Program

International Conference on Computational Science and Engineering
CSEConf2017

In memory of Hans Petter Langtangen

October 23 – 25, 2017
Oslo, Norway

Revised 2017-09-28
This book contains the program, including all abstracts for keynotes and contributed talks, of the CSEConf2017 – an International Conference on Computational Science and Engineering to be held October 23 – 25 in Oslo, Norway. The abstracts are listed according to their appearance in the program.

Simula Research Laboratory organizes the conference in the memory of professor Hans Petter Langtangen, who passed away on October 10, 2016. The conference topics of Software, Education, and Biomedical applications are selected specifically to honor Hans Petter’s impressing impact on the scientific computing community.

Conference web site: https://cseconf2017.simula.no/

Memorial web site: http://hpl-memorial.simula.no/
Monday, 13:00

Opening

Ole M. Sejersted
President of The Norwegian Academy of Science and Letters
Biographical note on scientific software

Are Magnus Bruaset, Kalkulo
Keynote

Riemann problems for hyperbolic PDEs: Theory, software, and education

Randall J. LeVeque
Boeing Professor of Applied Mathematics, University of Washington

Abstract

The Riemann problem is key to understanding the behavior of hyperbolic PDEs, and is the fundamental building block of many high-resolution shock-capturing numerical methods. The Riemann problem is simply the PDE together with piecewise constant data, and the solution is typically a similarity solution consisting of waves propagating at constant speeds away from the discontinuity. I will briefly review this theory and the way these methods are used in the Clawpack software package (http://www.clawpack.org). I will then describe an ongoing project to write a book exploring true and approximate Riemann solutions for a wide variety of wave propagation problems. Jointly with David Ketcheson and Mauricio del Razo, we are developing the book as a series of Jupyter notebooks that include Python code for the reader to experiment with, and that employ interactive widgets and animation tools to provide a more active experience for students or researchers grappling with this theory. We are still experimenting with the best approach to developing material that works well in the notebook and also translates well to static webpages and hardcopy, with the hope of expanding its accessibility and usefulness. The current state of the project can be found in the Github repository https://github.com/clawpack/riemann_book.
Monday, 14:00

A parallel finite element multigrid framework for geodynamic simulations with more than ten trillion unknowns

Dominik Bartuschat, University of Erlangen-Nürnberg
Uli Rüde, University of Erlangen-Nürnberg

Abstract

Numerical simulations are an indispensable tool in geosciences for understanding geodynamic processes inside the Earth. Due to the enormous spatial and time scales and the inaccessibility of the Earth's interior to direct measurements, studying these processes requires a combination of sophisticated computer simulations and mostly indirect observations.

Heating inside the Earth's core and mantle causes convection currents in the solid Earth mantle, which results in a viscous flow on geological time scales of millions of years. This mantle convection is the driving mechanism of plate tectonics, which causes mountain building, earthquakes and volcanism. However, many details of the physical processes in Earth mantle convection are poorly known, such as appropriate rheological parameters or the mantle viscosity structure.

To allow for the use of realistic physical parameters, Earth mantle convection simulations require extremely large grids for a sufficient resolution of the mantle volume of $10^{12}$ km$^3$ and many time steps. These simulations are only possible with highly efficient codes that exhibit excellent parallel scalability on modern supercomputers. In this talk, we present a framework for such large-scale time-dependent mantle convection simulations on a thick spherical shell with variable viscosity.

In the simulations a nonlinear coupled multiphysics problem of Stokes equation coupled to the energy equation is solved, modelling the conservation of momentum, mass, and energy. These equations are discretized with finite elements and the solution is computed in the Hierarchical Hybrid Grids (HHG) framework.

This framework combines the flexibility of unstructured tetrahedral meshes with the efficiency of structured grids for finite element discretizations. The design of HHG is motivated by the challenging goal of achieving high performance on large-scale and parallel finite element simulations on supercomputers. HHG exploits the performance and efficiency of nested structured grid hierarchies and hierarchically organized data structures combined with the flexibility of unstructured grids. To this end, HHG combines grid partitioning and regular refinement in such a way that an execution paradigm using stencils can be realized. Within uniform blocks of the mesh three-dimensional stencils are applied in the fashion of a finite difference method.

We present transient simulation results of the temperature distribution for the coupled flow and transport problem, as well as the stationary flow field for variable temperature-dependent viscosity with high viscosity contrasts. Moreover, scaling results are presented to show that our approach facilitates solving systems in excess of ten trillion ($10^{13}$) unknowns on Peta-Scale systems using compute times of a few minutes.
The p4est software for parallel AMR

Carsten Burstedde, University of Bonn

Abstract

As part of the software track of this conference, I would like to give an overview of the goals, functionality, and design principles of p4est. p4est is a free software library for managing adaptive meshes using distributed parallelism. This means that all mesh data is strictly divided between the parallel processes and global metadata replication is minimized. In combination with dedicated algorithms to create, adapt, partition, and interrogate an adaptive mesh, this enables scalability to the largest supercomputers available. p4est is used in many applications and fields throughout scientific computing.

p4est is developed on top of the MPI standard for message passing. It is a fairly strict representative of the two time-tested philosophies "Do one thing and do it well" and "keep it simple, stupid." It encapsulates all message passing for communication of mesh elements and partition markers, where mesh changes are alike MPI collective calls, some read-only accesses are formalized and some are not. While different opinions exist on the stylishness of its C-only, rudimentary object-based interface, its authors like its modularity and portability. From what we hear, p4est behaves exactly as advertised and is generally stable, reliable, and solves the problems it is meant to solve.

