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PhD Yearbook | 2016

DOCTORAL PROGRAM IN MATHEMATICAL MODELS AND METHODS IN ENGINEERING

Chair:
Prof. Roberto Lucchetti

Equations are everywhere! Between the atmosphere and the wing of a spaceship, in the blood flowing in an artery, on the demarcation line between ice and water at the poles, in the motion of the tides, in the charge density of a semiconductor, in the compression algorithms of a signal sending images from outer space. Such equations represent real problems. The Mathematical Engineer can see and understand the nature of these equations, and can develop models in order to understand their relevant qualities and solve real problems.
This PhD program aims at training young researchers by providing them with a strong mathematical background and with ability to apply their knowledge to the solution of real-world problems that arise in various areas of science, technology, industry, finance, management, whenever advanced methods are required in analysis, design, planning, decision and control activities. PhD students carry our their research both in the development of new mathematical methods and in the implementation and improvement of advanced techniques in connection with specific contexts and applications.
The Faculty of the PhD program is responsible for the organization of the training and research activities of the PhD students. Decisions of the Faculty comply with the requirements and standards of the Doctoral School of the Politecnico di Milano. A Chairman is elected within the Faculty, for representative and coordination activities. Admission of students to the PhD program is decided after examination of the candidates. Students applying to our program must provide their CV, along with reference and motivation letters. After admission, each student is assigned a tutor. The tutor is a member of the Faculty who assists the student in the early stages of his career, especially in the choice of the courses and in identifying a thesis advisor.
The overall activity of the PhD students can be quantified in 180 credits. The PhD program has a duration of three years. Activity can be classified into: introductory courses (no minimum number of credits required); main courses (at least 30 credits); specialized research training, including seminars, tutoring activity, participation to workshops/conferences, and scientific publications (at least 30 credits); development of a doctoral thesis (at least 90 credits).
At the end of each academic year, the PhD students report to the Faculty about their activity. The students report about attendance of courses and exams (and the corresponding grades), participation in various scientific activities (seminars, conferences, summer schools etc.), planning and intermediate results on their research project and preparation of the PhD thesis, and any other relevant activity. At the annual meeting the students also receive a grade by the Faculty. A negative grade may entail repetition of the current year of doctoral study (with suspension of the grant, if any) or exclusion from the PhD program, depending on the Faculty's decision. Mobility of PhD students to other institutions is strongly encouraged and financial support is provided to this purpose.
Among others, let us mention some typical types of professional skills and possible occupations of the graduated Doctors: analytic and numerical treatment of differential models for physical and industrial problems, quantitative methods in finance and risk management, operations research and optimisation, statistical modelling and data analysis.
Placement of graduated Doctors is expected in the following positions: research and development divisions of businesses, businesses involved in innovative design activities, financial institutions such as banks or insurance companies, public or private research centres, public and/or governmental agencies for social, economical, scientific study, planning or evaluation, Universities.
Since the PhD program in Mathematical Models and Methods in Engineering (formerly, Mathematical Engineering) has been active since the year 2001, we expect that a larger number of institutions and businesses will soon become more and more aware of the professional skills and expertise of graduated doctors.
Grants funded by external partners: ENI, SAES Getters, CINECA, European Project MathCard, FIRB-ID Project NUMQUES, I.I.T.

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PROBABILISTIC REPRESENTATION OF HJB EQUATIONS FOR OPTIMAL CONTROL OF JUMP PROCESSES, BSDES AND RELATED STOCHASTIC CALCULUS

