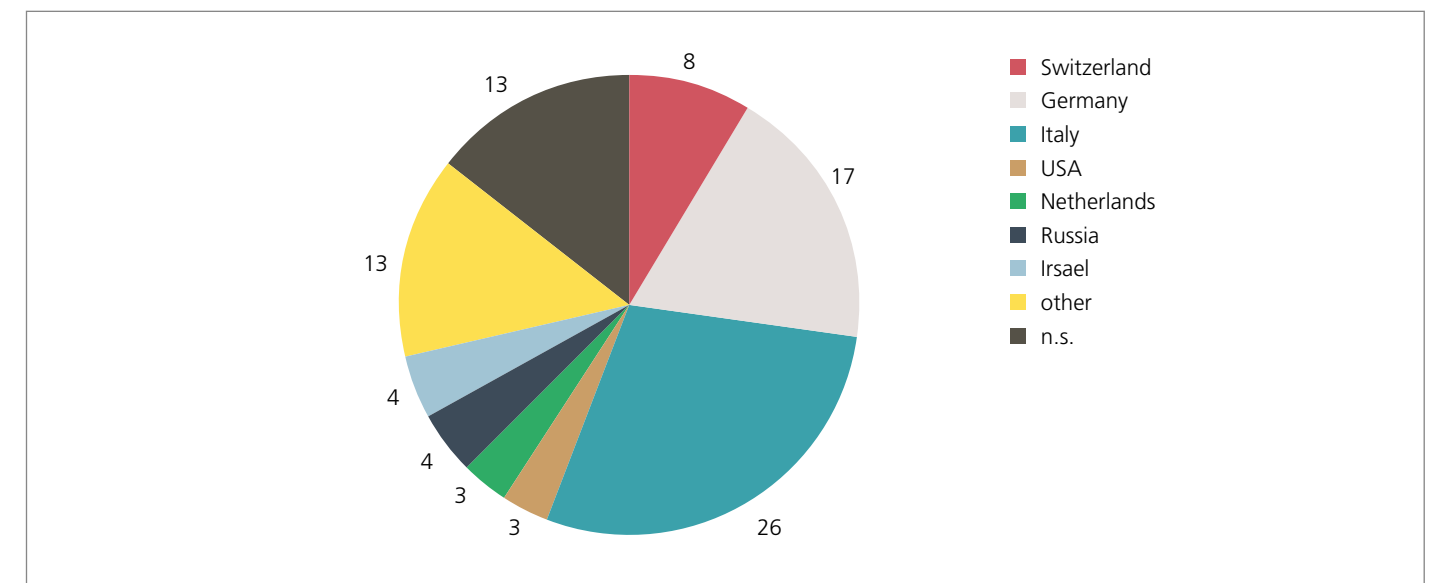
## PostDocs 2008-2014 by Country of Origin/Graduation



## SNF EU Funds

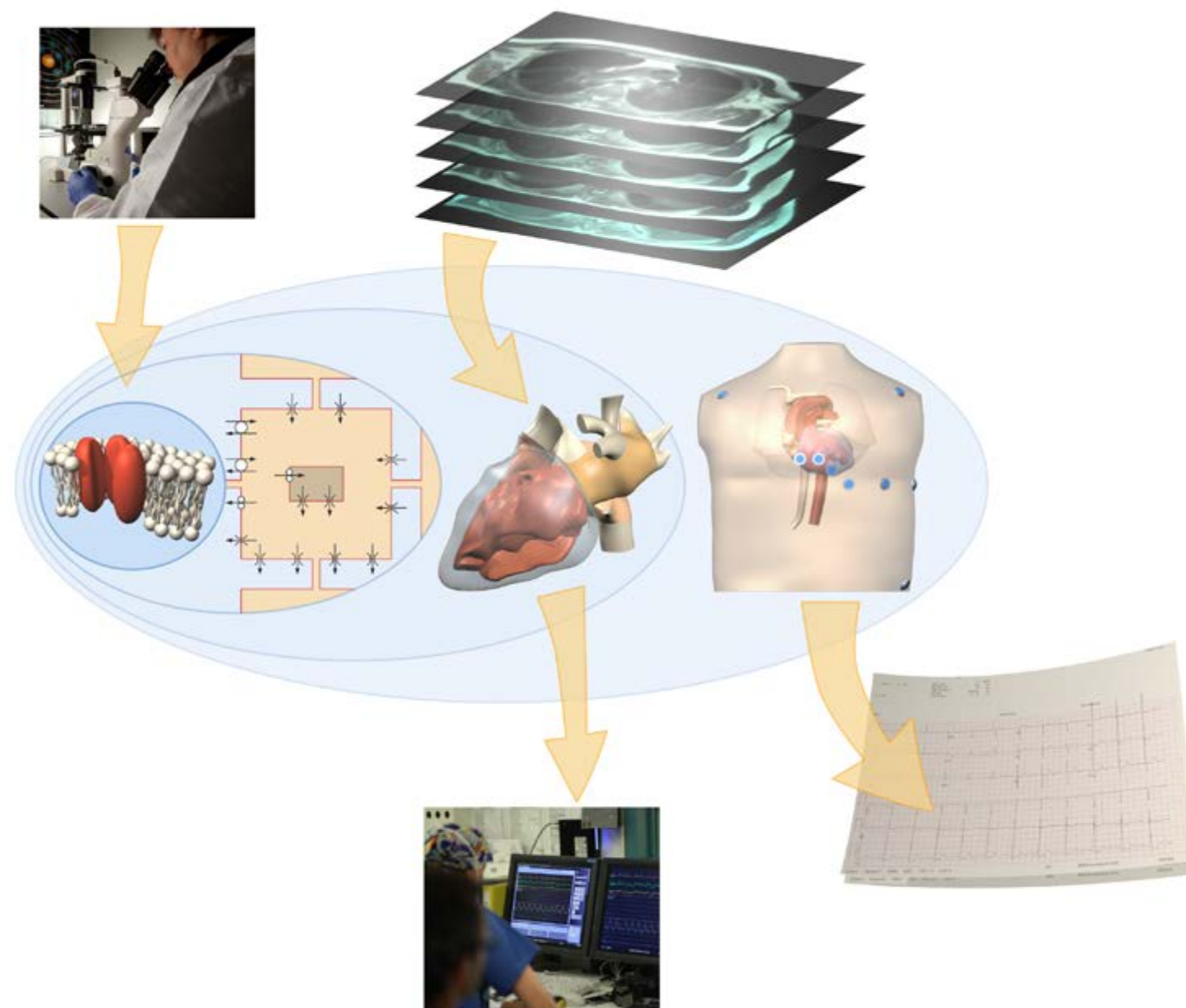


## PostDocs and PhD Candidates 2008-2014 by Country of Origin/Graduation





## CCMC CENTER FOR COMPUTATIONAL MEDICINE IN CARDIOLOGY



**The Center for Computational Medicine in Cardiology (CCMC), established in 2014, is run by the Institute of Computational Science in cooperation with the Cardiocentro Ticino.**

**The CCMC was founded based on the long lasting and strong interdisciplinary collaboration between Prof. Rolf Krause of USI and Prof. Dr. med Angelo Auricchio of Cardiocentro Ticino and is located at the university campus of Lugano. The mission of the new center is to foster the development of new computational approaches and methods as well as new simulation tools aimed at increasing our knowledge of the cardiovascular circulation system and thereby improving diagnostics.**

**This will allow for carrying out integrated analyses of large data resources, as well as customizing the use of various cardiological therapies and thus strive to predict the efficacy of these therapies in the median and long term.**

Computational science in cardiology has been at the frontier of computational medicine over the last decades. Cardiac function in health and disease is a particularly good example of the complicated interplay between the multiple physics (electrophysiology, mechanics, hemodynamics) and the different temporal scales (ranging from milliseconds for the dynamics of the cellular processes to years that the heart takes to adapt to changing loading conditions) and spatial scales involved (body, organ, cell, ion-channels).

As the efficiency of the cardiovascular system relies on the proper functioning and coordination of all of its constituent parts, malfunctions on any level can give rise to clinically relevant changes in cardiac performance, each of which can only be understood by considering the system as a whole. Considerable efforts have been directed towards computational modeling of biophysical systems (i.e. mathematical modeling and numerical simulation) and extended image analysis, but both fields of research have remained relatively separated. A main open challenge is thus to make integral use of the data obtained from image acquisition and analysis and to employ mathematical modeling the possibili-

ties of computational science for advancing research in heart disease.

The ongoing progress in computational science in combination with supercomputers allows for the numerical simulation of physical and biological systems, including the molecular, cellular, and organ level. However, due to the highly complex multi-scale and multi-physical behavior of the cardiovascular system and its components, the development of efficient, robust, and validated simulation tools for practical use in clinical applications is still a major challenge. Tackling this challenge requires the development of new computational methods, starting from image processing (e.g., segmentation), geometrical reconstruction, and ranging over new and problem specific discretization techniques, mathematical modeling of the underlying biophysics (e.g., constitutive relations that characterize the diseased tissue), to fast and robust (high performance) algorithms for the solution of the arising system of equations (e.g., preconditioning for linear and nonlinear problems). Realistic numerical simulations in cardiology can only be guaranteed through extensive validation against clinical measurements. In recent years, the initially generic models representing the average heart have evolved to enable simulation of patient-specific conditions.

The state of the art is that simulations of cardiac electrophysiology on high performance supercomputers can link ion-channel kinetics and tissue conductivities at the molecular level to abnormalities in the body surface ECG. In the near future, modeling of protein behavior will add another dimension, allowing the coupling of abnormalities in the ECG to abnormalities in anatomy, tissue properties and protein function. The continuously increasing computational capacity will set the stage for a wider application of such computational models in clinical practice.

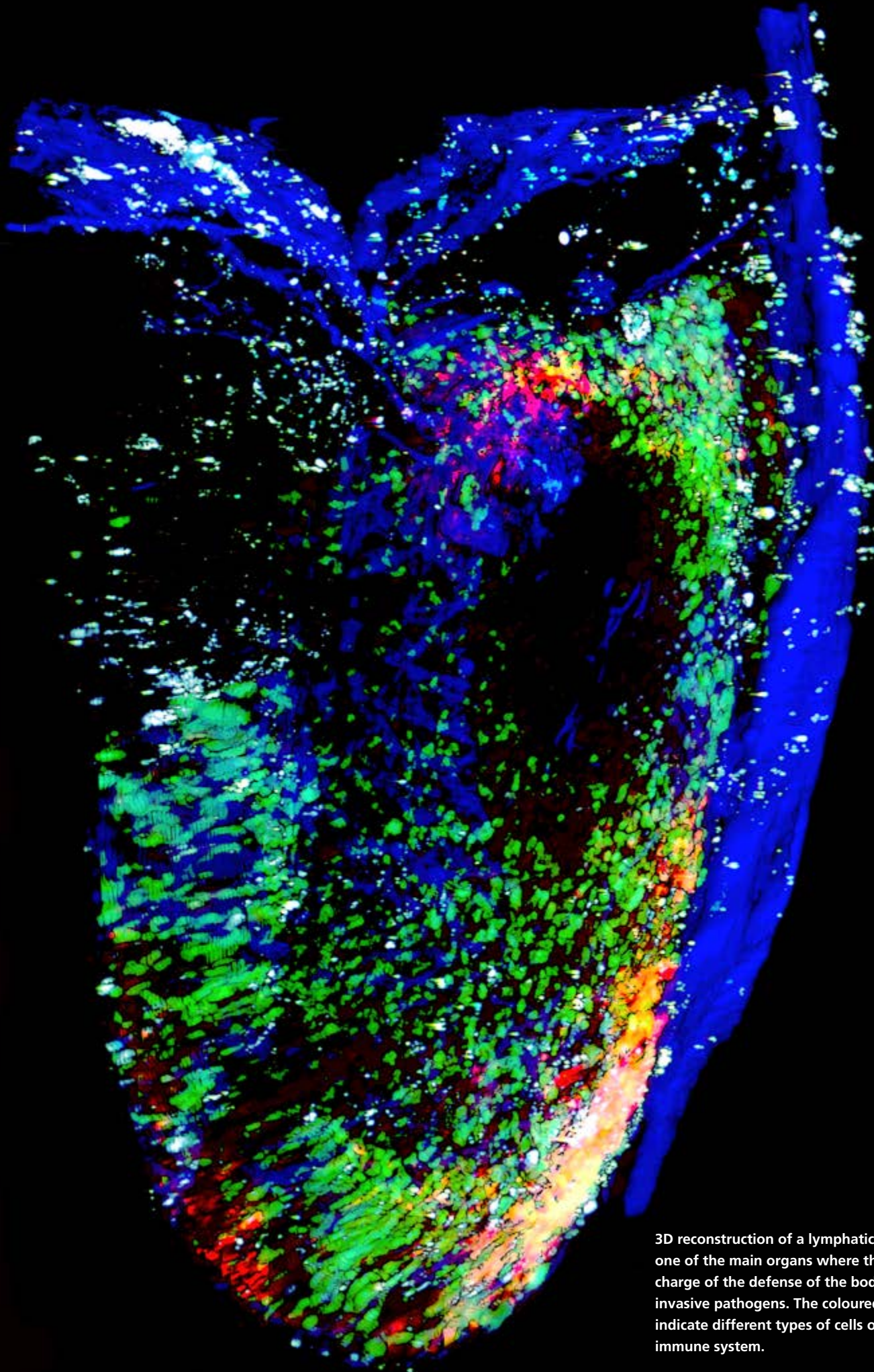


## INSTITUTE FOR RESEARCH IN BIOMEDICINE

# INVESTIGATING IMMUNE DISEASE

Immunology studies the mechanisms by which the body fights infections and unfamiliar cells, such as cancerous or transplanted cells. The defense of our body resides in specialized cells, which constantly patrol the organs to detect the presence of potentially dangerous challenges, such as bacteria or viruses or any foreign material. In the past the only possibility of examining the interaction between immune cells and pathogens was by performing in vitro assays. Recently, the development of powerful microscopes has allowed us to look inside the body of a living organism and monitor the behavior of these cells as never before. This technique is called intravital microscopy and is revolutionizing the way we observe immune reactions. The Institute for Research in Biomedicine in Bellinzona (IRB) has recently purchased, with the help of the Swiss National Science Foundation and the Maxi Foundation, one of the most advanced intravital microscopes in Europe. Thanks to this equipment, researchers at the IRB, have recorded movies which will allow for the study of events inside the body during an infection at high magnification and temporal resolution.

Typically, to study the behavior of specific types of cells and their interaction with other cells of the body, it is necessary to label them with different colors (figure on the left page). A major obstacle in the interpretation of the recorded movies is the quantitative analysis of the data. Following image acquisition, cells have to be identified and tracked using special computer software. However, currently available programs cannot clearly identify and track cells in an efficient way, due to the high number of events and the close interactions between cells. Therefore, new tools are needed to create more effective ways to study the movement of cells and to fully understand their function. To address this issue, IRB has joined forces with the Institute of Computational Science at USI and both have obtained a grant from SystemX, a platform which brings together scientific groups from different areas to find innovative solutions through multidisciplinary research. The funding allows a tight and fruitful collaboration.



3D reconstruction of a lymphatic node, one of the main organs where the cells in charge of the defense of the body finds invasive pathogens. The coloured dots indicate different types of cells of the immune system.



## KRAUSE GROUP

# EFFICIENT NUMERICAL METHODS FOR COMPUTATIONAL MECHANICS

Computational mechanics is at the heart of the simulation of several physical and industrial phenomena governed by the principles of mechanics.