I believe I am not saying too much when mentioning that Hans Petter was appreciative of the algorithmic design and capabilities of the software. While we did not directly work together, I am thankful for our conversations. It is good that different styles proliferate in scientific software, and we hope to contribute one example that performs a critical function while doing most of its work unnoticed in the background.
Center for Biomedical Computing (2007-2017)

Joakim Sundnes, Simula Research Laboratory

Abstract

The Center for Biomedical Computing (CBC) was established by Hans Petter Langtangen in 2007, and was running for 10 years. The Center has been devoted to three research tasks; computational middleware, robust solvers, and applications to biomedical problems with potential for high clinical impact. These highly integrated topics represent a broad, a medium, and a specialized scope, respectively, of advancing the current state of computational science. The challenging applications being addressed have driven new developments in computational methodologies and scientific software. A key mission of the CBC has been to make these useful developments accessible to computational scientists and engineers at large through professional, open source software. In addition to a high volume of published books and scientific papers, CBC has taken a central role in the development of the FEniCS finite element software, and has released a number of other open source software packages ranging from statistical tools for uncertainty quantification to optimization software geared towards patient-specific modeling of heart mechanics.
Keynote

Writing software for solving PDEs

Anders Logg
Professor of Applied Mathematics, Chalmers University

Abstract

In this talk I will present a brief history of the programming of PDE solvers, with a focus on the development of high-level abstractions, domain-specific languages and automated code generation. Several examples from well-known and widely used software libraries will be discussed. In particular, I will examine how early work of Hans Petter Langtangen on the Diffpack software has influenced the design of state-of-the-art software platforms for the solution of PDE. I will also reflect on the evolution of programming languages for the design of PDE solvers and speculate on how PDE solvers will or should be designed in the next 100 years.
On adjoint models, their implementation and applications

Simon Funke, Simula Research Laboratory
Marie E. Rognes, Simula Research Laboratory

Abstract

The adjoint equations of partial differential equations are essential in computational science. They enable the study of the sensitivity and stability of solutions, and the optimisation of free parameters. For practical problems however, the application of adjoints is often hindered by their difficult derivation and implementation, particularly for coupled, nonlinear and time-dependent models. In [1], the authors proposed an approach of automatically implementing adjoint models by exploiting the high-level mathematical structure inherent in finite element methods. In 2015, this idea was awarded the Wilkinson prize, and has since then been used to introduce adjoints to new application areas, ranging from renewable energy to biomedical computing.

In this talk, we give an introduction to adjoint models and the idea of high-level adjoint derivations. We then present a set of applications from biomedical computing and other disciplines where adjoint models have been used.

References

Automating the spectral Galerkin method in Python

Mikael Mortensen, University of Oslo
Miroslav Kuchta, University of Oslo
Lisandro Dalcin, King Abdullah University of Science and Technology

Abstract

The spectral Galerkin method employs globally supported spectral basis functions (e.g., Fourier, Chebyshev, Legendre) in the Galerkin approximation. Due to its accuracy, the method is often favoured in the study of fundamental physical phenomena in Cartesian domains, like turbulence and transitional flows in channels. Until now there have been few tools available for solving PDEs with this method, at least not if one is aiming at high performance supercomputers. With the shenfun Python module (github.com/spectralDNS/shenfun) an effort is made towards automating the implementation of the spectral Galerkin method for simple (yet large in scale) tensor product domains. The user interface to shenfun is intentionally made very similar to FEniCS (fenicsproject.org). PDEs are represented through weak variational forms and solved using efficient, order optimal direct solvers, that are made possible by exploiting the structure of the operators (e.g., tri-/penta-diagonality and upper Hessenberg), that arise from clever choices of modified Chebyshev or Legendre bases. MPI decomposition is achieved through the recently released mpi4py-fft module (bitbucket.org/mpi4py/mpi4py-fft), and all developed solver may, with no additional effort, be run on supercomputers using thousands of processors. This work is a continuation of M. Mortensen and H. P. Langtangen "High performance Python for direct numerical simulations of turbulent flows", Computer Physics Communications 203, p 53-65 (2016), that showed how a Python (Numpy+MPI for Python) implementation of a fully spectral Navier Stokes solver for triply periodic domains, could run as fast as C++ on thousands of processors. Since then, the shenfun package has also been used to create solvers for, e.g., turbulent channel flows and magnetohydrodynamics. This talk will give a demonstration of current capabilities and highlight Python as the powerful language it is for high performance scientific computing.
Scalable bifurcation analysis of nonlinear partial differential equations

Patrick Farrell, University of Oxford

Abstract

Computing the solutions of an equation as a parameter is varied is a central task in applied mathematics and engineering. In this work I will present a new algorithm, called deflated continuation, for this task, and describe a massively parallel implementation of it built on top of FEniCS.

Deflated continuation has three main advantages. First, it is capable of computing disconnected bifurcation diagrams; previous algorithms only aimed to compute that part of the bifurcation diagram continuously connected to the initial data. Second, its implementation is extremely simple: it only requires a minor modification to any existing Newton-based solver. Third, it can scale to very large discretisations if a good preconditioner is available.