Elena Bandini - Advisors: **Marco Fuhrman, Francesco Russo**

In the present document we treat three different topics related to stochastic optimal control and stochastic calculus, pivoting on the notion of backward stochastic differential equation (BSDE) driven by a random measure.
The three first chapters of the thesis deal with optimal control for different classes of non-diffusive Markov processes, in finite or infinite horizon. In each case, the value function, which is the unique solution to an integro-differential Hamilton-Jacobi-Bellman (HJB) equation, is probabilistically represented as the unique solution of a suitable BSDE. In the first chapter we control a class of semi-Markov processes on finite horizon; the second chapter is devoted to the optimal control of pure jump Markov processes, while in the third chapter we consider the case of controlled piecewise deterministic Markov processes (PDMPs) on infinite horizon. In the second and third chapters the HJB equations associated to the optimal control problems are fully nonlinear. Those situations arise when the laws of the controlled processes are not absolutely continuous with respect to the law of a given, uncontrolled, process. Since the corresponding HJB equations are fully nonlinear, they cannot be represented by classical BSDEs. In these cases we have obtained nonlinear Feynman-Kac representation formulae by generalizing the control randomization method introduced in Kharroubi and Pham (2015) for classical diffusions. This approach allows us to relate the value function with a BSDE driven by a random measure, whose solution has a sign constraint on one of its components. Moreover, the value function of the original non-dominated control problem turns out to coincide with the value function of an auxiliary dominated control problem, expressed in terms of equivalent changes of probability measures.
In the fourth chapter we study a backward stochastic differential equation on finite horizon driven by an integer-valued random measure p on R_+ x E, where E is a Lusin space, with compensator q(dt,dx)=dA_t Q_t(dx). The generator of this equation satisfies a uniform Lipschitz condition with respect to the unknown processes. In the literature, well-posedness results for BSDEs in this general setting have only been established when A is continuous or deterministic. We provide an existence and uniqueness theorem for the general case, i.e. when A is a right-continuous nondecreasing predictable process. Those results are relevant, for example, in the framework of control problems related to PDMPs. Indeed, when p is the jump measure of a PDMP on a bounded domain, then A is predictable and discontinuous.
Finally, in the two last chapters of the thesis we deal with stochastic calculus for general discontinuous processes. In the fifth chapter we systematically develop stochastic calculus via regularization in the case of jump processes, and we carry on the investigations of the so-called weak Dirichlet processes in the discontinuous case. Such a process X is the sum of a local martingale and an adapted process B such that [N, B] = 0, for any continuous local martingale N. Given a function u:[0,T] x R --> R, which is of class C^{0,1} (or sometimes less), we provide a chain rule type expansion for u(t,X_t), which constitutes a generalization of Ito's lemma being valid when u is of class C^{1,2}. This calculus is applied in the sixth chapter to the theory of BSDEs driven by random measures.
In several situations, when the underlying forward process X is a special semimartingale, or, even more generally, a special weak Dirichlet process, we identify the solutions (Y,Z,U) of the considered BSDEs via the process X and the solution u to an associated integro-partial differential equation.

MULTISCALE DOMAIN DECOMPOSITION METHODS FOR HIGH HETEROGENEOUS DARCY FLOWS

Davide Baroli - Supervisor: Prof. Luca Formaggia

One of the major challenges in reservoir flow simulation is posed by the existence of multiple scales and the resulting high resolution of the geophysical models.
A subsurface geological formation is usually of the scale of kilometers in the horizontal dimensions.

Reservoir properties, such as porosity and permeability typically show strong heterogeneity and may vary over many scales from the pore scale (10 μm), the core scale (10 cm) to the geological scale (1 km). In particular, permeability may show changes of several orders of magnitude from highly fractured rocks (10^8 millidarcy or 0.001 cm^2) to unweathered clay (10^{-15} millidarcy or 0.0001 cm^2). Thus, the accuracy of the simulation strongly relies on the detailed geophysical properties of the natural heterogeneous formation. However, the numerical solution of transport flows in heterogeneous media at the fine scale resolution is prohibitive.
In the last decades, multiscale approach has been shown to be very promising to bridge the gap between the geological and the flow-simulation scales. The multiscale methods resolve the flow process at the fine-scale resolution and their paradigm relies on the construction of basis functions that take into account the complex hierarchy of scales associated with natural geologic formations.

The governing equations for flow in porous media can be further expressed as a pressure equation. The main important geophysical parameter in this equation is the permeability field. In particular, the spatial variations of permeability result in complex distributions of the pressure.
In this thesis, we focus on flow processes, governed by Darcy Law in media characterized by high heterogeneous and fast-oscillatory permeability field. In particular, we address the geological scenarios of the multilayer faulting that is relevant for the secondary migration path of hydrocarbon and for the hydraulic fracturing.