Typical examples are crash tests, biomedicine, study of industrial plants, structural analysis, and geomechanics.

The determination of the effects of loads, parameters, and geometry are nowadays possible thanks to computational mechanics.

Simulations replace many laboratory tests, allowing for a speed-up in the development of new technologies and a reduction of experimental costs.

Accurate mechanical models are formed by a set of Partial Differential Equations (PDEs) and Ordinary Differential Equations (ODEs), that gives rise to coupled systems of non-linear equations.

The application of standard numerical strategies to these problems would be particularly expensive and impracticable and, hence, suitable HPC methods have to be developed.

The focuses of our research are the study of complex models in the biomedical and industrial fields, the development of suitable numerical methods for the resolution thereof, and sensitivity analysis of parameters on numerical results.

### POROELASTIC MODELS IN DENTAL BIOMECHANICS

Teeth can only virtually be thought of as rigidly linked to dental alveoli in the jaw bone.

These two structures are connected by the Periodontal Ligament (PDL).

It is a soft tissue, located between the root and the jaw bone, which absorbs the mechanical stresses exerted on the tooth, for example the forces generated by chewing, allowing micro-displacements.

The forces acting on a tooth can also be large, e.g., a tight bite can correspond to a force of 80 N.

Understanding the biomechanics of PDL is a fundamental and challenging task in dentistry.

Identifying a correct model and the right mechanical parameters may help in the early detection of parodontal diseases, such as gingivitis and periodontitis.

Indeed, these diseases can be identified by changes of the parameters which characterise a healthy PDL.

The mechanics of PDL are particularly complicated to describe because of its complex microstructures. It has an inherently biphasic structure. It is mainly composed of collagen fibers which form a solid matrix. This solid phase is infused with a interstitial fluid.

Because of this structure, the biomechanics of the PDL is highly complicated to describe.

The anisotropic elastic nature of the fibers and the damping behavior of the fluid are responsible for the non-linear and time-dependent response of the PDL.

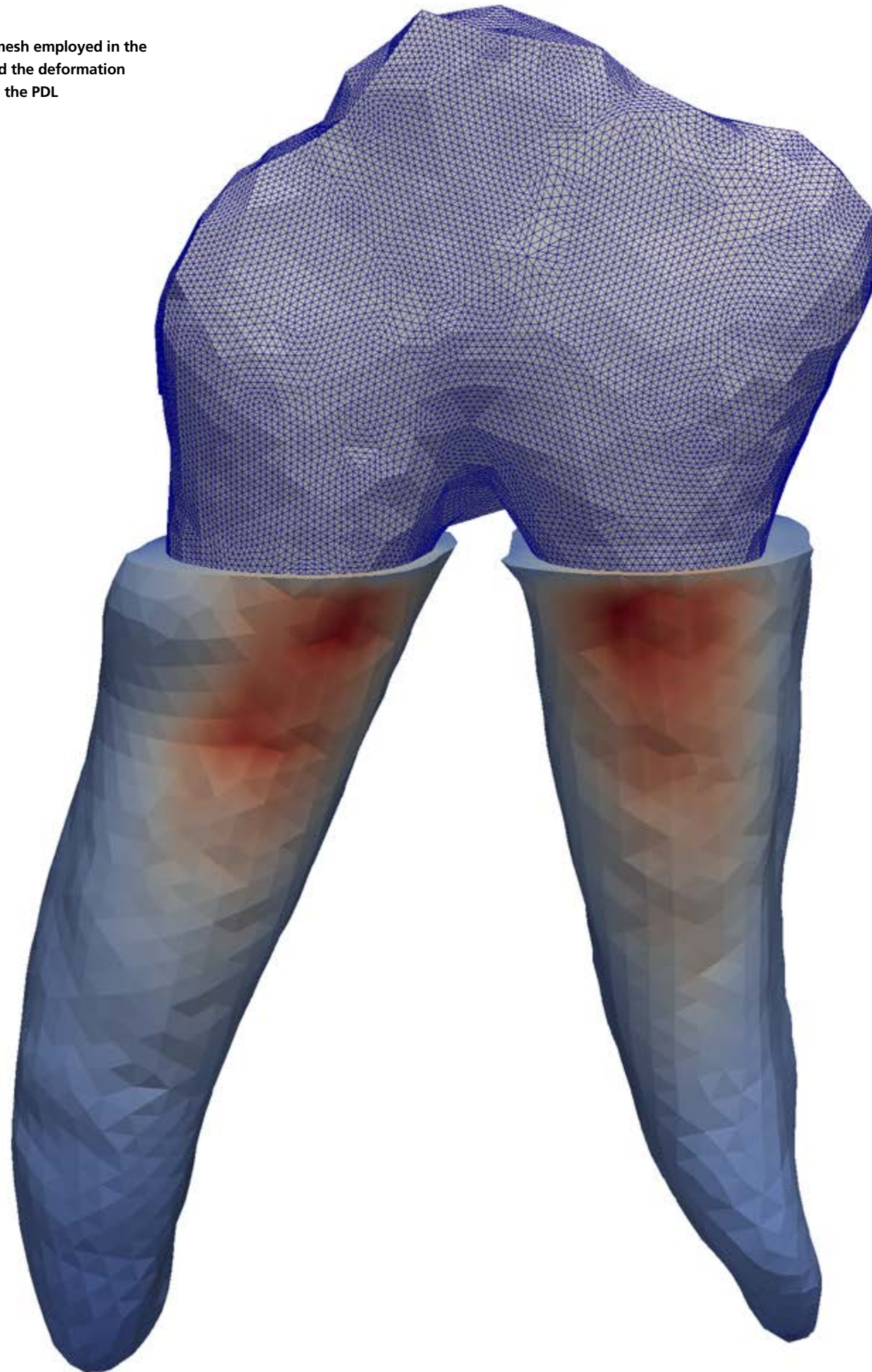
The poroelastic model naturally includes this biphasic nature but introduces several simulation challenges.

In order to describe the geometry of the PDL and to correctly estimate the generated forces, a very fine mesh is necessary.

Numerical simulation of an elastic body pushed and sheared against a rock-like rough substrate. The asymmetric stress distribution (concentrated in the footprint head) is visible.



The very fine mesh employed in the simulations and the deformation determinant in the PDL



## KRAUSE GROUP EFFICIENT NUMERICAL METHODS FOR COMPUTATIONAL MECHANICS

The application of standard HPC methods to the arising non-linear saddle-point system of equations is not possible.

Multigrid solvers are not optimal for these kinds of problems.

The presence of a high jump in the coefficients in the coupled problem introduces two main issues in the application of MG: it heavily reduces the convergence rate of the smoothers and it may prevent the convergence of iterative solvers on the coarse level.

Moreover, the use of a MG Newton's Method (MGNM) with a fixed number (15) number of W multigrid cycles improved convergence rates.

The use of a poroelastic model for the PDL allowed for a good representation of the mechanical force response of the tooth.

### In particular:

We derived two optimal values for the permeability and the mechanical parameters. We were able to reproduce the early stages of linear loading experiments up to 0.05 mm of applied displacement and 10 N of force. The derived parameters give a good agreement also in relaxation experiments.

### ROUGH CONTACT SIMULATION

Almost every surface, at some length-scale, is rough; even smooth-looking materials reveal a complex texture of fractal-like structures, when observed at micro or nano-scopic levels. As a consequence, every contact happening in the real world involves the interaction of small asperities, which determine crucial features of the contact itself, such as the real contact area and the surface stress distribution over it.

One of our projects consists in the determination of the influence on friction of particular roughness parameters, such as, for example, the root mean square roughness or the fractal dimension.

To do so, we simulated the contact of macroscopic bodies down to the microscopic level, solving problems with millions of unknowns, which are feasible only by employing state-of-the art techniques, such as our nonlinear multigrid solver algorithm, on machines with thousands of processors.

The results obtained, so far, allowed us to target specific phenomena, and, in particular, we are now applying our method to the study of the behavior

of cracked underground rocks, to understand what shear resistance they can oppose to external forces, such as those deriving from deep underground drilling or fracking.





## POTSE GROUP SOLVING THE PUZZLE OF HEART DISEASE

The contraction of the heart muscle is coordinated by an electrochemical activation mechanism. In the membrane of each muscle cell, millions of small channels, pumps, and exchangers allow the passage of specific ions into or out of the cell, each according to its own rules. The resulting complicated dance of ions allows for the cell to contract and relax, while signalling its neighbours to do the same. Various sensor mechanisms which influence the ion channels allow the cell to adapt its behavior to external circumstances. In a healthy heart this results in a perfectly tuned contraction leading to an efficient pumping function.

A variety of diseases can distort this complex system, causing the heart to pump less efficiently, or even resulting in a chaotic activation and a totally ineffective contraction, leading to sudden cardiac death. To diagnose such diseases, physicians rely on various electric signals which can be measured on the body surface (the well-known electrocardiogram) or inside the heart. However, these signals are often difficult to interpret, and are also influenced by other factors such as the patient's shape and posture.

In principle, we should understand these signals perfectly. We know the

behavior of the cardiac cells and their interactions, and by applying the universal laws of physics we should be able to compute what measurable signals result and how they would change with pathology. However, when this is tried it turns out that there are many unknowns in the sequence from ion channel to electrocardiogram. Identifying and filling these gaps in our knowledge helps us to better predict electrocardiogram changes from changes on the cell level. But it can also be valuable as a means of diagnosis, as some of the unknowns are interesting physiological parameters that tell something about the patient's disease.

Our approach is therefore to mimic the electrocardiogram and other signals in individual patients, by simulating them from the behavior of the cardiac cells and carefully adjusting the unknown parameters to improve the match. Thus we learn about physiology in general and about the patient's very individual disease.

From the magnetic resonance imaging, obtained in the hospital, we construct patient-specific models of the geometry of the heart, the torso surface, and several other organs. Using high-performance computing systems at the Swiss National Supercomputing Center

(CSCS) we then simulate the behavior of the muscle cells and their interactions on roughly a hundred million points in the heart. From the electrical currents that will flow between the model cells we compute the electrical potential field in the whole body, which gives us the electrocardiogram on the body surface, as well as signals inside the heart. All of these signals are compared to those measured in the hospital, and the model parameters are tuned until an optimal match is obtained.

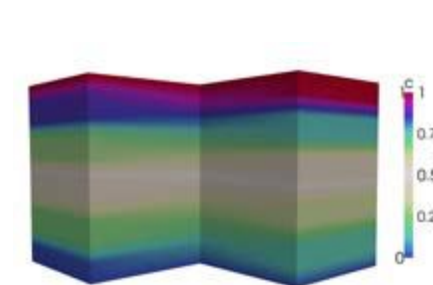
To make this possible, at ICS we have developed our own software to perform the simulations efficiently on the thousands of compute cores that the CSCS computers allow us to use. Apart from our work on understanding the heart and its diseases, at ICS and within CCMC this software is improved so that it can work, even faster, on tomorrow's computers, and hopefully one day in a computer standing on the physician's desk. An even more ambitious goal is to include the mechanical contraction of the heart in the simulations. Because the electrical and mechanical functions of the heart influence each other, such modeling would help us to reach the ultimate target: improving the efficiency of the mechanical contraction of the patient's heart.



## KRAUSE GROUP

SOFTWARE FOR  
EXASCALE COMPUTINGPERMEATION OF CHEMICALS  
THROUGH HUMAN SKIN

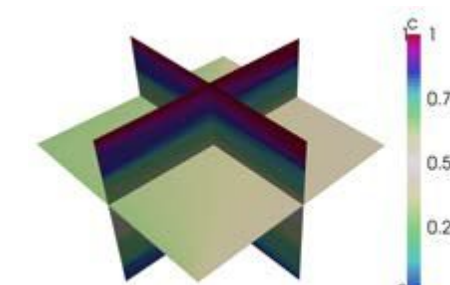
The in-silico modeling of how chemicals permeate through human skin is an important problem – be it for the development of drugs or cosmetics. Experiments here are limited by both practical and ethical concerns, so computer simulations are an invaluable tool. Such simulations are however difficult: The problem involves a vast range of scales and involves challenges from complex geometries, anisotropies and large jumps in diffusion coefficients. Therefore, sophisticated numerical algorithms together with high-performance computing resources are required to tackle this problem.



Some chemical is applied uniformly on the top of the brick and mortar geometry. Over time, it diffuses downwards.

## HIGH-PERFORMANCE COMPUTING

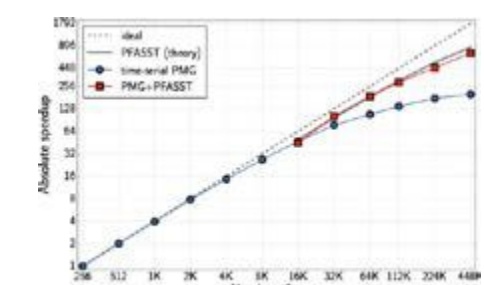
Because of its complexity, in-silico studies of skin permeation are computationally extremely expensive and require massive computing power to become tractable. Today's supercomputers already feature millions of cores and this number is anticipated to rise to more than 100 million over the next decade. This fundamental turn towards concurrency gives rise to many challenges for the development of numerical algorithms: we need new methods which are inherently designed for parallelism, in order to utilize the computing power provided by future supercomputers. Computational science therefore has to come up with novel numerical methods which can provide the required massive concurrency.



A cut through the employed brick and mortar geometry. Although the chemical is applied uniformly on the top, the anisotropic structure of the geometry leads to a strongly varying concentration.

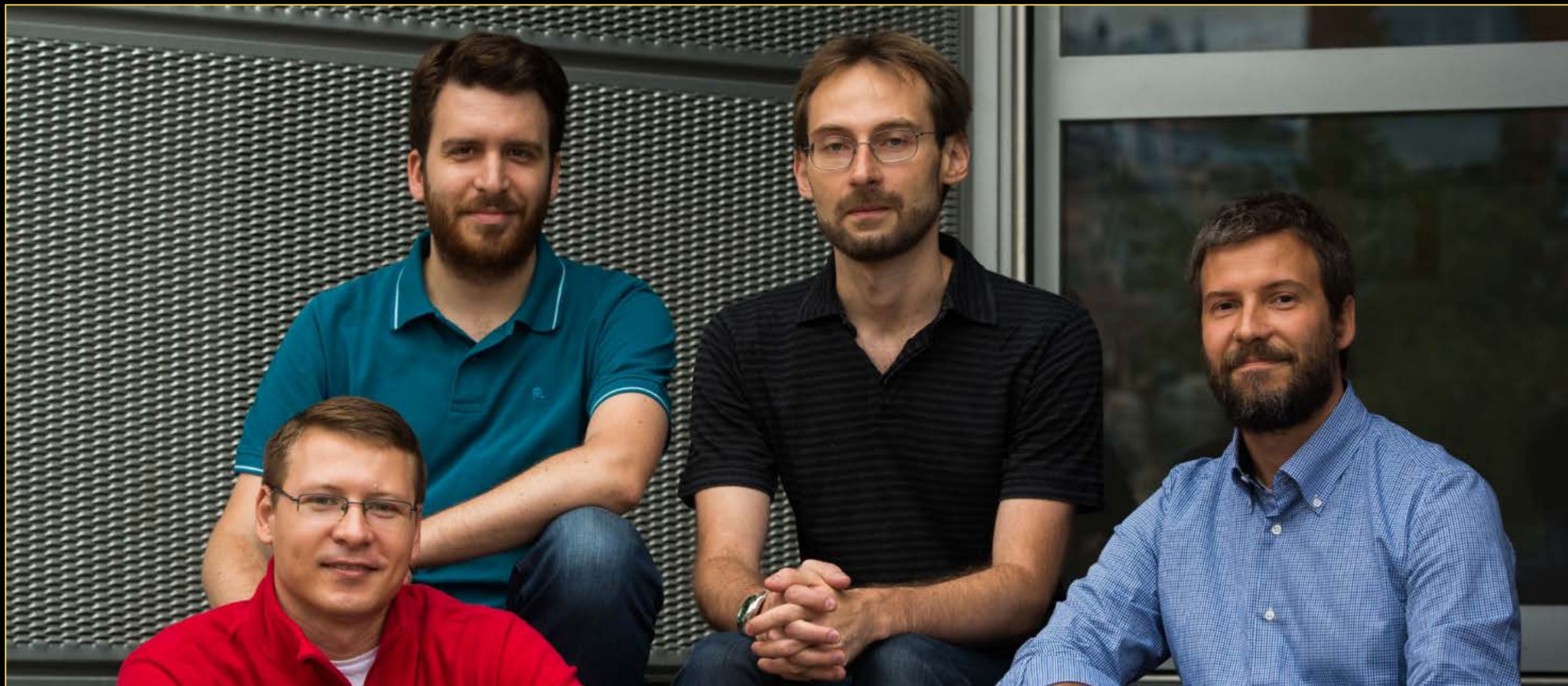
PARALLELISM IN TIME – NOVEL  
MATHEMATICAL ALGORITHMS

The project “Exasolvers – Extreme scale solvers for coupled problems” develops next generation numerical methods which will allow for a significant increase in resolution and accuracy. Researchers at ICS contribute to Exasolvers by developing novel parallel-in-time integration methods: These methods allow one to introduce an additional dimension for concurrency on top of already widely used parallelization in space. Using space-time parallelization allows one to improve utilization of parallel machines and can help to overcome the intrinsic limitations of classical approaches. As part of the work we did in Exasolvers, record-setting benchmarks of a space-time parallel code was provided using almost half-a-million cores on the IBM BlueGene/Q installation JUQUEEN at Juelich Supercomputing Centre.