Among other problems, we will apply our software to a famous singularly perturbed ODE, Carrier's problem. The computations reveal a striking and beautiful bifurcation diagram, with an infinite sequence of alternating pitchfork and fold bifurcations as the singular perturbation parameter tends to zero. The analysis yields a novel and complete taxonomy of the solutions to the problem, and demonstrates that a claim of Bender & Orszag (1999) is incorrect. We will also use the algorithm to calculate distinct local minimisers of a topology optimisation problem via the combination of deflated continuation and a semismooth Newton method.
Computing brain signals (CBra): Concurrent simulation of network activity, extracellular electric potentials and magnetic fields

Espen Hagen, University of Oslo
Solveig Næss, University of Oslo
Torbjørn Vefferstad Ness, Norwegian University of Life Sciences
Gaute T. Einevoll, Norwegian University of Life Sciences

Abstract

Recordings of extracellular electrical, and later also magnetic, brain signals have been the dominant technique for measuring brain activity for decades. The interpretation of such signals is however nontrivial [1], as the measured signals result from both local and distant neuronal activity. In volume-conductor theory the recorded extracellular potentials stem from a complicated sum of contributions from transmembrane currents of neurons near the measurement site. Further, given the same transmembrane currents the contributions to the magnetic field recorded outside the brain can be computed [2]. This allows for the development of computational tools implementing forward models grounded in the biophysics underlying the different measurement modalities [1].

LFPy ([3], LFPy.github.io) incorporated a now well-established scheme for predicting extracellular potentials of individual neurons with arbitrary levels of biological detail. It relies on NEURON ([4], neuron.yale.edu) to compute transmembrane currents of multicompartment neurons which is then used in conjunction with an electrostatic forward model [5]. We have now extended its functionality to populations and networks of multicompartment neurons with concurrent calculations of extracellular potentials and current-dipole moments. The current-dipole moments are used to compute non-invasive measures of neuronal activity, like magnetoencephalographic (MEG) signals [2,6] and, when combined with an appropriate head-model, electroencephalogram (EEG) scalp potentials. One such built-in head-model is the 4-sphere model including the different electric conductivities of brain, cerebral spinal fluid, skull and scalp [6].

The version of LFPy presented here is thus a true multi-scale simulator, capable of simulating electric neuronal activity at the level of cell-membrane dynamics, individual synapses, neurons, networks, extracellular potentials within neuronal populations and macroscopic EEG and MEG signals. The present implementation is equally suitable for execution on laptops and in parallel on high-performance computing (HPC) facilities.

References

Parallel stochastic simulation of cell-cell communication with spatially resolved reaction-diffusion kinetics

Adrien Coulier, Uppsala University
Andreas Hellander, Uppsala University

Abstract

Stochastic simulations are essential to the study of biological cells, yet there is no computational framework allowing for detailed spatial simulations of genetic regulatory network within large populations of cells. We fill this gap by developing a parallel simulation framework capable of spatially resolved stochastic simulation of cell-cell signaling in multicellular systems. We use an operator-splitting method to decouple the internal reaction-diffusion kinetics from the interactions on the cells' boundaries and allow for efficient and horizontally scalable simulations of large numbers of interacting cells on highly available, on demand distributed computing infrastructures, such as clouds. We use a small test model to study the convergence of our method as well as larger models to demonstrate weak scalability. Our method demonstrate the feasibility of detailed stochastic simulations of large populations of interacting cells and is the first step toward more complete simulations including both detailed reaction-diffusion simulations and cell mechanics.
Monday, 17:50

**On the Construction of Meshfree Finite Volume Particle Methods**

*Armin Iske, University of Hamburg*

**Abstract**

This talk discusses the utility of meshfree kernel techniques in adaptive finite volume particle methods (FVPM). To this end, we provide supporting arguments in favour of kernel-based reconstructions in the recovery step of FVPM, where our discussion addresses relevant computational aspects concerning numerical stability and accuracy, as well as more specific points concerning efficient implementation. Special emphasis is finally placed on more recent advances in the construction of adaptive FVPM, where WENO reconstructions by polyharmonic spline kernels are used in combination with ADER flux evaluations to obtain high order methods for hyperbolic problems.
GNSTLIB: a new numerical library for the evaluation of mathematical functions

Amparo Gil, Universidad de Cantabria
Guillermo Navas-Palencia, Universitat Politècnica de Catalunya
Javier Segura, Universidad de Cantabria
Nico M. Temme, IAA Alkmar

Abstract

We describe the numerical library GNSTLIB, a new ongoing project for the fast and accurate computation of mathematical functions in double precision floating-point arithmetic. GNSTLIB is a C++11 library with wrappers for the major programming languages used in scientific computing, such as Fortran, C and Python. GNSTLIB will provide support to R and Julia in future releases. GNSTLIB implements vectorized versions of all the routines, thus taking advantage of multi-core processors. Future releases of the library will expand the available set of routines to related numerical problems such as, for example, the evaluation and inversion of statistical distributions.
Optimizing memory layout and instruction order of a finite difference code

Gerhard Zumbusch, Friedrich-Schiller-Universität Jena

Abstract

Current processor and graphics processor architectures heavily use data and instruction parallelism at different levels. Floating point operations are grouped in vector instructions. Memory is organized in a hierarchy of registers, caches and local and distributed memories. Many numerical algorithms tend to be memory bandwidth limited. In this talk a finite difference stencil computation is discussed along with several techniques to optimize the implementation such as modified interleaved non-standard data layout, cache aware algorithms, loop unrolling, vectorization, parallelization and parameter tuning. This leads to performance levels much closer to compute peak performance than automatic compiler vectorization and optimization.
Education in CSE

Tuesday, October 24
Biographical note on education

Marie Rognes, Simula Research Laboratory
Virtual-classroom: An automated GitHub-tool for student-to-student peer-review of assignments

Aslak Bergersen, Simula Research Laboratory

Abstract

Background/Objective: Computer science is currently a key ingredient for all natural sciences, and Universities graduate thousands of candidates annually. However, there is a gap between working routines of successful industry and open-source projects, and how informatics is taught at the Universities. The aim of the open-source virtual-classroom project (https://github.com/hplgit/virtual-classroom) is to integrate version control systems for automated student-to-student peer-review of assignments.