The discretization of partial differential equation in the high heterogeneous Darcy flow at fine resolution leads to a large linear algebraic system, whose computational cost is prohibitive for a direct solver. Thus it is necessary to apply an iterative solver with preconditioning. However, the number of iterations strictly depends on the condition number of the stiffness matrix. In particular, in high heterogeneous Darcy flow, the upper an upper bound for the condition number depends not only on the inverse of mesh size (as standard in finite element formulations) but also on the global variations of heterogeneity and degrades when the variation is high. Hence, the resulting linear system is very ill-conditioned. The iterative solver thus requires a preconditioner which is robust with respect to global variations of heterogeneity (as well as mesh size).

In this thesis, we investigate the earlier multiscale domain decomposition framework based on the two-level Schwarz preconditioner, which combines the local correction on the overlapping subdomain covering with a global correction on a coarse space defined by a set of global basis functions.
The research in a multiscale framework is motivated by deteriorated of iterative solver equipped with traditional two-level Schwarz method when the distribution of coefficients exhibits high heterogeneity, fast-oscillation and jumps not aligned with subdomain boundaries. Thus, the robustness of preconditioner able to handle any position of the jumps and distribution of the coefficients with respect to each subdomain of the overlapping covering poses a challenge in domain decomposition framework.
The design guidelines of multiscale domain decomposition framework are: the construction of a coarse space, which is formed by multiscale basis functions, and of a partition of unity subordinated to the overlapping covering. The definition of multiscale basis functions, which incorporate information on the fine scale heterogeneity, allows to obtain a robust preconditioner with respect to the high heterogeneity. Whereas the partition of unity function provides not only a better local correction on the overlapping subdomain covering but also an improvement on the coarse correction when it is applied to the local multiscale basis functions. In literature, the original definition of multiscale basis functions is proposed by Hou and Obsorne. The proposed basis function can successfully incorporate the fine scale heterogeneity that occurs inside each subdomains. However, these functions are not able to capture accurately large variations that cross the subdomain boundaries. In the recent literature, an alternative construction of the coarse space basis functions is provided by multiscale functions based on energy minimization concept. In fact the multiscale preconditioner based on energy minimization coarse space is robust with respect to the large variation of heterogeneity also near and cross the subdomain boundaries.
In the thesis, an additional stage is introduced in the multiscale framework of two-level overlapping Schwarz preconditioners, with aim of reducing the number of iterations for the multiscale high-contrast problems. In our novel three stage multiscale preconditioner context, we present two algoritms. The first algorithm uses traces of local multiscale basis functions and modifies multiscale basis functions. The second approach uses smoothing procedure of Chebychev (or Jacobi) to modify multiscale basis functions. In both cases, the original multiscale basis functions are computed by energy minimization technique using local eigenvalue problems and partition of unity functions. The second procedure based on the smoothing remove artificial effects due to partition of unity functions via smoothing steps and it is also robust with respect to minimal overlaps.
The improvement of these novel procedures with respect to the multiscale two-level Schwarz method are validated by several numerical experiments. In the validation, we focus on synthetic multilayer scenario whose permeability in each layer exhibits high heterogeneity and high-oscillating behavior. synthetic discrete fracture network where the permeability exhibits high-contrast due to thin fracture network. In addition, the novel numerical method is tested on a realistic configuration of discrete fracture network.
Furthermore, since we investigate the Darcy flow in high heterogeneous complex geological formation, like multilayer faulting, the permeability field is affected by epistemic uncertainty.
We distinguish two different stochastic modeling of multilayer faulting: parametric and non-parametric case. The first randomness description consider each layer of the multilayer faulting scenarios is considered a high or low conductivity regions, where the boundaries that separate these regions are stochastic, while within each region, the heterogeneities have Gaussian nature. Whereas the parametric scenario does not consider stochastic position of the boundaries between each layers.

The main computational drawback of the forward uncertainty analysis is the large amount of Darcy flow simulation with input permeability random field. The aim of forward uncertainty analysis is the forecast and the evaluation of some quantities of interest. To reduce the computational demand and obtain a robust multiscale domain decomposition preconditioner accounting for uncertainties, we apply the reduced order model technique with scope of construct a real-time preconditioner method. The proposed reduced order method is based on uncertainty sampling and is capable to handle both parametric and non-parametric configuration of permeability scenarios, which poses a challenge in reduced order methods.