Scaling of a space-time parallel code (red) versus a code that is parallelized only in space (blue). The former provides significantly better total speedup on all the 458,752 cores of the machine.

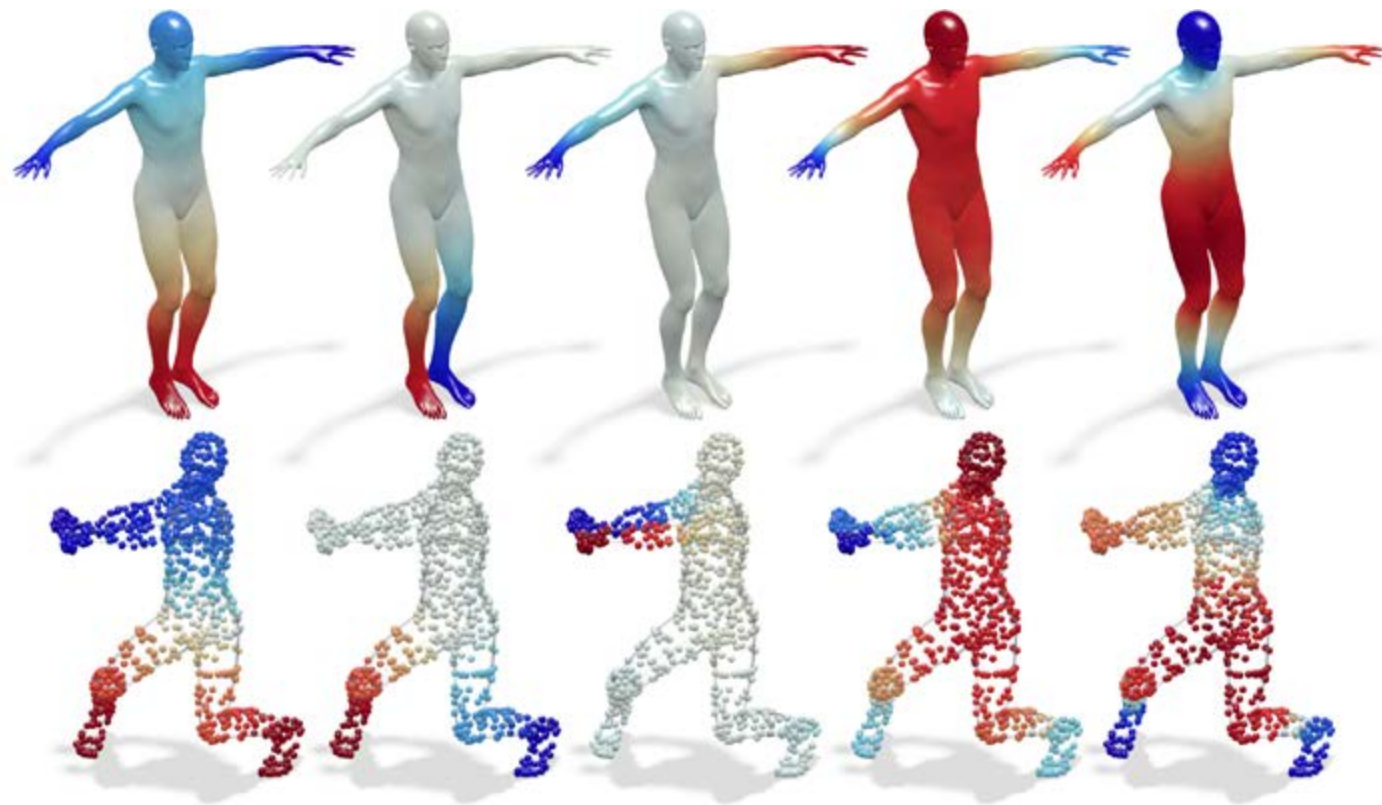




BRONSTEIN GROUP

# COMPUTATIONAL SHAPE ANALYSIS





BRONSTEIN GROUP

# GEOMETRIC AND VISUAL COMPUTING

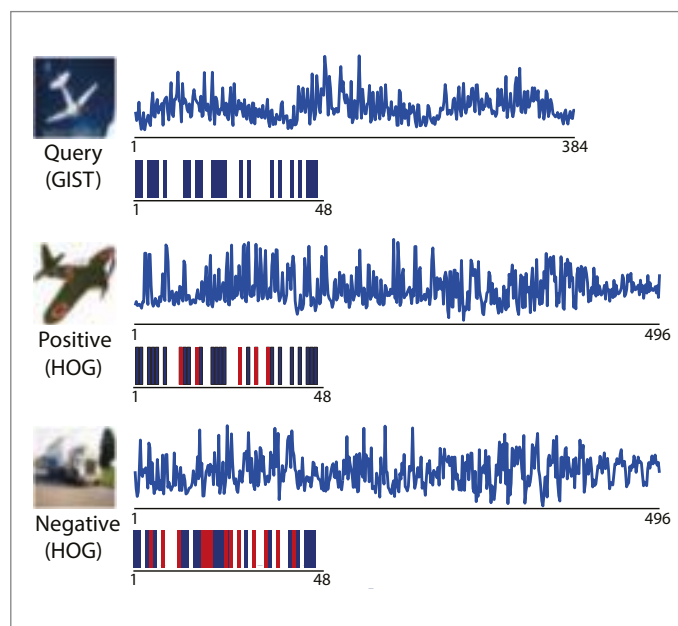
Vision is one of the most important sense for human beings, allowing us to perform a variety of extremely complex tasks in our everyday life. Prof. Michael Bronstein's Geometric and Visual Computing group conducts multi-disciplinary research dealing with different facets of visual information: acquisition, processing, analysis, indexing and retrieval. Our research encompasses three pillars: theory, computational methods, and applications. Our group is supported by the ERC Starting Grant and extensively collaborates with the industry and leading research labs in Switzerland, USA, France, and Israel.

## COMPUTATIONAL SHAPE ANALYSIS

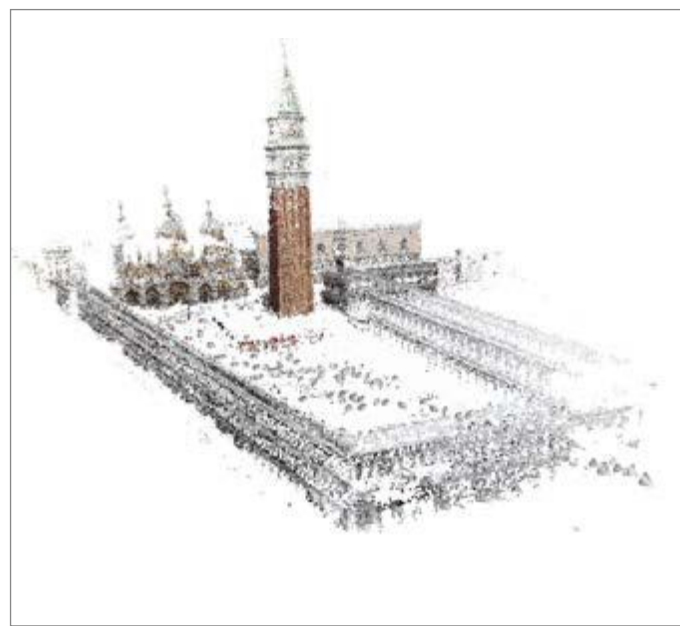
The last decade has witnessed a silent revolution in the maturity of commercial technologies for 3D data acquisition, display, and printing, creating a complete ecosystem. While 3D data processing bears some resemblance to classical signal and image processing, it is fundamentally different in many aspects, due to the need to deal with non-Euclidean structures. In our group, we are developing spectral analysis methods which allow for the handling of a variety of problems related to the 3D ecosystem: 3D shape acquisition, shape correspondence, comparison, editing, and retrieval.

## LARGE-SCALE VISUAL DATA SEARCH

Each second, megabytes of visual information are generated and published, in the form of videos uploaded to YouTube or photos posted on Instagram or Facebook. Organizing, indexing, and searching visual data is one of the most challenging problems in the domain of "big data" analysis. In our group, we are developing methods for efficient representation and retrieval of such data by embedding them into binary spaces, where computation of similarity boils down to finding binary code collisions or computing the Hamming metric.



Visual search through multi-modal similarity-preserving hashing. Our methods allow mapping different image descriptors such as Histograms of Gradients or Gist into compact binary codes which preserve semantic similarity between images and are mutually comparable (image from Masci et al., PAMI 2014)



Reconstruction of a 3D city model from photos requires extracting and matching millions of keypoints (local image features). This task can be achieved efficiently and reliably using our similarity-preserving hashing techniques (image of Piazza San Marco from Strecha et al., PAMI 2011)

## IN A NUTSHELL

- Acquisition, analysis, and retrieval of geometric and visual information is among the most challenging "big data" problems today
- Our research is on the crossing between geometry, computer vision, graphics, and machine learning
- We develop methods based on metric and spectral geometry for modeling high-dimensional multi-modal data
- Our methods are applied to a broad spectrum of problems, ranging from social network analysis to medical imaging and image search





HORENKO GROUP

# COMPUTATIONAL TIME SERIES ANALYSIS



### IN A NUTSHELL

- Modeling and prediction of risk is increasingly important in finance, weather/climate research, health care etc.;
- Many challenges (limited statistics for risk-inducing extreme events, multiscale nature of problems, missing/incomplete data);
- Four main directions of research of the “Computational Time Series Analysis” group at ICS are: (1) data-driven methods for modeling of extremes, (2) risk minimization methods for investments, (3) credit and equity risks in finance, (4) analysis of cardiac arrest risks in cardiology.

### HORENKO GROUP

## DATA-DRIVEN MODELING AND PREDICTION OF RISKS

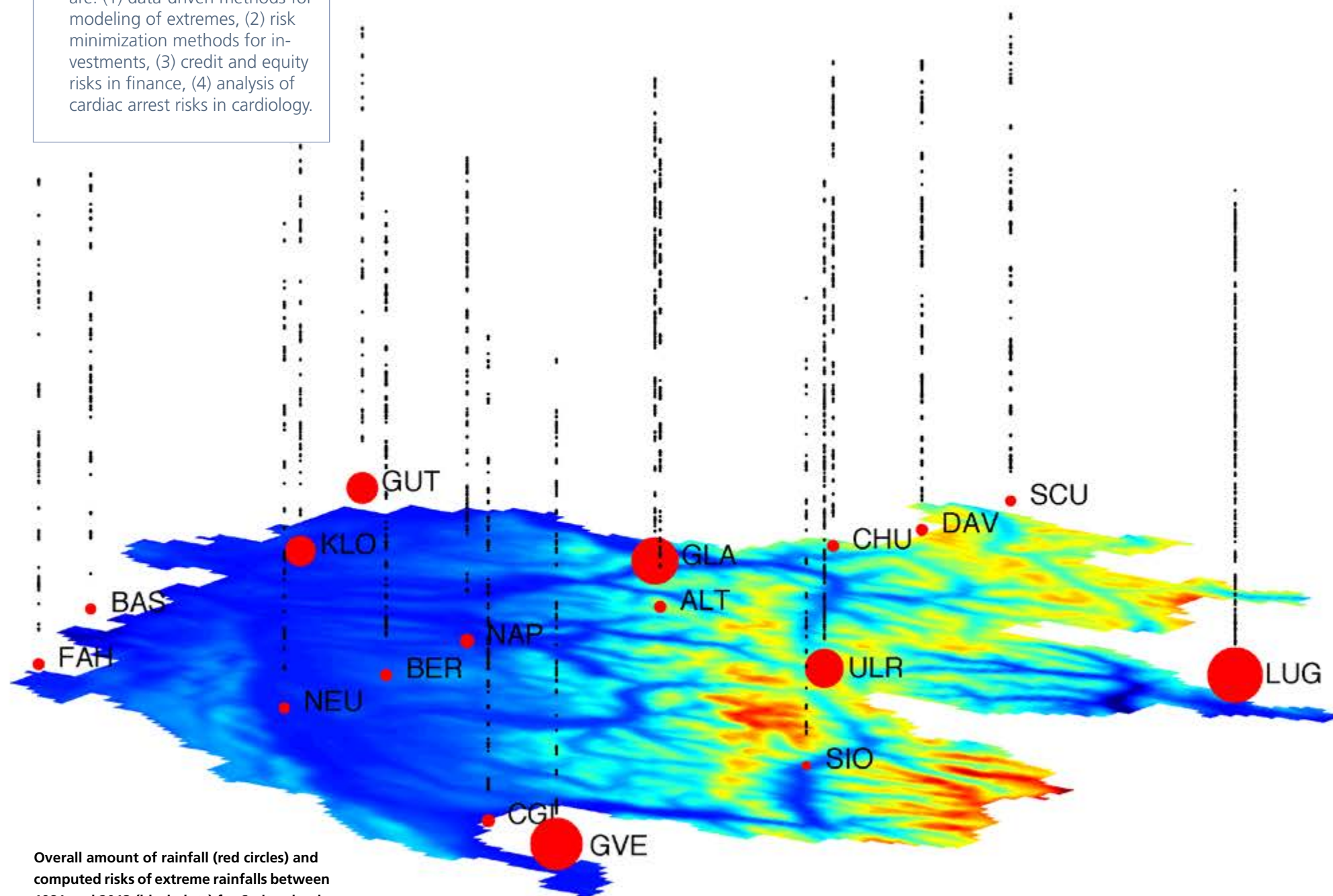
scale quantities that are not statistically-independent or identically-distributed may result in the violation of assumptions which are necessary for applicability of standard approaches and tools. The application of the standard stationary risk modeling approaches common to machine learning and statistics (e.g., methods like artificial neuronal networks, support vector machines, generalized linear models, homogeneous Markov processes, Generalized Extreme Value theory or standard GARCH methods from econometrics) in such situations leads to biased and even completely wrong predictions of the risks.