Methods: The virtual-classroom project is an extension of the Classroom platform on GitHub where administrators (teachers) have access to teams (students) repositories. From the virtual-classroom, one team with one repository is automatically created for each student. The students or groups can complete course work directly in the repository. During peer-reviews, virtual-classroom gives the reviewer temporary access to the to-be-reviewed repositories. The feedback is then provided orally if the work has been evaluated within groups, and in written form if reviewed between groups.

Results/discussion: The tool has been used at the University of Oslo in both undergraduate and graduate courses, with up to 250 students per course. The students rapidly grasp how and why to use version control systems, and thus become more professional developers. By reviewing the work of peers, the students quickly learn to how to produce readable code, including naming conventions, commenting, coding style, and structure of the program.

A particular feature of the virtual-classroom is that it enables basic informatics courses to be given to hundreds of students simultaneously, and reduces the load, or eliminates the need for teaching assistants. As all students both receive and give feedback, the result is feedback that is quantitatively and qualitative better; the latter because it is personal. That being said, the feedback may be less precise than what is expected of a more experienced teacher.

Conclusion: We have introduced an automated GitHub-tool for student-to-student peer-review of assignments that has shown highly effective in basic informatics education. The tool could be easily expanded or applied to create new workflows tailored to specific courses.
Tuesday, 10:40

Keynote

Computing in science education

Knut M. Mørken
Professor of Mathematics, University of Oslo

Abstract

Computers and computing have had a tremendous impact and changed society in ways few would have thought possible. The impact on research is just as dramatic: Most fields now depend on methods that are crucially dependent on computers.

In education, computers have provided new channels of communication, online courses have become common, and computers have had a marked impact on the practice of teaching. However, the effect has been much less visible in the content of the teaching; it is difficult to derive the existence of computers from a description of the curriculum in most undergraduate science programs.

In this presentation we will reflect on this apparent anomaly and describe some of the work at the University of Oslo to address the situation by renewing general science education with an integrated, computational perspective. This was a favourite topic of Hans Petter Langtangen and we will of course discuss his central role in this work.
Teaching modelling to first-year biology students

Simen Tennøe, University of Oslo
Milad Hobbi Mobarhan, University of Oslo
Svenn-Arne Dragly, University of Oslo
Andreas Våvang Solbrå, University of Oslo
Lex Nederbragt, University of Oslo

Abstract

The field of biology relies heavily on computations. This is not well reflected in education and the current undergraduate curriculum has little computational content. This results in a discontinuity between the education received by the students and the problems they face after graduation. The end result is that the students are not equipped to meet the requirements of modern research nor the tasks awaiting them in the industry. To remedy this problem, a new course, BIOS 1100 - Introduction to Modelling in Biology, will be held for the first time at the University of Oslo in fall 2017.

Currently, no available book combines biology and programming at an introductory level in a satisfactory way. Most textbooks teach both topics separately or expect the reader to know either biology or programming from before. We have therefore written our own textbook to be used as curriculum in this course. This book aims to teach programming and modelling to first year biology students through examples from biology. The book is based on a philosophy of just-in-time teaching where the programming concepts are introduced just when they are needed to solve the problem in hand. This puts the programming content in an unusual order in comparison to the traditional computer science curriculum while keeping the biology students motivated by the problems they solve. The examples are mainly from the three branches of biology: population dynamics, bioinformatics and evolution. The purpose is to give biology students a practical understanding of programming and mathematical models. This will enable the understanding of mathematical models and encourage critical thinking. Programming allows much more realistic and inspiring problems to be addressed, enabling students to work on current research topics early on. The textbook is written using DocOnce (created by Hans Petter Langtangen), which enables us to compile the book to both LaTeX/PDF, HTML and Jupyter Notebooks.
Neuronify: An educational simulator for neural circuits

Svenn-Arne Dragly, University of Oslo
Milad Hobbi Mobarhan, University of Oslo
Andreas Våvang Solbrå, University of Oslo
Simen Tennoe, University of Oslo
Anders Hafreager, University of Oslo
Anders Malthe-Sørenssen, University of Oslo
Marianne Fyhn, University of Oslo
Torkel Hafting, University of Oslo
Gaute T. Einevoll, Norwegian University of Life Sciences

Abstract

Neurons are cells in the brain that are able to rapidly change the electric field across their cell membrane. These changes allow neurons to communicate with each other and is the basis for the complex computations in the brain. Understanding how neurons communicate and the properties of neuronal networks is essential for neuroscience students. Traditionally, students draw networks with pen and paper and qualitatively deduce features of the network by analyzing the static drawings. Here, we present Neuronify, an app that allows students to draw the same networks on a computer or mobile device and run dynamic simulations without programming. The students can test their analysis by running the network and check their predictions against the outcome.

Educational software (apps) can improve science education by providing an interactive way of learning about complicated topics that are hard to explain with text and static illustrations. Such software is readily available in many areas of natural science such as physics and electrical engineering. However, few educational apps are available for simulation of neural networks. Neuronify allows the user to easily create and explore neural networks in a plug-and-play simulation environment. The user can drag and drop network elements such as neurons, electrical stimulation tools and recording devices. The components can then easily be connected to one another.