COMPRESSED SOLVING: SPARSE APPROXIMATION OF PDES BASED ON COMPRESSED SENSING

Simone Brugiapaglia - Advisor: Prof. Simona Perotto
Co-advisor: Prof. Stefano Micheletti

In this thesis, we deal with a new framework for the numerical approximation of partial differential equations which employs main ideas and tools from compressed sensing in a Petrov-Galerkin setting. The goal is to compute an s-sparse approximation with respect to a trial basis of dimension N (with s N) by picking m N randomly chosen test functions, and to employ sparse optimization techniques to solve the resulting m × N underdetermined linear system. This approach has been named COmpRessed SolvING (in short, CORSING).
First, we carry out an extensive numerical assessment of CORSING on advection-diffusion-reaction equations, both in a one- and a two-dimensional setting, showing that the proposed strategy is able to reduce the computational burden associated with a standard Petrov-Galerkin formulation.
Successively, we focus on the theoretical analysis of the method. In particular, we prove recovery error estimates both in expectation and in probability, comparing the error associated with the CORSING solution with the best s-term approximation error. With this aim, we propose a new theoretical framework based on a variant of the classical inf-sup property for sparse vectors, that is named Restricted Inf-Sup Property, and on the concept of local a-coherence, that generalizes the notion of local coherence to bilinear forms in Hilbert spaces. The recovery results and the corresponding hypotheses are then theoretically assessed on one-dimensional advection-diffusion-reaction problems, while in the two-dimensional setting the verification is carried out through numerical tests.
Finally, a preliminary application of CORSING to three-dimensional advection-diffusion-reaction equations and to the two-dimensional Stokes problem is also provided.