Research aims of the “Computational Time Series Analysis” group were organized in several connected research directions, imposing special emphasis on extending the currently available concepts and methods towards a non-parametric, non-stationary and non-homogeneous setting and involving the new opportunities that are provided by the emerging HPC facilities. These research directions in the project were: (1) data-driven methods for modeling of extreme events (2) risk minimization methods for investments; (3) data-driven modeling, inference and prediction of credit and equity risks in finance (in collaboration with P. Gagliardini from USI Economics department); (4) data-driven analysis and understanding of the sudden cardiac arrest risk (in collaboration with A. Auricchio from the Center for Computational Medicine in Cardiology (CCMC Lugano and Cardiocentro Ticino).

Main application areas for the tools and methods developed by the “Computational Time Series Analysis” group in context of this research domain so far have included: (1) climate/atmosphere/ocean science (in collaboration with experts from the CSIRO in Hobart/Tasmania and Max Planck Institute in Hamburg/Germany); (2) economics and finance (in a close collaboration with experts from USI Economics Department); (3) medicine/cardiology (in collaboration with experts from CCMC Lugano).

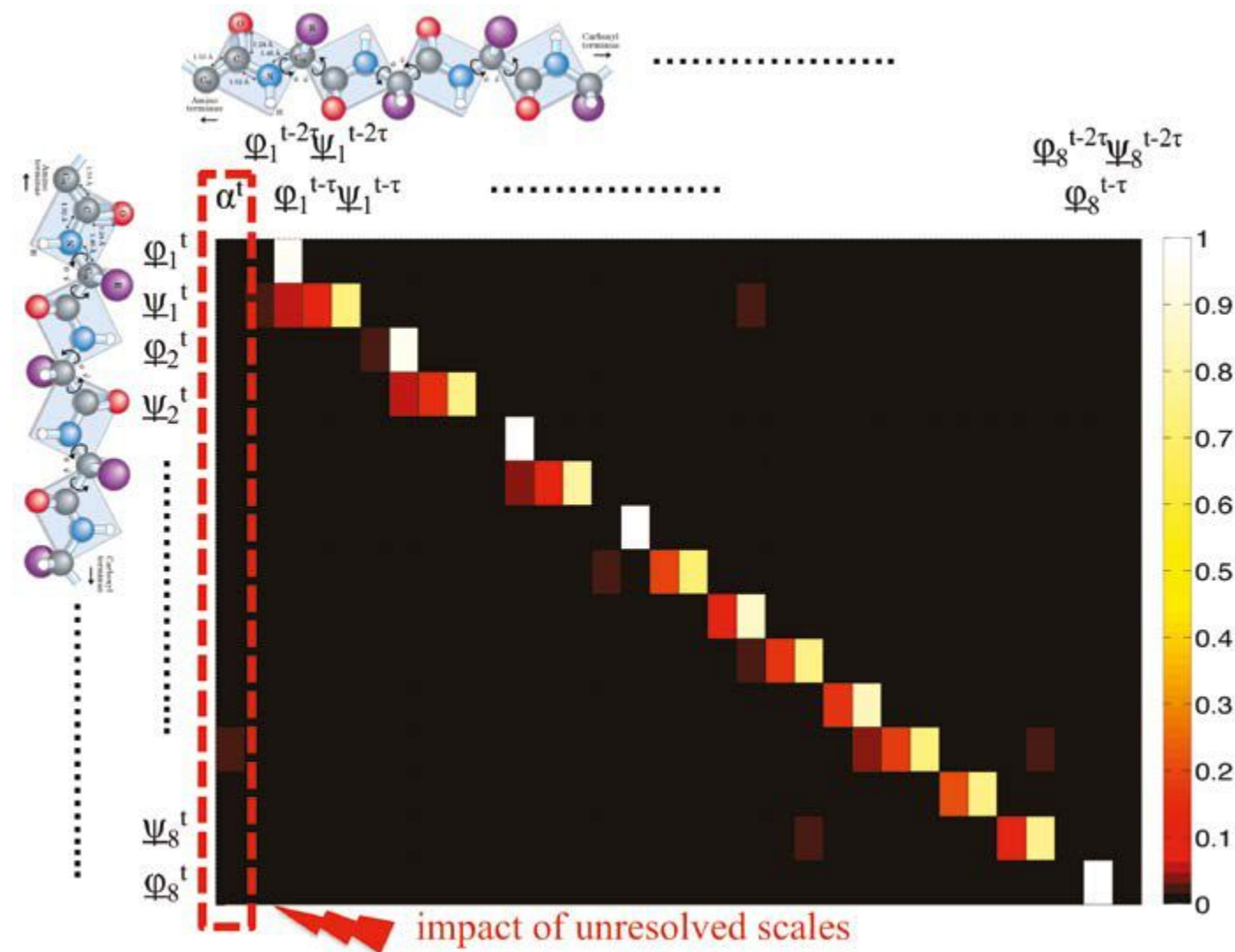
Data-driven modeling of risks, such as market and credit risks, weather-induced risks and health risks (e.g., a risk of a heart attack), is one of the central problems in many application areas. The task of an adequate mathematical description and prediction of the available risk data in its multiscale nature (resulting from the presence of different temporal and spatial, i.e. regional, sectorial and global scales) becomes more and more important in all spheres of human activity. Important questions thereby are: (1) an investigation of the mutual influence of different risks and their spatial (e.g., regional) and temporal evolution, (2) identification of the most important exogenous impact factors that play a role in the dynamics of risks, (3) proper mathematical and statistical description of the influences coming from the unresolved/latent scales and factors. This problem has many challenges, e.g., since risk is usually associated with some more-or-less extreme events and the more extreme these events are the less times they were observed and the less data is available for their analysis.

Moreover, as was recently demonstrated by the members of the “Computational Time Series Analysis” group in a context of multiscale discrete systems, the presence of unresolved/missing



Overall amount of rainfall (red circles) and computed risks of extreme rainfalls between 1981 and 2013 (black dots) for Switzerland.





Optimal causality matrix which was inferred from an output of the Molecular Dynamics (MD) simulation of a polypeptide in water (S. Gerber and I. Horenko, Proc. Natl. Acad. Sci USA (PNAS), 111 (41) 14651-14656, (2014)).

### IN A NUTSHELL

- How to learn causality relations from the data and to distinguish them from simple correlations?
- Standard methods and tools have significant limitations for real life systems, because of the multiple interacting scales that are not measurable (in time and in space);
- New HPC-scalable framework for data analysis beyond usual limitations was developed in the ICS group "Computational Time Series Analysis".

### HORENKO GROUP

# CAUSALITY OR CORRELATION? NEW DATA ANALYSIS METHODOLOGY FOR MULTISCALE SYSTEMS

Causality belongs to the most fundamental concepts in science. Besides providing a better insight into a system, appropriate discarding of the insignificant causality relations reduce the computational complexity of the corresponding models and methods. Given two sets of data variables  $y$  and  $x$ , one of the main challenges in statistical data analysis is to distinguish between the correlation and the causation relations between them. There are a lot of examples which demonstrate the well-known fallacy that "correlation does not imply causation" and although there exist a lot of methods for measuring the correlation, there is just a handful of possibilities available for data-driven causality inference. Another serious challenge comes from the multiscale nature of the real-life data, i.e., from the fact that the considered data for a process of interest

are embedded in a hierarchy of other processes and data on a wide range of temporal and spatial scales. Most of the data on the processes that are involved in interactions with the considered process is not directly measurable, i.e. the approaches must deal with the problem of missing data and systematically-unobserved (latent) and potentially-important processes.

Research conducted in the "Computational Time Series Analysis Group" of ICS has resulted in development of non-parametric, non-stationary, non-homogeneous data analysis framework which goes beyond the conceptual and computational limitations of standard approaches and allows to infer the causality relations in a multiscale context. In a close collaboration with partners from other disciplines, this framework was tested against and

applied to real-life data from a range of multiscale systems in biophysics, geosciences, sociology, economics and medicine.



KRAUSE GROUP

HIGH PERFORMANCE METHODS FOR NUMERICAL  
SIMULATION IN SCIENCE, MEDICINE AND ENGINEERING



## KRAUSE GROUP

# HIGH PERFORMANCE METHODS FOR NUMERICAL SIMULATION IN SCIENCE, MEDICINE AND ENGINEERING

Whereas, development of the methods require deep insight into their mathematical properties and their abstract structure, we nevertheless aim at testing and validating our new approaches along “real life” problems. Close cooperations with partners from industry and medicine is therefore as important an ingredient of our work as mathematical modeling and numerical analysis.

An additional challenge is posed by the fact that nowadays computational power comes “in parallel”. Current supercomputers are extremely powerful, but their computational possibilities are based on massive parallelism: thousands and hundreds of thousands of cores are connected in order to build a modern high performance computer. Exploiting these massively parallel machines for numerical simulation requires specially adapted numerical methods – and of course their careful realization in terms of numerical software.

One central aspect of our work is therefore to make our simulation tools capable of running on the fastest parallel machines available today and tomorrow. This often requires one to rethink or to redesign traditional algorithms, or even to develop completely new approaches.

This combination of mathematical abstraction and know-how from informatics allows us to develop methods which not only run on current super-computers, but also are capable of dealing with complex problems on multiple scales – be it from physics, engineering, or medicine.

Current projects in the group of R. Krause include biomechanics, contact problems in elasticity with and without friction, nonconforming domain decomposition methods, nonlinear and non-smooth multigrid methods, parallel nonlinear solution methods, adaptive finite elements for complex geometries, cardiac simulation, and parallel-in-time integration.

The optimization of mechanical parts in engineering, the design of prostheses or implants, or the development of new therapies for personalized treatment: mathematical modeling and numerical simulation is nowadays an indispensable tool for research and development in science, medicine, and engineering. Using numerical simulation, development processes can be shortened and costs for development can be significantly reduced.

Moreover, numerical simulations allow for the virtual testing of new designs for things such as, e.g., prostheses or implants, which might be difficult or undesirable to realize using studies involving human beings or animals.

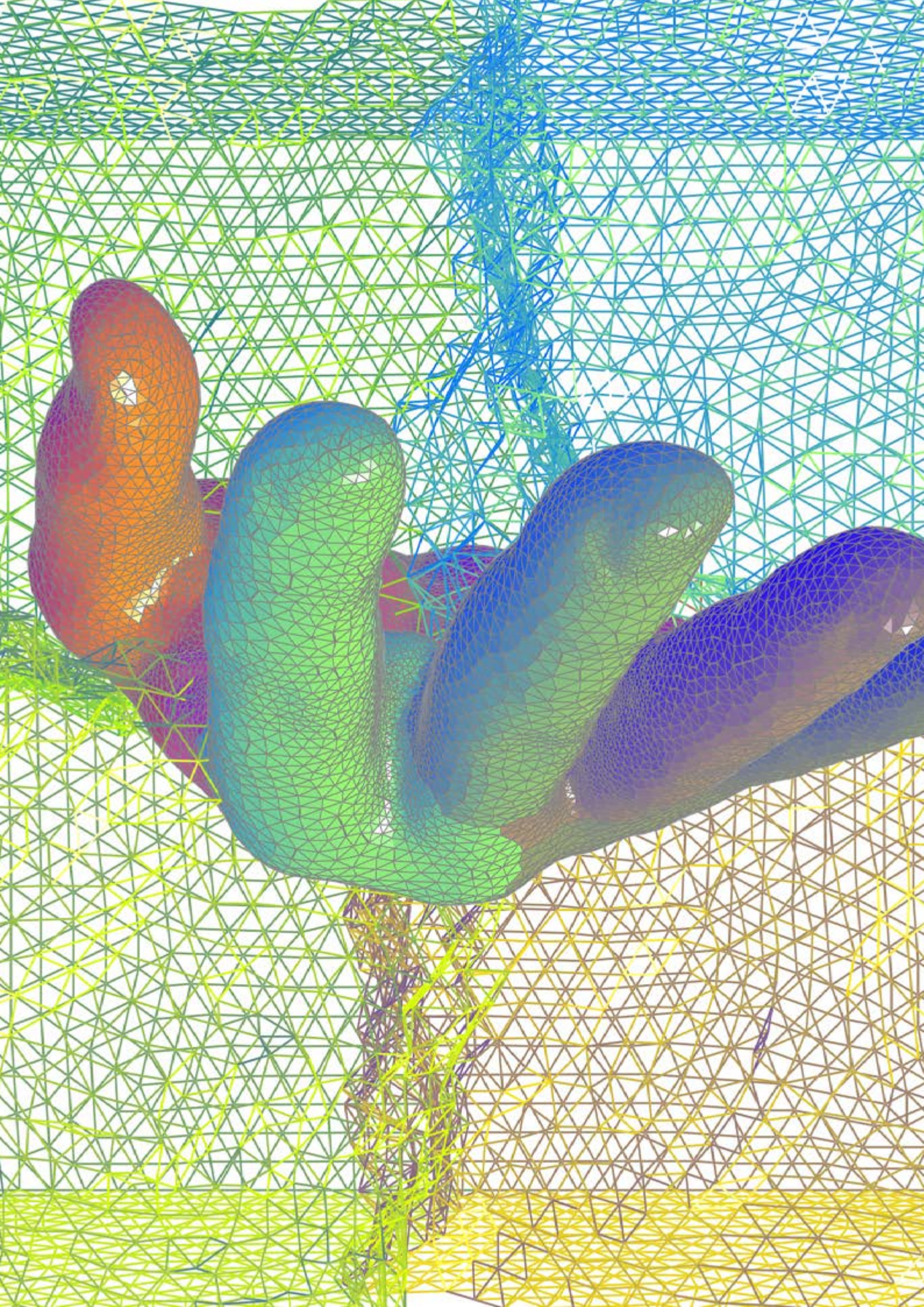
Clearly, in order to be as realistic as possible, any numerical simulation should involve all aspects which are relevant to the considered problem. Very often, this means to consider different physical behaviors at different scales in space as well as in time. One prominent example here is friction, as

it will occur in gear boxes, joints, or prostheses.

Friction is a complicated effect which takes place on a micro-scale. Thus, any numerical method for the simulation of frictional effect has to take care of these micro-scales. In combination with the mechanical deformation of the object under consideration, e.g., the prosthesis, this gives rise to a problem on multiple scales: friction on the micro-scale and the mechanical deformation on a larger scale, usually referred to as macro-scale.

From a numerical point of view, the simulation of such multi-scale effects is far from trivial. Reliability and efficiency of the simulation method are of the utmost importance, as well as their robustness.

Within the group of R. Krause, we aim at the efficient modeling and simulation of nonlinear processes on multiple scales in space and time for scientific, medical and biomechanical applications.