Building intuition for how neurons and neural networks behave has been a top priority in designing Neuronify. We aim to provide a low entry point to simulation-based neuroscience. Most undergraduate students do not have the computational experience to create their own neural simulator. Neuronify offers them an opportunity to build and experiment with neural networks in a graphical and easy-to-understand interface. By playing around with the networks, the students can develop a good understanding of their properties.

To facilitate the use of Neuronify in teaching, a set of premade common network motifs is provided, performing functions such as input summation and detection of direction of stimulus movement. Neuronify is developed in C++ and QML using the cross-platform application framework Qt. It has been downloaded more than 30,000 times since its launch and is available on smart phones (Android, iOS), tablet computers as well personal computers (Windows, Mac, Linux).
Jupyter notebooks in science and education

Min Ragan-Kelley, Simula Research Laboratory
Fernando Perez, UC Berkeley

Abstract

Jupyter notebooks are interactive documents, combining prose, code, and rich media output. The notebook environment facilitates interactive exploration as well as recording analyses for communication and reproducibility. These documents are now widely used in computational science and education, from the LIGO experiment publishing notebooks to accompany their results, enabling anyone to follow along with their signal analysis observing gravitational waves, to classrooms ranging from high school programming through graduate school courses in computational sciences.
Abstract
We have recently developed an online digital compendium to be used in an introductory course in numerical methods for engineering students (applied mechanics and civil engineering). In our approach, we blend the theory of the numerical methods with their corresponding implementation, in a practical manner which encourages the students to actually make use of their computers while reading the theory. At first sight our digital compendium may look similar to an iPython Notebook, however the important difference is that we allow the python code to be directly downloaded to the student’s computers, whenever the compendium is rendered in the popular integrated development environment (IDE) Eclipse. The compendium is written in the simple and minimally tagged markup language DocOnce, whereas a web-parser for code-snippet parsing was developed as a plugin for Eclipse. With our approach, we embed the teaching resource in the IDE, as opposed to the iPython Notebook which embeds code in the teaching resources. In this way we lower the threshold for the students to exploit the teaching resources in their programming practices, and they may easily make use of examples from this course in later courses. Didactically we reduce the need for task switching and multitasking which are well known pedagogical challenges.
Tuesday, 13:40

Keynote

Mathematical models and simulation in biomedicine

Adélia Sequeira  
Professor of Mathematics, Instituto Superior Técnico, Universidade de Lisboa

Abstract

Over the past few years, developments in computational science and technology became increasingly important in the progress of biomedical research and predictive biomedicine. The growing dominance of computerized information (medical imaging, electronic patient records, automation of clinical studies) is considerably enhancing further progress in medical practice and research together with its empirical tradition. As a result, medicine is developing closer links to bioengineering, computer science and mathematics. The advancements in the power of modern computers along with the progress in imaging, visualization and geometry reconstruction techniques, as well as the improvement of sophisticated numerical algorithms, allow for the development and analysis of highly complex models. The final goal is to set up patient-specific models and simulations incorporating data and measurements taken from each single patient, that will be able to predict the results of medical diagnosis and therapeutic planning with reasonable accuracy and using non-invasive means.

According to the most recent statistics, cardiovascular diseases represent the major cause of death in developed countries, having a significant impact in the cost and overall status of healthcare. Consequently, the understanding of the fundamental aspects of the pathophysiology and treatment of these diseases are subjects of the greatest importance around the world, giving a key impulse to the progress in mathematical and numerical modeling of the associated complex phenomena governed by heterogeneous physical laws. However, the circulatory system is highly integrated and modeling its various functions is an incredibly challenging problem, which still requires many fundamental issues to be addressed.

Mathematical Models and Simulation in Biomedicine is a Master’s course addressed to students of Applied Mathematics and Biomedical Engineering, dedicated to an introduction to modeling and simulations of the human cardiovascular system. This includes fundamental topics such as an overview of blood rheology, constitutive models for blood flow dynamics, mathematical models for the vessel wall, FSI techniques for blood flow in compliant vessels, reduced 1D models, geometrical multiscale modeling of the circulatory system. Applications to some clinical cases are also included in the program.

The course requires solid basis provided in standard mathematical undergraduate courses, knowledge of advanced computational methods and interest in biology, medicine, mathematics and computations.

This lecture is devoted to the presentation of the main topics of the course, the requested computational background, the supporting bibliography, as well as the evaluation practices. Numerical simulations of some test cases in idealized and realistic geometries of blood vessels will be shown.
Tuesday, 14:10

Image-based biomedical modeling, simulation and visualization

Chris Johnson, University of Utah

Abstract

Increasingly, biomedical researchers need to build predictive computational models from images (MRI, CT, EM, etc.). The “pipeline” for building such computational models includes image analysis (segmentation, registration, filtering), geometric modeling (surface and volume mesh generation), large-scale simulation (parallel computing, GPUs), large-scale visualization and evaluation (uncertainty, error). In my presentation, I will present research challenges and software tools for image-based biomedical modeling, simulation and visualization and discuss their application for solving important research and clinical problems in neuroscience, cardiology, and genetics.
When counting flops is not enough: Optimization of data access viewed from programmers' perspective