PARALLEL MIXED–MODE 3D–TCAD SIMULATION OF POWER SEMICONDUCTOR DEVICES

Davide Cagnoni - Advisor: Prof. Carlo De Falco
Co-advisor: Dr. Marco Bellini

The push for deployment of renewable energy technologies across the European Union is generating transformation pressure on the transmission infrastructure. In particular, the role High Voltage Direct Current (HVDC) technology in the grid is growing. Novel Power Semiconductor devices such as the BiGT or improvements in well–proven devices such as the thyristor are a key enabling technology allowing for the feasibility of HVDC grids. Technology Computer Aided Design (TCAD) simulations play a key role in the development and optimization of new devices. As complex geometries are an important ingredient for optimal performance of high power, large area semiconductor devices, full scale 3D simulations are required. Large current densities and fast switching speeds, lead to non–negligible multi–physics effects such as interactions of charge transport with substrate heating. The complexity of the physical phenomena that govern the performance of new and advanced device structures makes it extremely difficult to develop compact models for them. Furthermore, available compact models depend on a very large number of parameters, that require a lengthy and expensive tuning procedure in order to be accurate over a wide range of operating conditions. For such reason in the technology design phase it is often required to perform mixed–mode simulations, i.e., to simulate the device performance when coupled to controlling circuit and load. The thesis was carried out in the framework of a collaboration between the Modeling and Scientific Computing (MOX) lab of Politecnico di Milano, and the Power Electronics department in the Corporate Research Center of ABB in Baden–Dättwil, Switzerland aimed at implementing a parallel 3D TCAD simulator especially tailored for the needs of the Power Semiconductors industry in general and for those of ABB in particular. The resulting C++ code, named CGDD++, was developed from scratch during the preparation of the thesis, building on the experience gained during a preliminary feasibility study comprehensive of the development of a Fortran 2003 code (CGDD) phase and was based on the FEMilaro library. CGDD++ relies on the BIM++ library (also developed in the course of this thesis) for spatial discretization of differential operators, and for interfaces with MUMPS and LIS libraries for the solution of linear systems of algebraic equations. The development of CGDD was partially supported by the SuperComputing Applications and Innovations (SCAI) department of CINECA, Italy through the Interdisciplinary Laboratory for Advanced Simulation (LISA) projects 3DSPEED (3D Simulation of PowEr Electronics Devices, 2014) and PDDD (3D Power electronics Drift Diffusion Device simulation, 2013). The main feature of CGDD++, which were the objective of this thesis, is the ability to allow implementation and testing of a wide range numerical algorithms suited for very large scale parallel mixed–mode simulation of Power Semiconductor devices, including electro–thermal effects. Particular emphasis was devoted during the development of this thesis to the implementation and assessment of various linear and nonlinear iteration strategies. The thesis starts with the introduction of differential model, universally known as drift–diffusion model, and the choice of the various physical coefficients forms for the model. In particular the models for the band gap energy and effective intrinsic density, for the mobility of carriers and for the different types of carrier generation and recombination are introduced with their dependence on mterial, doping, temperature. In power electronics devices, temperature effects are particularly important due to the high powers being dissipated. The decision hereby taken of limiting the model to deal with uniform, constant temperature as a parameter is due to the necessity of taking a first step, and being able to investigate different regimes in a simpler way. The framework presented in this thesis, however, provides means of including either lumped or distributed temperature models, task we can consider as a future research objective. The introduction of the distributed model is followed by a review of conditioning of the drift–diffusion system and nondimensional reformulations which help defining the solution algorithm. A switch to lumped modeling is necessary to test and simulate power devices response and behavior during usage. Settings suited to reproduce realistic usage conditions are emulated by means of a controlling electric circuit, comprising static and dynamic, linear and nonlinear components, and providing the dynamic boundary conditions needed to our system.
The framework we use to model the behavior of electric circuits is that of Modified Nodal Analisys (MNA), and investigation of the general form of the lumped models grants us insight on analogies allowing for a similar treatment of distributed models, and their coupling with circuital elements. Some analytical results with respect to the coupling of distributed and lumped circuital elements are reported. After linearization and discretization, approximating the solution of the drift–diffusion equation and the coupled differential–algebraic description of the controlling circuit ultimately results in the successive solution of a number of linear systems. We discusses the choice of linear solvers suitable for the specific problems at hand, trying to exploit peculiarities stemming from the form of the original problem. Standard iterative solvers do not prove convergent on the fully coupled system, while direct solvers ultimately require too much computer memory to be exploited in the case of big devices represented with refined meshes. We propose and validate a specifically tailored strategy which allows for a staggered solution of the coupled PDEs, but calls for fundamental adjustments deriving from the previously presented analysis: proper non diagonal scaling, treatment of the dynamic boundary conditions, acceleration through vector extrapolation. This kind of algorithm proves enabling for the solution of a problem which is intractable with standard methods.

STATISTICAL METHODS FOR OMICS DATA

Marzia A. Cremona - Supervisor: Piercesare Secchi
Co-advisors: Laura M. Sangalli, Simone Vantini

The Human Genome Project has been completed more than a decade ago, with the sequencing of the human genome. From that moment on, many techniques have been developed to study genetic and epigenetic processes, i.e. all the processes that involve the genetic material and the heritable changes in gene activity. Next Generation Sequencing (NGS) methods have revolutionized the genomic field by allowing fast, accurate and not very expensive genome-wide sequencing. Currently, many NGS techniques are available and produce different types of data whose common characteristics are their high-dimensionality and complexity. For instance, DNA-seq can be used to find mutations in an individual genome, while RNA-seq permits to study gene expression, Dnase-Seq investigates the open chromatin regions of the genome and ChIP-seq analyzes protein-DNA interactions.
The heterogeneous and high-dimensional omics data generated by high-throughput experimental technologies pose several challenges for reliable statistical methods and biological interpretation. Moreover, significant computational challenges are introduced by the massive nature of omics data. Although much progress has been made, data analysis and interpretation still represent the bottleneck in genomic knowledge. The present work addresses this need, introducing novel statistical methods that are expected to have broad applicability in genomics. With the aim to fully exploit omics data and unveil the complexity of the genome, existing techniques are extended, novel methods are developed and appropriate analysis pipelines that cleverly combine them are established.
The leading idea of this work consists in considering genomics data at high resolution, treating them as "curves" made of measurements along the DNA sequence. This innovative approach is relatively underused in genomics, although it has several advantages. The most important one is that the consecutive ordering of the measurements along the genome is naturally embedded by the curves. Moreover, the fact that the whole curves are the objects of the study contribute to increase the ability of the statistical methods to extract the global information, without losing the meaningful details present in high resolution data. This central idea is applied, through different statistical methods, to multiple types of omics data in three genomics contexts. First, ChIP-seq peaks are clustered and analyzed selecting indices reflecting their shape (both complexity and intensity of the peaks). Second, the genomic landscape of endogenous retroviruses is studied, both in mouse and in human, using Functional Data Analysis techniques. Third, a novel statistical methodology, called Functional Motif Discovery, is developed with the aim to identify "signatures shapes" in multiple high resolution genomic tracks related to mutagenesis and genome dynamics.