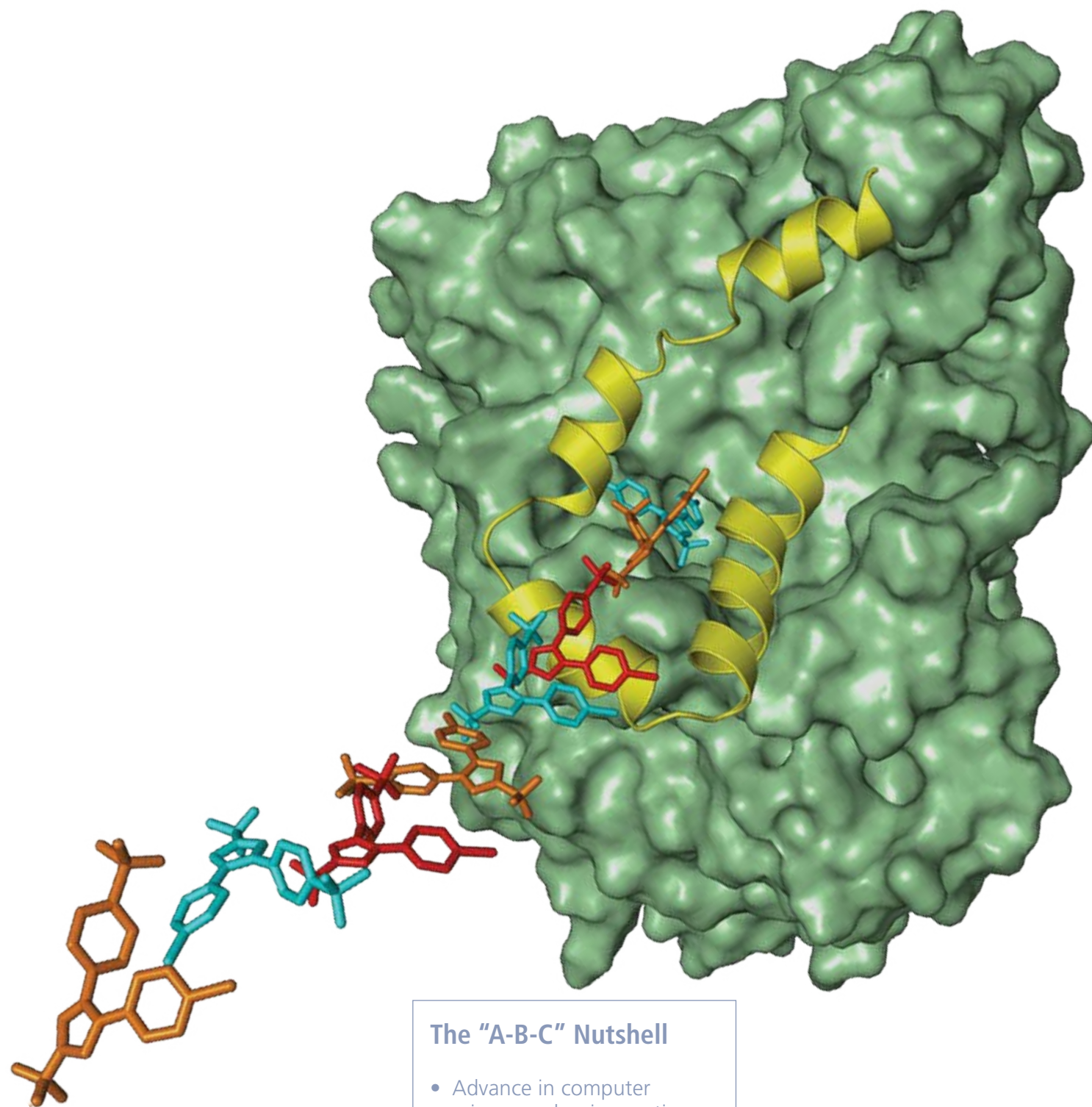




LIMONGELLI GROUP

MEDICINAL CHEMISTRY  
& DRUG DESIGN





### The "A-B-C" Nutshell

- Advance in computer science makes imperative to increase the accuracy of in-silico models
- Biological processes generally occur on long timescales and in complex multi-component environment
- Calculations able to model the physiological condition and reach biologically relevant timescales, increase the success rate of molecular predictions and drug design

Pictured is the binding process of a ligand to the Cyclooxygenase 2 enzyme.

## LIMONGELLI GROUP COMPUTATIONAL RESEARCH IN MEDICINAL CHEMISTRY AND MOLECULAR BIOLOGY

### DRUG DESIGN

Disclosing the events ruling the binding process of a drug to its target is of invaluable help in understanding its mechanism of action and develop new medications. Atomistic simulations, such as molecular docking and molecular dynamics, represent a natural choice to investigate ligand/protein interaction (1). In particular, docking algorithms are very useful to develop automated protocols to virtually screen databases of thousand ligands and identify new lead compounds. However, such fast methods are based on approximated estimation of the binding free energy, while this information is crucial to improve computer-aided drug discovery. To this end, we have recently developed a new approach, called Funnel-Metadynamics (2), that allows describing the binding and unbinding path of a ligand to its target, leading to an accurate estimate of the binding free energy. This kind of simulations is suitable to study even complex molecular binding processes such as protein/membrane and protein/protein interaction, where conformational flexibility and environment play a determinant role.

Taking advantage of this and other recent innovations, one can choose the most appropriate computational strategy for the system under investigation to increase the success rate of drug design.

### MOLECULAR MODELING

Biopolymers regulate activities fundamental for cellular lifespan adopting specific topologies. In this paradigm, revealing new structures is a major finding that provides the molecular bases to elucidate cellular mechanisms otherwise unexplained and the way to interact with them. This goal can be achieved combining standard and advanced computations with experiments. Example is our recent work where the existence of a novel DNA structural motif, named G-triplex, was predicted through enhanced-sampling folding simulations on the G-quadruplex thrombin binding aptamer (3). This important discovery was confirmed by a series of experiments.

In an ideal situation, biomolecules should be simulated in their biological context. However, the size and complexity of the physiological environ-

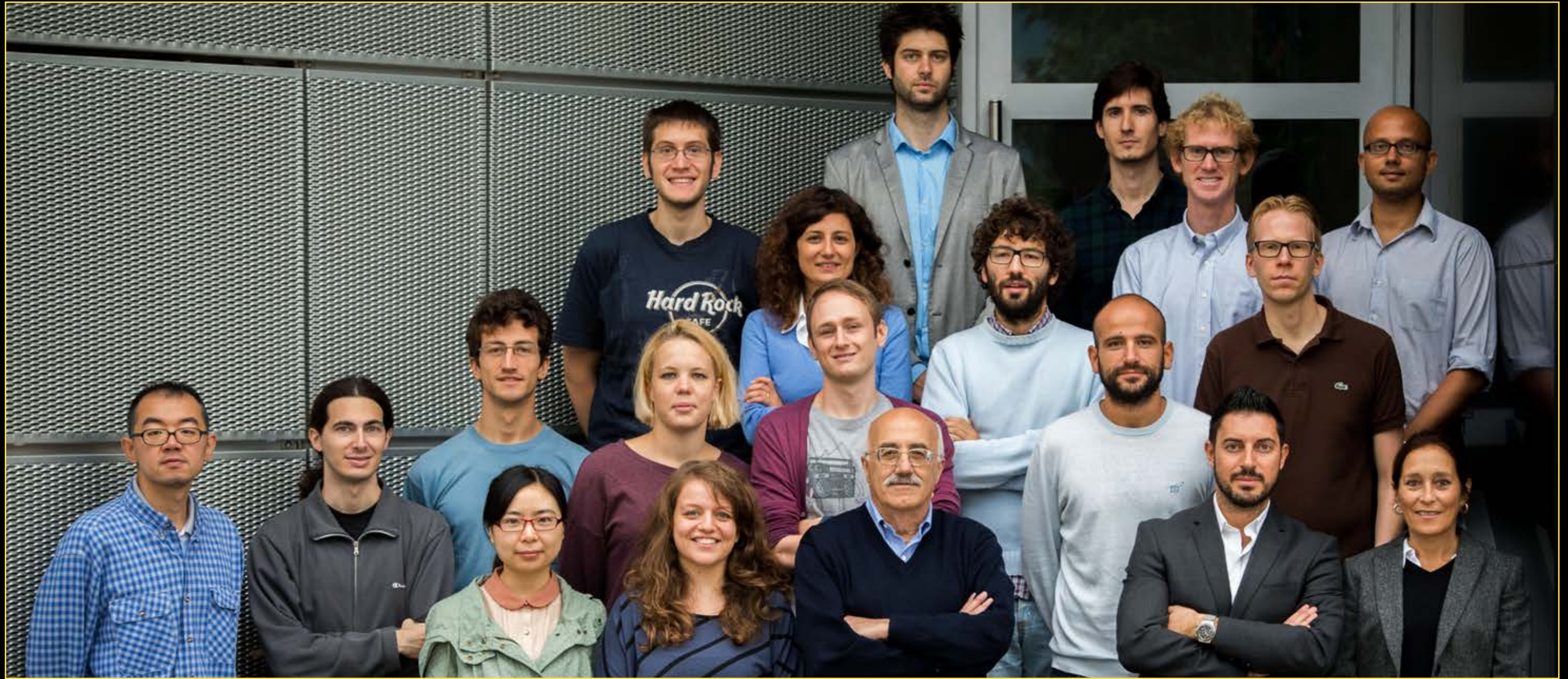
ment represent a major hurdle even for the most modern computational approaches. We achieved an important advance in this field by setting up a multiscale protocol that combines Coarse-Grained molecular dynamics and Metadynamics (CG-MetaD) (4,5). This approach allows describing long timescale events in large and complex systems at an affordable computational cost. In particular, using CG-MetaD simulations we have elucidated the second timescale dimerization process of the transmembrane helices of the epidermal growth factor receptor, computing also the associated free-energy landscape. This process is at the base of the activation mechanism of this kind of receptors, thus determining the mode and the energy cost of the dimerization process is instrumental to shed light on the functional mechanism of these receptors and understand the malfunction of the oncogenic variants.

The CG-MetaD approach opens new areas of investigation on membrane proteins (e.g. ion channels), protein clusters (e.g. GPCRs) and other biologically relevant systems, such as antigen/antibody complex, which are difficult to study using standard calculations.

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3. Limongelli V. et al. *Angew. Chem. Int. Ed. Eng.* **2013**, 125, 2325-2329.
4. Lelimosin M, Limongelli V and Sansom MSP. *Biophys. J.* **2013**, 104, 32.
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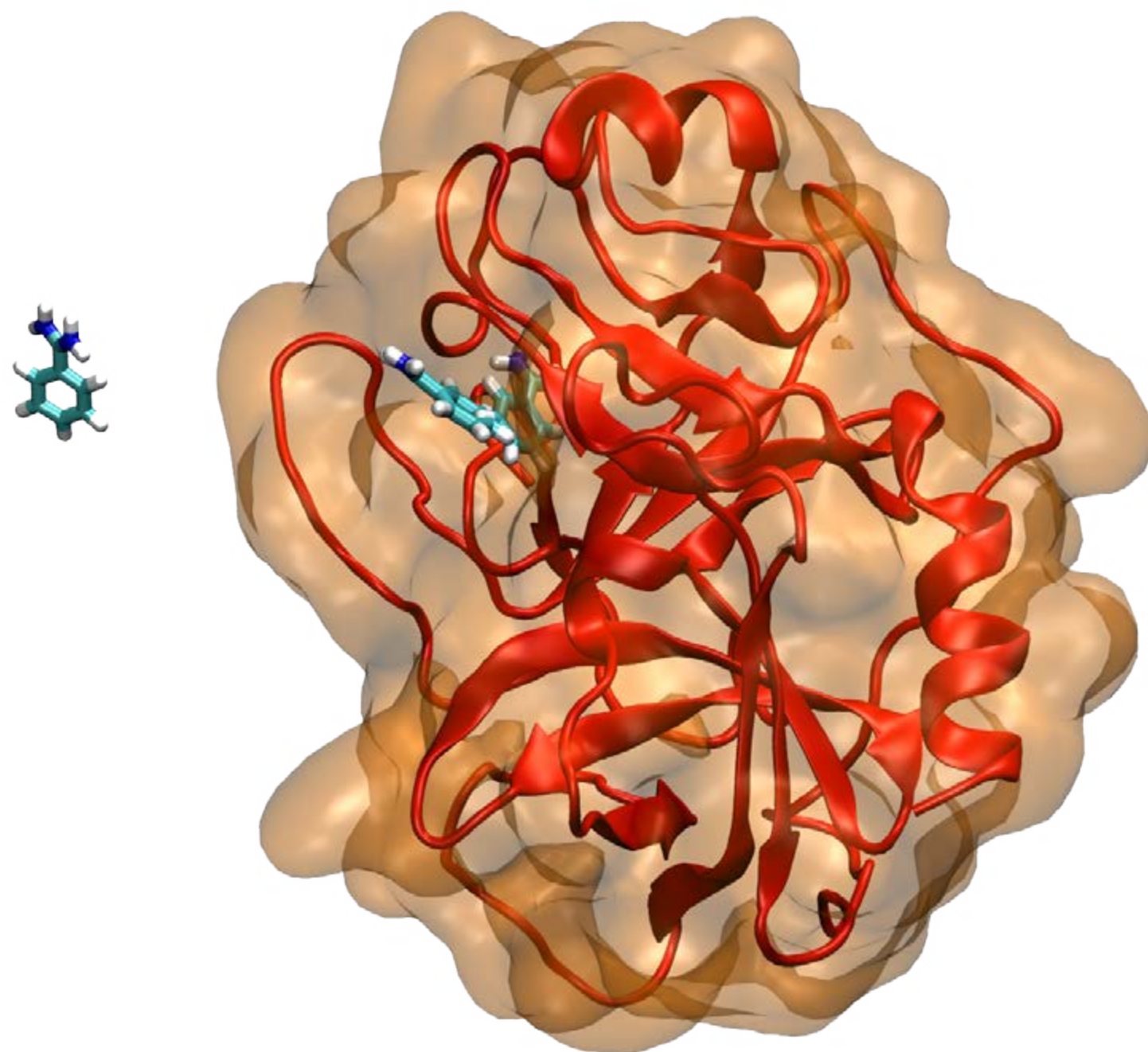




PARRINELLO GROUP

COMPUTATIONAL  
BIOLOGY





#### IN A NUTSHELL

- Biological systems are extremely complex
- Many scientific fields are related to biomolecular chemistry including pharmaceutical and medical areas
- Computational modeling allows for detailed and inexpensive prevision of realistic bio-environment

## PARRINELLO GROUP ADVANCED METADYNAMICS METHODS FOR BIOMOLECULAR SIMULATIONS

### DRUG UNBINDING

It is of paramount importance in the early stages of drug discovery to predict both how strongly and for how long does a drug stay bound to the protein. So far the major emphasis has been on predicting the strength of interaction as determined by the binding affinity. In contrast it has not been possible to use computations to predict the duration for which a drug stays bound. The dissociative half-life of the protein-ligand complex is defined as the time during which the ligand remains in the binding site. In principle this should be amenable to calculations through molecular dynamics (MD) simulations. However, in spite of the potential of MD simulations no such simulation has yet been reported. This is a consequence of the limiting timescales of MD simulations.

Metadynamics developed in our group is a popular technique that complements MD and allows studying complex systems. Using our recent significant extensions of metadynamics, we can now for the first time study protein-ligand dissociation pathways and determine associated rates, reaching well into longer than seconds regime while maintaining full atomic resolu-

tion for protein, drug and solvent. This work will open up new horizons in the ability to calculate mechanisms and rate constants, and have a transformative effect on the process of drug design, hopefully making it cheaper and faster.

### ALLOSTERIC REGULATION

Allosteric regulation plays an important role in a myriad of biomacromolecular processes. Specifically, in a protein, the process of allostery refers to the transmission of a local perturbation, such as ligand binding, to a distant site. Decades after the discovery of this phenomenon, models built on static images of proteins are being reconsidered with the knowledge that protein dynamics plays an important role in its function. Molecular dynamics simulations are a valuable tool for studying complex biomolecular systems, providing an atomistic description of their structure and dynamics.