Shahadat Hossain, University of Lethbridge
Trond Steihaug, University of Bergen

Abstract

Until recently, the exponential growth in processor performance as predicted by “Moore’s Law” enabled automatic speed-up of compute-intensive applications. In the last decade the industry has witnessed a shift from high-frequency single-CPU systems to ones that feature a large number of compute cores of modest processing power. Independent of whether programmers write code for sequential or parallel systems one of the fundamental challenges to achieving high performance is to do with getting data from slower memory to processors. The main purpose of this paper is to elucidate basic concepts of locality of reference to data in a hierarchical memory system. We have chosen (sequential) matrix-matrix multiplication (BLAS 3) as the representative application to illustrate the identification and exploitation of data locality. However, we depart from the usual textbook illustration of starting with triple-loop multiplication code and then showing data access pattern under different loop permutations. Instead, we express matrix-matrix multiplication in terms of elementary operations of inner-products, outer-products, and linear combinations. Triple-loop multiplication codes follow naturally thereof depicting pattern of data access such that the most convenient storage of matrix elements can be observed directly. The code is then extended to incorporate blocked multiplication to demonstrate temporal locality. As an example of structured problem we introduce storage by diagonals to perform banded matrix multiplication. From our experience, students find indexing in diagonal storage rather complicated. We use diagrams and derive indexing formulas to access the matrix elements by diagonals. The effect of memory hierarchy on performance is demonstrated by numerical experiments.
Springer Nature and MOOCs

Francesca Bonadei, Springer Nature

Abstract

Massive Open Online Courses (MOOCs) and variations of them have changed education both in the corporate and in the academic world. Springer Nature aims to innovate also taking advantage of MOOCs both for internal education and for external training as well, using a large variety of platforms, and offering content at different levels (from students to researchers to professionals) in different forms. Examples of some interesting initiatives will be mentioned.

During this session we will also focus on the presentation of a unique publishing project, born in cooperation with Federica Web Learning, one of the largest European provider of open access multimedia courses developed by the outstanding Italian University of Naples Federico II. This project consists of an editorial cooperation concerning the MOOCs in the English language developed by Federica Weblearning, that will promote international authorship, topical coverage, and dissemination to a global readership of scholars, students, researchers, professionals and policymakers.
Tuesday, 15:30

Discussion on education in CSE

*Introduction by*
*Uli Rüde, University of Erlangen-Nürnberg*

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**Tuesday**

17:00 Free time / relocation to Oslo Opera House

18:00 Tour of the Opera House (optional, registration required)

19:00 Aperitif (Opera House)

19:30 Conference dinner at Restaurant Argent (Opera House)
Biomedical Applications

Wednesday, October 25
Biographical note on biomedical applications

Kent Andre Mardal, University of Oslo and Simula Research Laboratory
Keynote

Computational Physiology and the Physiome Project

Peter Hunter
Distinguished Professor, University of Auckland

Abstract

Computational physiology models deal with multiple physical processes (coupled tissue mechanics, electrical activity, fluid flow, etc) at multiple spatial and temporal scales, and in some cases analyze integrative biological function in terms of underlying structure and molecular mechanisms. These models are intended both to help understand physiological function and to provide a basis for diagnosing and treating pathologies in a clinical setting. The Physiome Project of the International Union of Physiological Sciences (IUPS) and the Virtual Physiological Human (VPH) project funded by the European Commission are together developing model and data encoding standards, web accessible databases and open source software for multiscale modelling. A new journal called Physiome has recently been launched to publish reproducible and reusable models.

This talk will provide an update on the Physiome Project infrastructure. It will also discuss the use of bond graph theory as a means of ensuring that computational biology models involving multiple physical mechanisms are compliant with principles of mass and energy conservation.
Wednesday, 10:10

Assessment of regional myocardial work through adjoint-based data assimilation

Henrik Finsberg, Simula Research Laboratory
John Aalen, Oslo University Hospital
Camilla Kjellstad Larsen, Oslo University Hospital
Joakim Sundnes, Simula Research Laboratory
Otto A. Smiseth, Oslo University Hospital
Samuel Wall, Simula Research Laboratory

Abstract

**Introduction.** To achieve efficient pumping of blood to the body, the healthy heart contracts in a synchronous manner. However, heart disease can alter how the heart is activated during a beat, and dyssynchronous contraction can occur, reducing the overall pumping efficiency. Advanced treatments exist for such cases, but selecting patients likely to respond can be challenging. The existing selection criteria, based on organ level measures of activation and contraction, have relatively low specificity. It is therefore of interest to extract new biomarkers to help better identify potential responders. Here we explore one example of a potential biomarker, the regional myocardial work [1], a measure of cardiac efficiency, using a computational model of cardiac mechanics optimized to patient specific data using a high level adjoint based data assimilation method.

**Methods.** Left ventricular (LV) geometry was obtained from 4D echocardiography, and the segmented chamber was modelled as an incompressible, continuous hyperelastic body described via an transversely isotropic material law [2]. Active force development was modeled through additively decomposing stress into passive and active stresses, the latter added along the cardiac fiber direction, defined by a rule based architecture.

The model was fit to 4D imaging of the LV through the cardiac cycle using an adjoint-based data assimilation technique, which automatically solves for the gradient of the solution with respect to local active stress, for highly efficient minimization of model misfit against collected data. Simulations were optimized both globally and regionally in 17 delineated segments [3]. With these simulations, the amount of mechanical work performed between time point \(t_m\) and \(t_n\) could be regionally calculated through –

\[
W(t_m, t_n) = \int_{t_m}^{t_n} S : \dot{E} \, dt \approx \sum_{i=m}^{n} (S_{t_i} : dE_{t_i}).
\]

where

\[
S_{t_i} = \frac{1}{2} (S_{t_i} + S_{t_{i-1}})
\]

and

\[
dE_{t_i} = (E_{t_i} - E_{t_{i-1}}).
\]

\[
W(t_m, t_n) = \int_{t_m}^{t_n} S : \dot{E} \, dt \approx \sum_{i=m}^{n} (S_{t_i} : dE_{t_i}).
\]
Here subscript $t$ indicates the time point, $S$ is the Second Piola-Kirchhoff stress tensor and $E$ is the Green-Lagrange strain tensor.