Unfortunately, their predictive power has been limited by the complexity of the biomolecule free-energy surface and by the length of the allosteric timescale (in the order of milliseconds). Combining all-atom molecular dynam-

ics with enhanced sampling methods developed in our group, we are able to probe the origins of the allosteric changes that transcription factor mixed lineage leukemia (MLL) causes to the interactions of KIX domain of CREB-binding protein (CBP) with phosphorylated kinase inducible domain (pKID). We compare our results with previous experimental studies. Through this research we are able to develop a general simulations protocol to study allosteric phenomena and many other biological processes that occur in the micro/milliseconds timescale.



PARRINELLO GROUP

# NOVEL COMPUTATIONAL TOOLS FOR MODELLING CRYSTAL NUCLEATION AND GROWTH

## PHASE CHANGE MATERIALS

Phase change materials are the building blocks of state of the art optical storage devices and of the next generation of non volatile memories, which foreshadow multi level programming, nanowires based architectures and an important role in neuromorphic computing. All of these applications rely on the fast and reversible switching from the disordered phase to the crystalline state, which takes place in the nano domain with respect to both the time and the length scales. In order to unravel the atomistic details of the fast crystallization, we have taken advantage of Neural Network based interatomic potential for GeTe that obliterates the well known computational limitations of first principle calculations, in terms of system size and timescale while retaining the accuracy of a density functional theory framework. Thanks to this powerful tool, we have been able to perform large scale molecular dynamics simulations of the crystal growth of GeTe at the interface between the crystalline and the supercooled liquid phase, employing models that really bring our simulation playground extremely close to the actual crystallization scenario so extensively explored experimentally.

### IN A NUTSHELL

- Crystal engineering is one of the most challenging fields in materials science
- Its applications span from pure crystal growth to material surface functionalization
- Combination of new mathematical algorithms and machine learning approaches open up to ambitious technological applications

## GROWTH OF ORGANIC CRYSTALS

Nucleation and growth of a crystal phase from solution is a ubiquitous phenomenon of primary importance both in natural and industrial processes. Biomineralization phenomena as well as the production of sophisticated synthetic drugs or expensive fine chemistry compounds are just some of the processes that crucially depend on the nucleation and growth of a crystal from a dispersed and disordered phase.

The identification of nucleation mechanisms, the mechanistic description of crystal shape evolution during the growth process or the influence of foreign molecules on both nucleation and growth, represent only a fraction of the open problems in this field.

In this framework, molecular simulations play a primary role, allowing to obtain an insight into the elusive phenomena that occur at the molecular scale. In our research we apply enhanced sampling simulations to investigate both nucleation and growth of organic molecules from solution. Obtaining molecular-level information regarding nucleation is an essential step towards a thorough comprehension of crystallization processes.

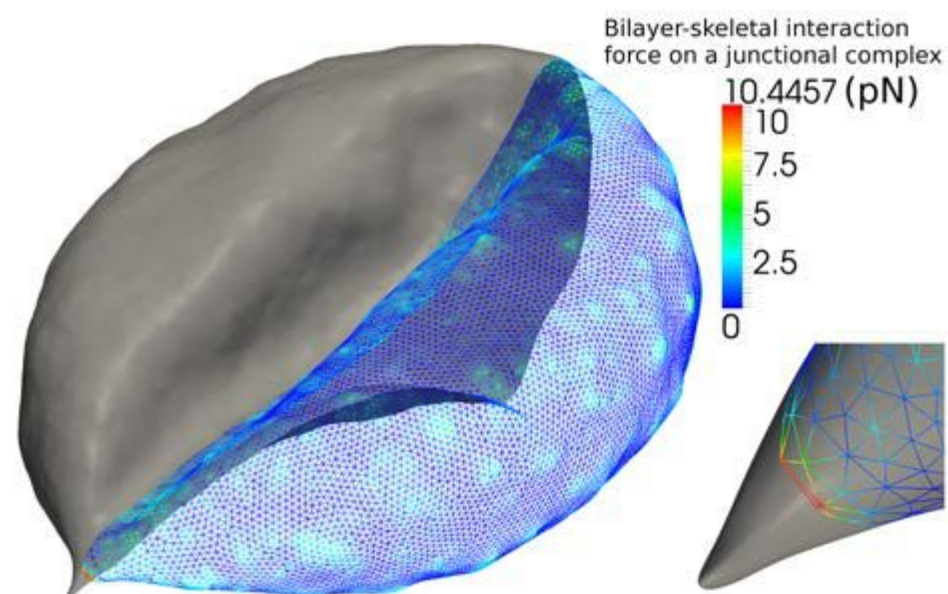
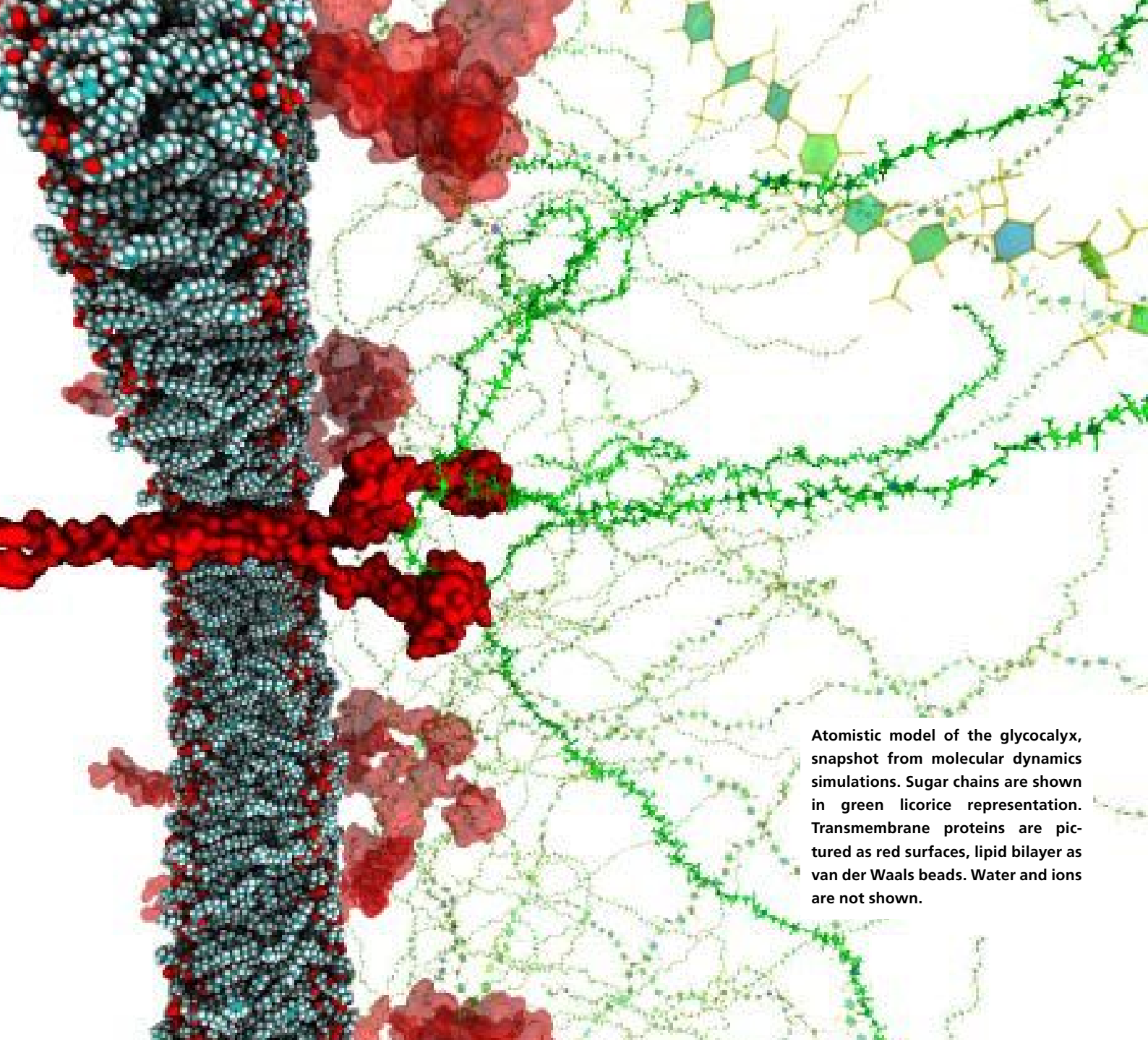




PIVKIN GROUP

SCIENTIFIC  
COMPUTING GROUP





Snapshot from the simulation of the whole RBC cell stretched under the flow with a line attachment to the microfluidic channel wall. The inset is the local view of the bilayer-cytoskeletal interaction. The bilayer is shown as gray surface while the cytoskeleton is shown as a triangular network with the contour. The contour is the magnitude of the bilayer-cytoskeletal interaction force on a junctional complex.

## PIVKIN GROUP

# CELL BIOMECHANICS

## CELL BIOMECHANICS

We developed a systematic coarse-graining procedure for modeling red blood cells (RBCs) using arguments based on mean-field theory. Our spectrin-based RBC model lies between continuum and atomic scales and can be used for arbitrary levels of coarse-graining. The model takes into account bending and in-plane shear energy, viscous effects of the membrane, and constraints of total area and volume. We performed systematic fully three-dimensional computational simulations as well as microfluidic experiments to quantitatively study the flow dynamics of the RBCs at the smallest relevant scale and different physiological conditions. Recently, we have extended this model by representing the lipid bilayer and the cytoskeleton of spectrin network as two distinct components. We employed this new model to investigate the effects of the bilayer-cytoskeletal viscoelastic interactions. Currently there are no experimental techniques that directly measure the mechanical characteristics of these interactions. By applying this new two-component whole-cell model, we reconciled and resolved several controversies and issues in RBC mechanics. Our computational framework provides a broad general methodology for mesoscale simulations of the flow of cells. In addition, it can be used to explore important problems involving cell physiology and pathological states mediated by protein mutations, such as the bilayer loss in hereditary spherocytosis and the bilayer-cytoskeleton uncoupling in sickle cell anemia.

## TRANSPORT PROCESSES IN TUMOR INDUCED MICROCIRCULATION

Over 85% of human cancers are solid tumors. In order to grow tumors require supply of oxygen and nutrients. Therefore the blood flow in tumor vasculature networks are a key regulator of the tumor development in the vascular phase. In collaboration with the group of Petros Koumoutsakos from ETH Zurich, we study the transport processes in healthy and tumor induced microcirculation. We build on our combined expertise in modeling of blood flow using experimentally validated multiscale models, on the development of continuum, discrete and hybrid angiogenesis models, and on the capability to implement highly-scalable particle codes on emergent computer architectures. Within the project, we recently built an atomistic model of the glycocalyx. To the best of our knowledge this is the most detailed model to date. The glycocalyx is a polymeric layer that is the first barrier for solute exchange between the blood and tissues and as such it is involved in key metabolic processes. It is now well established that information about molecular motions within the glycocalyx is necessary to advance our knowledge of its function. Current experimental techniques are not yet sensitive enough to elucidate the detailed dynamic interplay among the different glycocalyx components. Here, molecular dynamics simulations act as the unique exploratory tool, not only to complement experimental findings but also to propose testable predictions. We envision that the present study will enhance our understanding of transport phenomena in healthy and tumor induced microcirculation thus contributing to the development of rational strategies for cancer therapy.