**Results.** We tested the method on healthy control subjects and patients suffering from left bundle branch block (LBBB). The results show an excellent fit between measured and simulated strain ($R^2 = 0.8$) and volume ($R^2 = 1.0$). The estimated regional myocardial work, assessed in these segments, shows clear differences between the healthy and diseased patients (e.g. Mid Septal longitudinal wasted work ratio[1]: 1.45 (LBBB), 0.24(Healthy)) and can potentially be used as a biomarker to map regional cardiac dysfunction.

**References**

Constructing dyadic geometries from super-resolution imaging for computing structure-function relationships in cardiac contraction

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Abstract

The microanatomical structures responsible for cardiac excitation-contraction (EC) coupling in ventricular myocytes are degraded in many cardiac diseases. How these structural changes impact function is not well understood. The small size of the structures, combined with the multi-scale nature of EC coupling, makes computations a fundamental tool for understanding structure-function relationships across these scales. A major bottleneck, however, is the lack of detailed geometric data to properly constrain computational models. We are developing a pipeline to construct detailed and structurally accurate geometries from three dimensional super-resolution dSTORM imaging of ryanodine receptor (RyR) localization. Beginning with the dSTORM-defined RyR distributions and a t-tubule map identified from caveolin 3 labeling, we use rule-based heuristics to define t-tubular and sarcoplasmic membrane structures. We then combine the generated geometries with a finite volume reaction-diffusion model of calcium-induced calcium release (CICR) to explore the impact of structural degradation occurring within and between dyads, on microscopic and macroscopic EC coupling. Importantly, our model combined spatially distributed calcium diffusion and buffering at sub-dyadic resolution (non-compartmental dyadic dynamics) with stochastic RyR release, both of which are necessary to capture how dyadic break-up affects spark dynamics. We have used our pipeline at the dyad-level to explore how changing the shape and size of local membranes affects RyR-triggered spark fidelity, amplitude, duration, and termination. We will use our pipeline and calcium model to move to larger volumes and explore ensembles of calcium release units to better understand structural impact on emergent multi-scale EC properties.
Verification and validation in biomedical computing

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Abstract

In traditional engineering disciplines, geometries, boundary conditions, flow conditions, and fluid properties are well defined. However, such information is often not well defined in biomedical computing and engineering. We often rely on medical image-based segmentations that involve a significant amount of manual labor, which again could result in inter-laboratory variability. In addition, many studies in the biomedical domain are retrospective and lack patient-specific boundary conditions like flow rates, loads, etc. Verification & validation (V&V) is therefore especially important in biomedical computing. Since the concepts of V&V are fairly broad, we will provide a brief introduction to the topics. Although the material is relevant for all branches of image-based modeling where assumptions have to be made, the trends in biomedical computing will be exemplified by an overview of the recent challenges held in the aneurysm computational fluid dynamics community. Finally, we will address whether or not V&V is actually needed, or just additional noise.
Numerical challenges and ideas for "Next Generation" CFD tools for flow problems with complex rheology

Stefan Turek, TU Dortmund

Abstract

We present numerical simulation techniques for incompressible fluids with complex rheology due to 'extreme' changes of the viscosity which may vary significantly by several orders of magnitude, for instance due to non-isothermal behavior and pressure, resp., shear dependency. Such fluids may include viscoplastic as well as viscoelastic effects which is typical for biological fluids, yield-stress fluids, granular material as well as polymer melts and rubber (caoutchouc). We discuss special discretization and solver techniques in which case the coupling between the velocity, pressure and additional variables for the stresses, which leads to restrictions for the choice of the FEM approximation spaces, and the (often) hyperbolic nature of the problem are handled with special Finite Element techniques including stabilization methods. The resulting linearized systems inside of outer Newton-type solvers are (special) nonsymmetric saddle point problems which are solved via geometrical multigrid approaches. We illustrate and analyze numerically the presented methodology for well-known benchmark configurations as well as prototypical industrial and biomechanical applications for several nonlinear flow models.
Coronary bypass graft surgery (CABG) is performed on approximately 500,000 patients every year in the United States. Because most patients require multi-vessel revascularization, roughly 70% of CABG surgeries employ saphenous vein grafts, despite the superior performance of arterial grafts. Vein graft failure continues to be a major clinical problem, with as many as 50% of grafts failing within 5 years of surgery. When a vein graft is implanted in the arterial system it adapts to the high flow and pressure of the arterial environment by changing composition and geometry. Though hemodynamics is known to play an active role in growth and remodeling of blood vessels, the underlying mechanisms of vein graft failure remain poorly understood. We will describe our two-pronged approach to investigating the biomechanical underpinnings of vein graft failure following CABG. First, we perform patient-specific simulations of coronary and bypass graft hemodynamics to compare the biomechanical forces acting on venous and arterial grafts. We will present recent advances in computational methodology in which we employ multiscale modeling methods to couple closed loop lumped parameter models of the coronary physiology to 3D hemodynamics simulations with fluid structure interaction and variable material properties. Second, we adapt a constrained mixture theory of growth and remodeling for use in vein grafts, and explore potential causes and amelioration of vein graft failure. Parameter estimation in these models is accelerated via optimization. Finally, we present a Bayesian framework for uncertainty quantification combining automated parameter estimation for clinical data assimilation and efficient multi-resolution expansion for uncertainty propagation to simulation predictions.