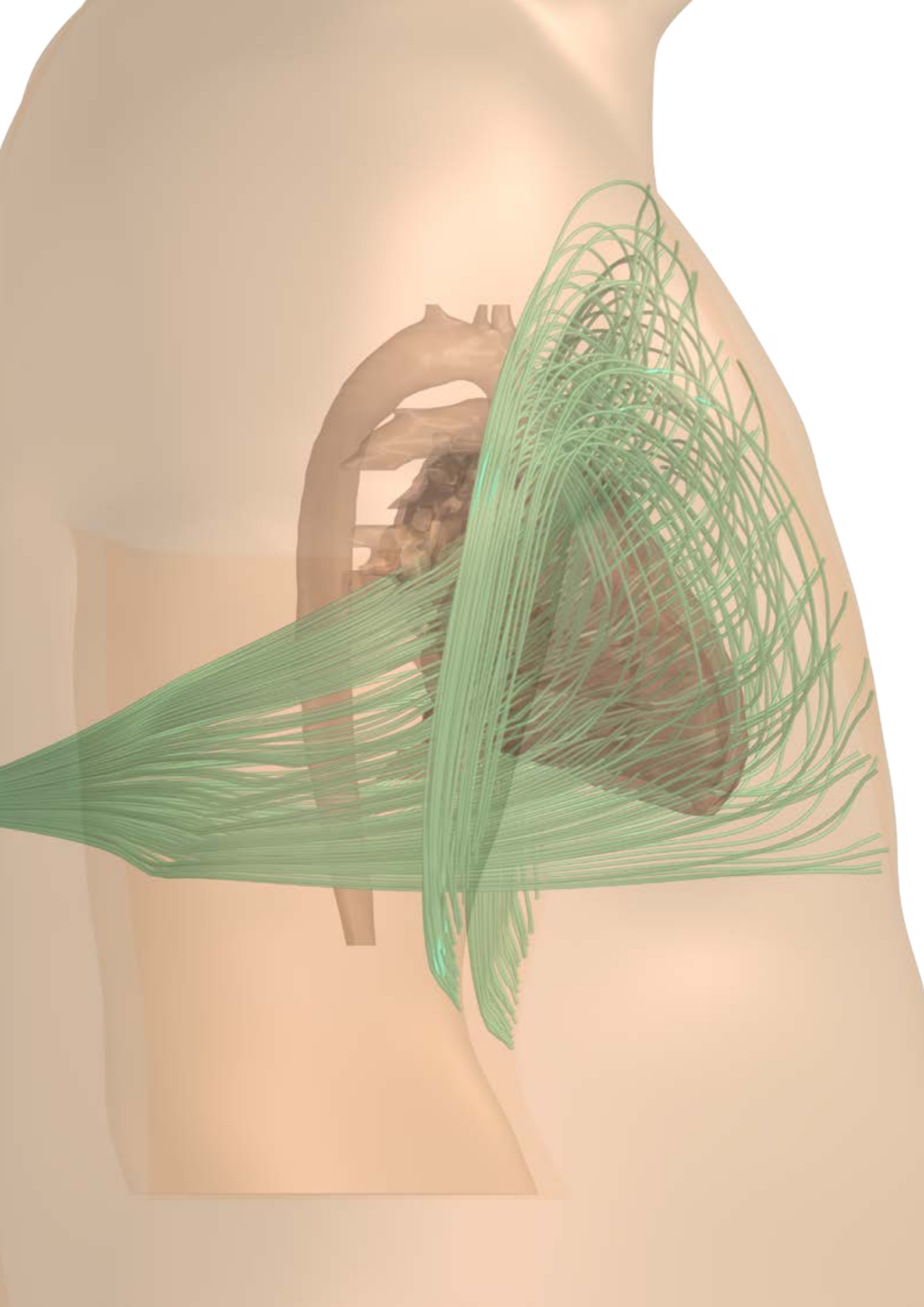
POTSE GROUP

# MODELING CARDIAC ELECTROPHYSIOLOGY



POTSE GROUP

# UNDERSTANDING THE ELECTROCARDIOGRAM



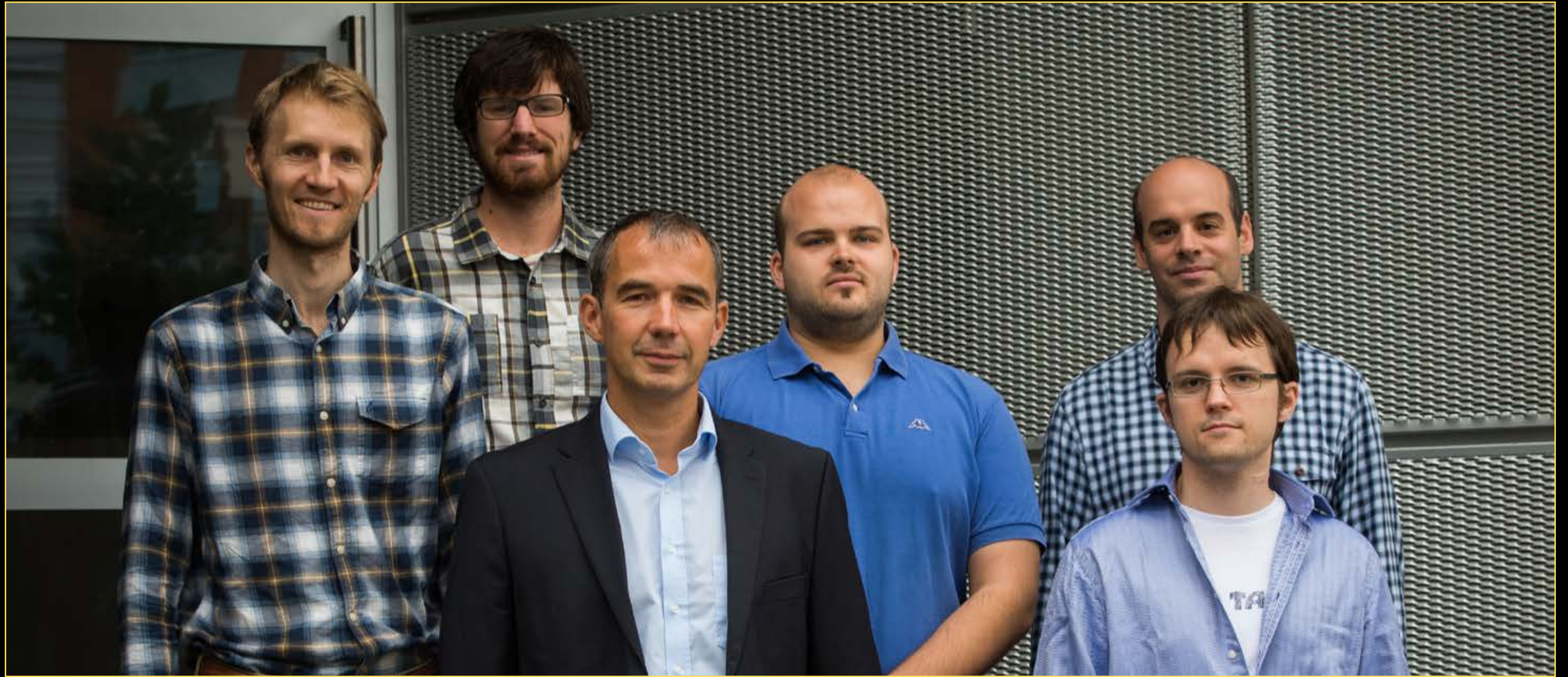
Electrocardiograms are measured using groups of electrodes on the skin of the patient. One electrode serves as the positive pole, and two or three others as the negative pole of the "lead". The way an electrocardiographic lead sees the heart can be computed by virtually injecting – in a computer model of the body – a current in the positive pole and extracting it from the negative pole. The direction in which this current crosses the heart is the same as the direction in which the lead is most sensitive, at that point of the heart. The green curves show how a positive electrode on the back and three negative electrodes on the arms and left leg would view the heart.

To let the heart work efficiently, all of its muscle cells must contract simultaneously. This requires rapid communication between the cells, which is achieved by an electrical activation mechanism. The same electrical activation that causes each cell to contract is also propagated to its neighbors. This causes an activation wave to sweep the ventricles of the heart in less than one tenth of a second. Due to this organized activity, the beating of the heart causes clear electrical signals, which can be measured as electrocardiograms.

Electrocardiograms are useful for diagnosis of heart diseases but their interpretation can be difficult. The cellular mechanisms that cause the electrical activation are highly complex, activation and deactivation take place in large parts of the heart simultaneously, and the different electrical conductivities of the heart, lungs, and other organs influence the way in which the activity of the heart translates into signals that can be measured with electrodes on the skin.

We provide insight in these mechanisms, and help cardiologists to better understand the signals, using computer simulations of the heart and the conduction of the electrical currents that it generates. With these simulations we can test hypotheses: does a given change in the behavior of the cardiac cells cause the same electrocardiogram changes as seen in the patient – or should we suspect that something else is going on? We can also use computations to visualize phenomena, or to show how signals and diseases relate to each other. This work spans a wide range of disciplines such as cardiology, physiology, biomedical engineering, mathematics, informatics, and computational science.

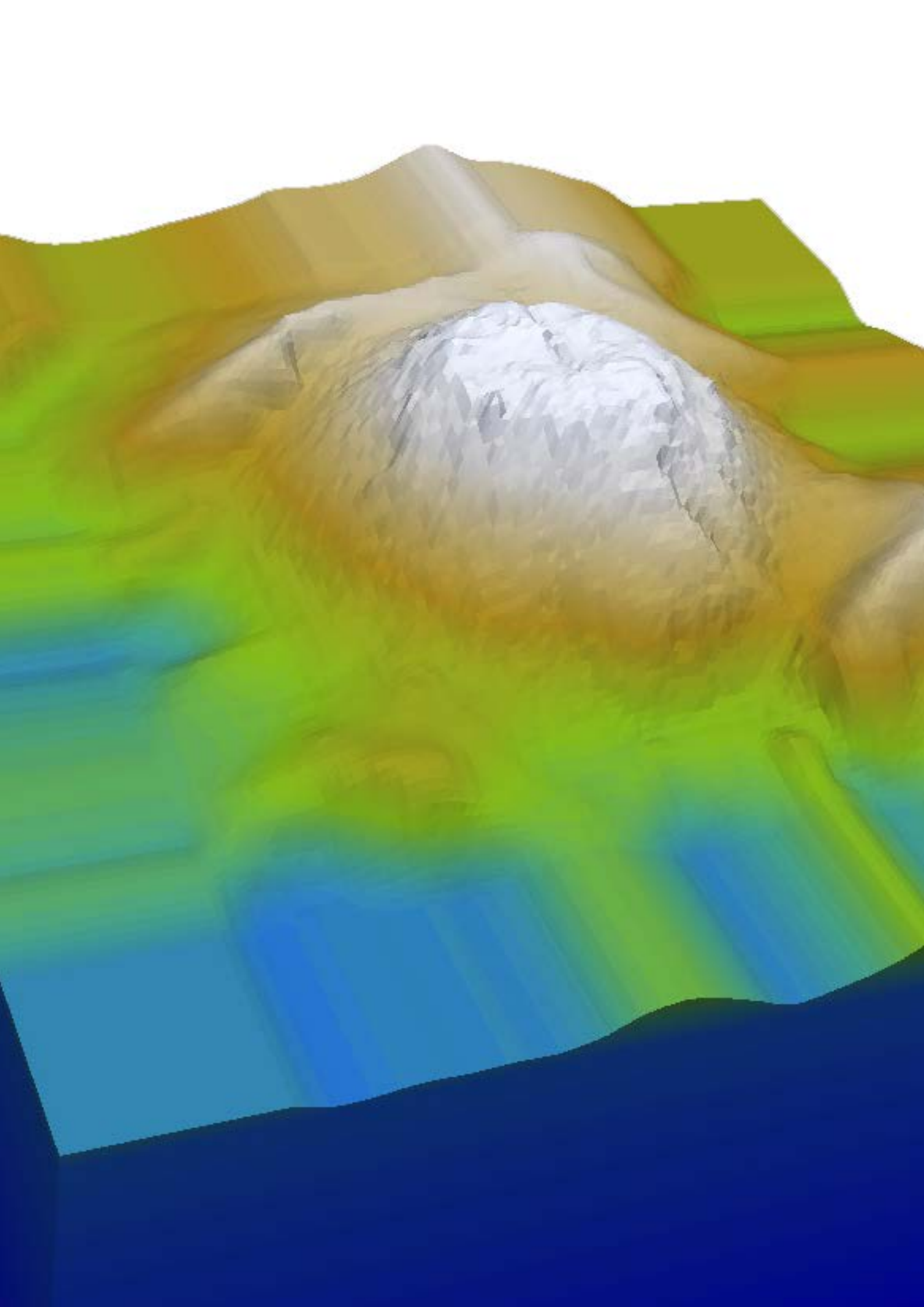




SCHENK GROUP

# ADVANCED COMPUTING LABORATORY IN COMPUTATIONAL SCIENCE





## SCHENK GROUP EXASCALE ALGORITHMS AND ADVANCED COMPUTATIONAL TECHNIQUES

The Advanced Computing Laboratory was established in 2012 as a research group at the Institute of Computational Science. It is dedicated to interdisciplinary research activities in the domains of extreme-scale high performance computing, numerical optimization, and scientific computing. Our challenge is to enable research by employing leading-edge supercomputing technologies and innovative numerical algorithms. We conduct research in high performance computing and computational science, especially in the design and prototype development of scalable numerical software systems. Working in our group often involves developing innovative mathematical approaches, methodologies, and technological tools in supercomputing. Underlining the importance of application-driven research, part of the research is currently dedicated to transferring these developments to various application areas. In cooperation with national and international academic institutes and industrial partners, we currently work on supercomputing topics in the areas of, e.g., computational geophysics, computational nanoelectronics, and energy research.

### SOLVER ALGORITHMS AT THE EXASCALE

Numerical simulation is a crucial part of science and industry in Europe. The advancement of simulation as a discipline relies on increasingly compute intensive models that require more computational resources to run. This is the driver to achieve exascale. Due to the limits in the increase in single processor performance, exascale machines will rely on massive parallelism on and off chip, with a complex hierarchy of resources. The large number of components and the machine complexity introduce severe problems for reliability and programmability. The former of these will require novel fault-aware algorithms and support software. In

addition, the scale of the numerical models exacerbates the difficulties by making the use of more complex simulation algorithms necessary, for numerical stability reasons. A key example of this is increased reliance on solvers. Such solvers require global communication, which impacts scalability, and are often used with preconditioners, increasing complexity again. Unless there is a major rethink of the design of solver algorithms, their components, and software structure, a large class of important numerical simulations will not scale beyond petascale. This interdisciplinary research brings together, at the cutting edge of the development of solvers, related algorithmic techniques, and HPC software architects for programming models and communications. It is supported within the EU FP7-ICT program.

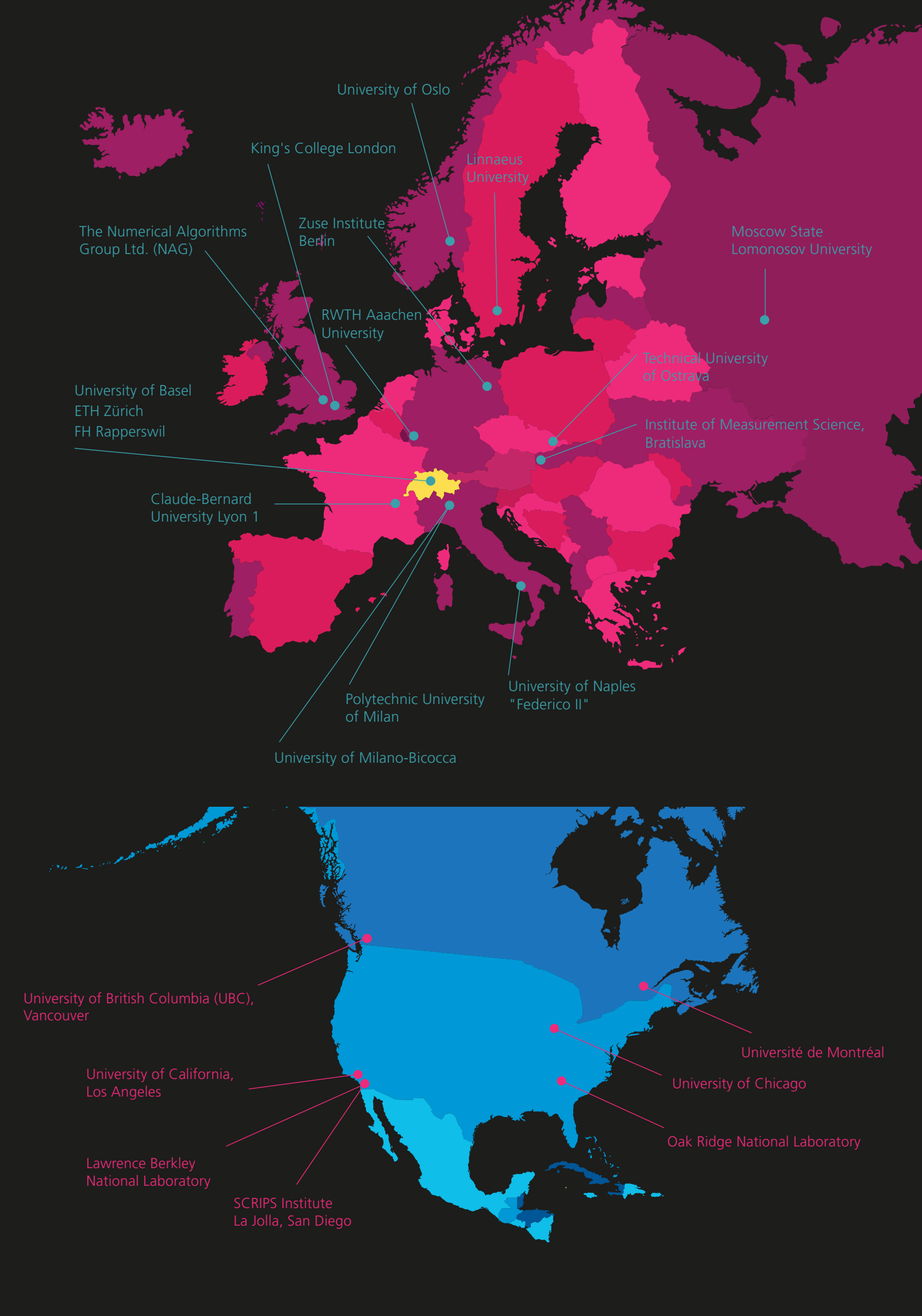
### FULL-WAVEFORM INVERSION IN STRONGLY HETEROGENEOUS MEDIA

Resolving structures and processes on a wide range of interacting spatio-temporal scales is a grand unifying challenge in all branches of geophysics which must be addressed in order to achieve a comprehensive understanding of the Earth as a multi-physics system. Geophysical modeling and inversion across the scales heavily relies on modern HPC resources. To achieve this goal, we combine recent developments in computational methods for nonlinear optimization and wave propagation, such as high-order finite element discretizations, local time-stepping, iterative methods, and inexact parallel interior-point methods.

### STENCIL PROGRAMMING IN COMPUTATIONAL EXASCALE SCIENCE

The performance of a processor unit is limited by the memory bandwidth rather than the available compute power. This so-called memory wall causes many scientific applications on structured grids to perform poorly. Solving this problem is of utmost importance for explicit time integration applications on semi-structured or structured grids. A key example is the application of smoothers in massively parallel multigrid solvers. Such multigrid solvers require global communication, which impacts scalability, and they heavily rely on complex parallel smoothers based on structured grid computations. In such types of solvers, stencil kernels are often the dominant part of the computation, and an efficient parallel implementation of the kernel is therefore crucial in order to reduce the time to solution. However, in current complex hardware microarchitectures, meticulous architecture-specific tuning is required to elicit the machine's full compute power. Unless there is a major rethink of the design of solver algorithms, their components, and software structure, a large class of important numerical simulations will not scale beyond petascale. We are addressing the issues of stencil programmability, stencil efficiency, and their application in the design of exascale multigrid solvers.





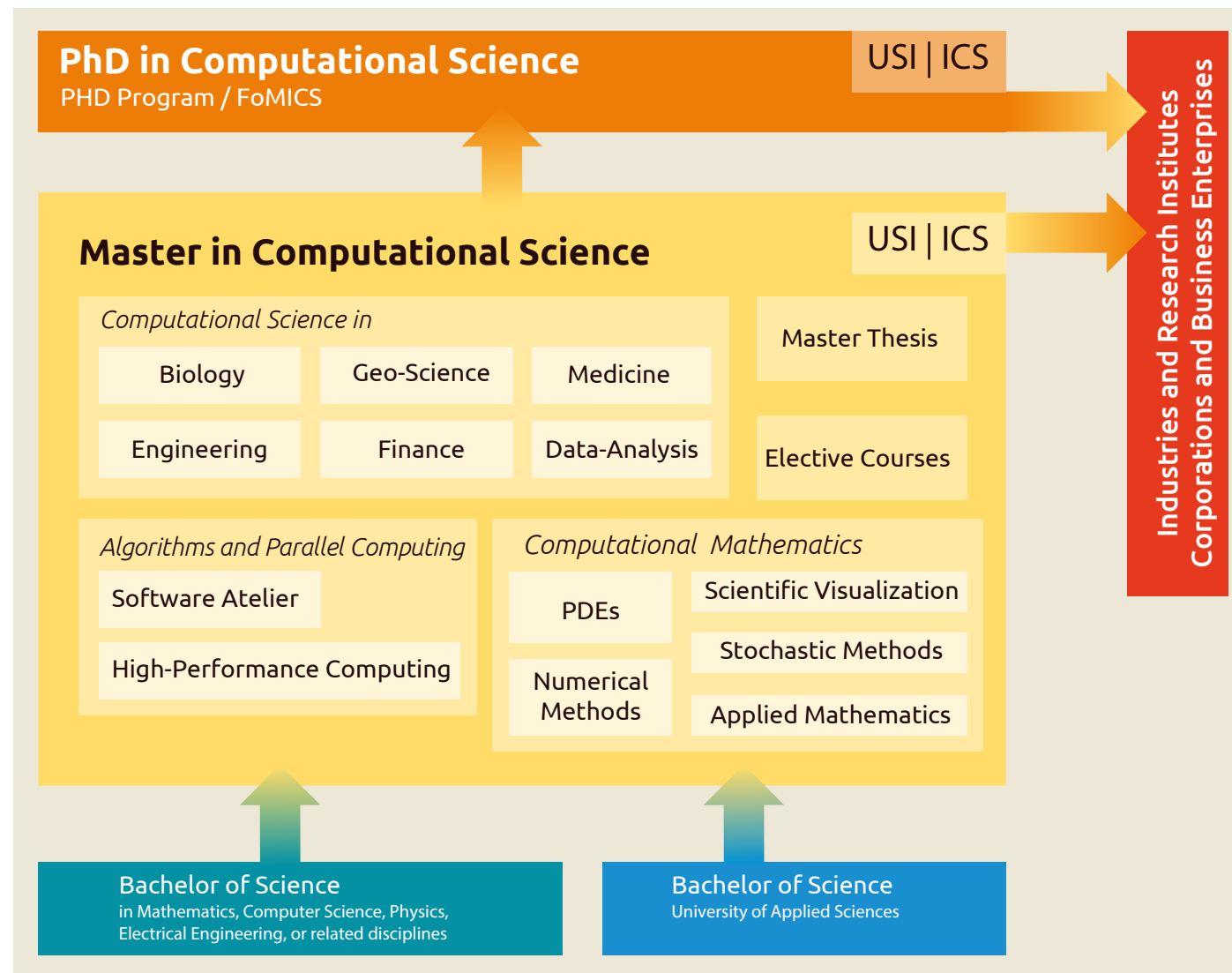
## LIST OF ICS PARTNERS IN RESEARCH AND INDUSTRY

Argonne National Laboratory  
 Brandenburgische Technische Universität  
 Deutscher Wetterdienst Zentralamt/German Meteorological Service  
 Deutsches Zentrum für Luft- und Raumfahrt DLR/German Aerospace Center  
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 Max-Planck-Institut für Meteorologie/Max Planck Institute for Meteorology  
 Moscow State Lomonosov University

The Numerical Algorithms Group Ltd. (NAG)  
 Oak Ridge National Laboratory  
 Politecnico di Milano/Polytechnic University of Milan  
 Private Foundation TI  
 Rheinisch-Westfälische Technische Hochschule Aachen/RWTH Aachen University  
 Ruhr University Bochum  
 SCRIPS Institute La Jolla  
 Simula Research Laboratory  
 SUPSI/University of Applied Sciences and Arts of Southern Switzerland  
 Swiss National Supercomputing Centre  
 TATAA BIOCENTER AB  
 Technical University of Ostrava Czech Republic  
 T-Systems Germany  
 University of British Columbia (UBC) Vancouver  
 University of California, Los Angeles  
 University of Perugia  
 University of Milano-Bicocca  
 University of Duisburg-Essen  
 University of Stuttgart  
 Claude-Bernard University Lyon 1  
 Université de Montréal  
 University of Antwerpen  
 University of Basel  
 University of Bern  
 University of Chicago  
 University of Luxembourg  
 University of Naples "Federico II"  
 University of Oslo  
 University of Oxford  
 University of Versailles Saint-Quentin-en-Yvelines France



## Structure of the Computational Science Master Program



## GRADUATE AND POST-GRADUATE PROGRAMS AT ICS

### Master of Science Program in Computational Science

The multidisciplinary Computational Science Master program at ICS provides a high level education, offering a blend of cutting edge scientific research and practical application, thus providing an excellent foundation for a corporate, industrial or academic career. By combining a solid and deep theoretical background in applied mathematics and numerical analysis with state-of-the-art knowledge in computer science and high-performance computing, students will get the best of two worlds: A general and abstract view on computational techniques provided by the mathematical framework, and a hands on / application oriented education in modern informatics and software engineering.

With the resources available at ICS and our partners at the Swiss National Supercomputing Centre CSCS, ETH Zurich, or Cardiocentro Ticino, the students are trained to exploit the power of mathematics and of large supercomputers for real-world simulations in a broad range of application areas. Students receive a firm grounding in programming, mathematical modeling and numerical simulation as well as a strong orientation towards applied mathematics. The unique scope of our Master program creates an exceptionally wide spectrum of occupations for our graduates in a large variety of different application domains. Our graduates are sought-after experts in data evaluation, data modeling and prognosis.



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ICS**

## PH.D. AND FOMICS

The Ph.D. program at ICS promotes the development of new professionals interested in academic or industrial research careers. ICS hosts the Swiss Graduate Program FoMICS "Foundations of Mathematics and Informatics in Computational Science". FoMICS is an education network between Swiss Universities for training PhD students in Computational Science. It is based on the two key components mathematical modeling and high-level engineering of scientific software. FoMICS offers a curriculum comprised of foundations of mathematical models and algorithms, as well as on computing and simulation skills, which

enable participating PhD students to develop tailored mathematical models and efficient software, exploiting the capabilities of recent hardware environments - from local, specialized architectures to Swiss-wide large-scale HPC systems.





## MICHAEL BRONSTEIN

Michael Bronstein is an assistant professor in the Institute of Computational Science, Faculty of Informatics. He received the B.Sc. summa cum laude (2002) from the Department of Electrical Engineering and Ph.D. with distinction (2007) from the Department of Computer Science, Technion (Israel Institute of Technology). Prior to joining USI, he held a visiting appointment at Stanford university. His main research interests are theoretical and computational methods in metric geometry and their application to problems in computer vision, pattern recognition, shape analysis, computer graphics, image processing, and machine learning.

Prof. Bronstein has authored over 70 publications in leading journals and conferences, over a dozen of patents and the book "Numerical geometry of non-rigid shapes" (published by Springer Verlag). His research was recognized by numerous awards and was featured in CNN, SIAM News, and Wired. Michael Bronstein was the co-chair of the Workshop on Non-rigid shapes and deformable image alignment (NORDIA) in 2008-2012, Third International Conference on Scale-Space and Variational Methods in Computer Vision (SSVM) in 2011, and the Eurographics Workshop on 3D Object Retrieval (3DOR) in 2012. He has

served on review and program committees of major conferences in computer vision and pattern recognition and was invited and keynote speaker in numerous international symposia. He is a Senior Member of IEEE and member of SIAM.

Besides academic work, Dr. Bronstein is actively involved in industrial applications, technology transfer and commercialization, and consulting to technological companies in the computer vision, image processing, and pattern recognition domain, both in technical and management positions. His track record includes developing and licensing algorithms for large-scale video analysis applications at the Silicon Valley start-up company Novafora (2004-2009 as co-founder and VP of video technology) and developing coded-light 3D camera based on his patents at the Israeli start-up Invision (2009-2012 as one of the principal technologists). Following the acquisition of Invision by Intel in 2012, Michael Bronstein currently serves as advisor and research scientist at Intel.



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## ILLIA HORENKO

Illia Horenko is an associate professor in the faculty of informatics at the University of Lugano. He received a Ph.D. in applied mathematics from the Free University (FU) of Berlin in 2004 and spent several years as a postdoctoral research fellow at the Biocomputing Group and Climate Research Group at the FU Berlin, before joining the faculty of mathematics and computer science of the FU Berlin as an assistant professor in 2008.

His research interests are focussed on the development and practical implementation of data analysis algorithms, inverse methods and time series analysis approaches. Application areas for the developed methods are problems from climate/weather research, computational finance and econometrics, biophysics, computational fluid mechanics, sociology and gottarun). Special emphasis is put on data-based investigation of socio-economical and climate-related processes. Prof. Horenko has published over 30 papers in the professional literature. He was an organizer of several big programs on mathematical and computational aspects of scientific computing (Oberwolfach program in 2008) and climate research (IPAM program at the UCLA in 2010) and is a frequent reviewer for international funding agencies and the top journals in his field.



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## ROLF KRAUSE

Rolf Krause is chair of advanced scientific computing and the director of the institute of computational science in the faculty of informatics. From 2003 to 2009, he was professor at the University of Bonn. During that time he spent a sabbatical at UC San Diego (USA) and Columbia University New York (USA). In 2002 he was on a Postdoctoral research visit at the Courant Institute (NYU, New York). He holds a Diploma and a PhD (2000) in Mathematics from the FU Berlin (Germany).

His research focuses on numerical simulation and mathematical modeling in scientific computing and computational sciences, in particular the development of theoretically well founded simulation methods, which show excellent performance also in real world applications. He is associate editor of the SIAM Journal on Scientific Computing (SISC) as well as the Springer Journal Computing and Visualization in Science (CVS). Together with Prof. Dr. med. A. Auricchio of the Cardiocentro Ticino, Rolf Krause established the "Center for Computational Medicine in Cardiology" (CCMC) in 2014, which they are leading as co-directors.



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## VITTORIO LIMONGELLI

Professor Limongelli took his Master Degree in Chemistry and Pharmaceutical Technology at University of Napoli "Federico II" (Italy) in 2004 and took at the same university his PhD degree in 2007. During those years, his research was focused on standard computational methodologies (e. g. molecular docking, homology modeling) applied to the study of systems of biopharmaceutical interest. In 2007 he was visiting PhD first at University of Bologna (Italy) and then at ETH Zurich (Switzerland). Here he did his PostDoc working in the field of enhanced sampling simulations used to study rare events in biosystems with a special focus on molecular binding processes. In December 2010 he got a permanent position as Researcher at the University of Naples "Federico II" (Italy) and in 2014 he got the qualification to function as Associate Professor in Italian Universities. In 2015 he moved back to Switzerland as Senior Assistant Professor at USI Lugano (Switzerland).



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## MICHELE PARRINELLO

Professor Parrinello is known for his many technical innovations in the field of atomistic simulations and for a wealth of interdisciplinary applications ranging from materials science to chemistry and biology. Together with Roberto Car he introduced ab-initio molecular dynamics, also known as the Car-Parrinello method, marking the beginning of a new era both in the area of electronic structure calculations and in molecular dynamics simulations. He is also known for the Parrinello-Rahman method, which allows crystalline phase transitions to be studied by molecular dynamics. More recently he has introduced metadynamics for the study of rare events and the calculation of free energies. For his work he has been awarded many prizes and honorary degrees. He is a member of numerous academies and learned societies, including the German Berlin-Brandenburgische Akademie der Wissenschaften, the British Royal Society and the Italian Accademia Nazionale dei Lincei, which is the major academy in his home country Italy. Born in Messina in 1945, he got his degree from the University of Bologna and is currently professor of Computational Sciences at Università della Svizzera italiana (at the ICS) and ETHZ in Switzerland.



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## MARK POTSE

Mark Potse is a researcher at Inria, the French national institute of applied mathematics and informatics, and as a visiting professor coordinates the electrophysiological modeling work at the CCMC. He obtained his PhD in physics at the University of Amsterdam, The Netherlands, for a thesis in computerized analysis of high-resolution electrocardiological data. Interested in understanding cardiac electrical signals, he did postdoctoral fellowships in Montreal, Canada, with Ramesh Gulrajani and Alain Vinet, and in Maastricht, The Netherlands, with Frits Prinzen and Ulrich Schotten, developing and using a large-scale cardiac modeling code. This code, extensively enhanced at ICS, now suits the requirements of modern-day supercomputers and has been used in studies of Brugada Syndrome, myocardial ischemia, ventricular hypertrophy, and ventricular conduction disturbances.

Mark's research combines signal analysis and modeling to improve understanding of cardiac pathologies and their effects on measurable signals. His current research interests are in the areas of J-wave syndromes, ventricular conduction disturbances, and atrial fibrillation. To make this work possible he also pays a great deal of attention to the maintenance and further development of this modeling code, as well as mesh creation and data visualization techniques.



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## IGOR V. PIVKIN

The research interests of Igor Pivkin lie in the area of multiscale/multiphysics modeling, corresponding numerical methods and parallel large-scale simulations of biological and physical systems. Specific areas include biophysics, cellular and molecular biomechanics, stochastic multiscale modeling, and coarse-grained molecular simulations. He received his B.Sc. and M.Sc. degrees in Mathematics from Novosibirsk State University, Russia, M.Sc. degree in Computer Science and Ph.D. in Applied Mathematics from Brown University, USA. Before joining ICS, he was a Postdoctoral Associate in the Department of Materials Science and Engineering at Massachusetts Institute of Technology, USA.



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## OLAF SCHENK

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He graduated in Applied Mathematics from Karlsruhe Institute of Technology (KIT), Germany, and earned his PhD in 2001 from the Department of Information Technology and Electrical Engineering of ETH Zurich and a *venia legendi* from the Department of Mathematics and Computer Science from the University of Basel in 2009. He conducts research in applied algorithms, computational science, and software tools for high-performance scientific computing.

Olaf Schenk is a member of the Society for Industrial and Applied Mathematics (SIAM), the Association for Computing Machinery (ACM) and the Institute for Electrical and Electronic Engineers (IEEE). He is a recipient of an IBM faculty award (2008) and two leadership computing awards from the U.S. Department of Energy (2012, 2013). He serves on the editorial board of the SIAM Journal for Scientific Computing.



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