References


In silico FRAP and FLIP experiments

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Abstract

Fluorescence Recovery after Photobleaching (FRAP) and Fluorescence Loss in Photobleaching (FLIP) are microscopy methods for visualization of molecular transport processes in living cells. While in FRAP experiments the local recovery after photobleaching is investigated, a FLIP sequence observes fluorescence loss after repeated bleaching over time and throughout the entire cell.

In this contribution we simulate both FLIP and FRAP experiments on segmented cell images based on the reaction-diffusion system from [1,2]. The PDE model is solved by a Discontinuous-Galerkin method implemented in FEniCS [3].

The simulation results are compared to in vivo FLIP and FRAP microscopy images using the Enhanced Green Fluorescent Protein (eGFP). Also simulated FRAP recovery curves will be compared to experimental data.

References

Pelvic construct prediction of trabecular and cortical architecture: a comparison between structural and continuum approaches

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Abstract

The pelvic construct is an important part of the body as it facilitates the transfer of upper body weight to the lower limbs and protects a number of organs and vessels in the lower abdomen. In addition, the importance of the pelvis is highlighted by the high mortality rates associated with pelvic trauma. Although computational models of the pelvis have been used to assess its structure or behaviour under loading, no attempt has been made to develop a model using a structural mechanics approach as opposed to a continuum mechanics approach. This study presents a comparison between a mesoscale structural model and a continuum orthotropic model of the pelvic construct and the joints and ligaments associated with it. For the first model, shell elements were used to model cortical bone, while truss elements were used to model trabecular bone and the ligaments and joints. The continuum model was developed using shell elements to represent cortical bone, solid tetrahedral elements to represent trabecular bone and truss elements to represent the ligaments and joints. Both finite element models were subjected to an iterative optimisation process based on a strain driven bone adaptation algorithm [1, 2]. The pelvis models were adapted to a number of common daily living activities (walking, stair ascent, stair descent, sit-to-stand and stand-to-sit) by applying joint, muscle and inertial loads derived using a musculoskeletal modelling framework. The cortical thickness distribution and trabecular architecture of the adapted models were compared qualitatively with computed tomography scans. A third model derived directly from the CT scans was used as a benchmark to compare the response of the adapted models for a load case corresponding to standing up.

Both models have shown good agreement with the CT images in terms of overall bone architecture. The comparison between a structural and a continuum model is useful as it highlights a number of potential advantages of using the former approach. The structural modelling approach was shown to be less computationally demanding and it enables a number of applications such as fracture modelling, design and additive manufacturing of frangible surrogates. In addition, the structural model could be developed further by assigning the elements an initial directionality derived from the elasticity matrices associated with elements of the continuum model.

References


Non-linear least square fitting of a hyperelastic model to soft tissue experimental data

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Gerhard A. Holzapfel, NTNU and Graz University of Technology
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Abstract

In this work we present some practical challenges when fitting soft tissue experimental data to a hyperelastic model, and point out methods which will help obtain a good fit. As an example, experimental data from biaxial mechanical testing of porcine pericardium will be fitted to an incompressible anisotropic hyperelastic strain energy function. The pericardium serves the mechanical function of preventing excessive torsion and displacement of the heart. Having a thickness of <1 mm it acts as a membrane subjected to internal pressure. Biaxial experiments are therefore a relatively simple way of obtaining the mechanical properties. For each sample, different stretch ratios for circumferential and longitudinal directions are tested (1(Circ) : 1(Long), 1 : 0.75, 0.75 : 1, 1 : 0.5 and 0.5 : 1) in order to capture the directional dependency and obtaining a larger data set leading to unique material parameters. Based on the knowledge of the microstructure of the material, governed collagen and elastin, and also from its non-linear anisotropic behaviour, the strain energy function

$$\Psi = c \left( I_1 - 3 \right) + \frac{k_1}{k_2} \left( \exp \left( k_1 \left( \kappa I_1 + \left( 1 - 3\kappa \right) I_4 - 1 \right)^2 \right) - 1 \right),$$

is chosen [1]. Using a non-linear least square scheme the objective function is implemented as

$$\chi^2 = \sum_{i=1}^{n} \left[ (\sigma_1 - \sigma_{1,w})_i^2 + (\sigma_2 - \sigma_{2,w})_i^2 \right],$$

where $n$ is the number of data points and $c, k_1, k_2$, and $\kappa$ are the parameters to be found. While the implementation of this method may not be very challenging, several choices must be made which are not obvious, and the question of what is a good fit and how is it obtained is further discussed. We investigate several challenges and strategies: (i) comparing a fit using only equibiaxial data to using the complete data set, (ii) fitting $\kappa$ (governing the amount of anisotropy) to the equibiaxial data before fitting the remaining parameters to the complete data set and (iii) weighting the objective function from parts of the data set to improve the fitting in a certain area. This may lead to a better fit in spite of the error estimate being higher. Further, the initial guess of the material parameters is shown to be important for the fitted result and thus exemplify the lack of uniqueness, which may greatly affect the result in further use of the model [2].

References


Wednesday

13:20 – Closing remarks

13:30 – Lunch