Clustering and analysis of ChIP-seq data using peak shape

ChIP-seq (Chromatin Immunoprecipitation Sequencing) is a NGS technique largely used to investigate the interactions between DNA and various types of proteins. These interactions result as peaks in ChIP-seq segnals. While in standard ChIP-seq analysis only peak intensity is usually considered, the proposed analysis method consists in selecting five shape indices reflecting both the complexity and the intensity of the peaks. Multivariate clustering is then used to identify different peak shapes. The obtained clusters are then characterized using a wide range of statistical and bioinformatics techniques. The methodology is applied to ChIP-seqs for the transcription factor GATA-1 in different cell types (K562, primary human and mouse megakaryocytes), and to a set of ChIP-seqs for nine different proteins in K562 cells, demonstrating that peak shape depends on the protein under investigation, that it is associated with characteristic regulatory complexes and is correlated with gene expression. The same principles used in this study can be applied to the investigation of ChIP-seq data for other types of proteins (e.g. histone modifications) as well as to ChIP-exo data, possibly leading to more complete results. The central part of the presented methodology (SIC-ChIP, Shape Index Clustering for ChIP-seq peaks) is available online as a command line R script.

Studying the genomic landscape of endogenous retroviruses using Functional Data Analysis techniques

Endogenous retroviruses (ERVs) are a particular type of transposable elements, segments of DNA that can move within the genome of an organism and have an important role in genome evolution and in many diseases. The distribution of ERVs in the genomes is neither random nor homogeneous, hence it is very interesting to study the integration and fixation preferences of these elements. For the first time in this field Functional Data Analysis techniques such as the Interval Testing Procedure and multiple Functional Logistic Regression models are extended and employed to address three questions about the biology of ERVS: 1) what genomic features are significant for ERV integration and fixation? 2) at what genomic scales and locations are these features influential? 3) how do genomic features work in concert to provide signals essential for integration and fixation? These analyses show evidence of the existence of genomic features associated with fixation and integration preferences for ERVs.

Functional motif discovery and its application to mutagenesis and genome dynamics

This work focus on the identification of "signatures shapes" in multiple genomic tracks. The motivating genomic problem is the study of mutagenesis and genome dynamics, i.e. the investigations of the processes that generate mutations in the DNA sequence of an organism. The proposed methodology involves the study of multiple neutral mutation rates and employs Functional Data Analysis techniques to efficiently reduce the noise present in high resolution (e.g. 1 kb windows), naturally incorporating the consecutive ordering of the measurements. In particular, a novel approach to identify functional motifs (that is, typical "shapes" that may recur within each curve, or across several curves in a given set) is elaborated. Given the nature of the considered data, the Functional Motif Discovery (FMD) is capable of handling multidimensional curves and allowing for missing values (gaps in the curves). Since an extensive pre-processing is needed to prepare the raw data to be handled as functional data, a collection of techniques adapted from FDA and other fields of statistics, called SPA (Smoothing after Predicting not Available data), is also developed.

STABILITY PROPERTIES OF EVOLUTION SYSTEMS WITH MEMORY

Valeria Danese – Supervisor: Prof. Vittorino Pata

The dominating theme of this thesis is the study of the stability properties of dynamical systems, with particular interest towards evolution systems with memory arising from relevant models in Mathematical Physics. Our analysis is mainly oriented to models encompassed by a suitable abstract memory equation, which generates a semigroup of solutions on a proper Banach space endowed with a further component accounting for the presence of memory. The focus of this work is not restricted to a specific model. Indeed, the most interesting part is perhaps the development of new theoretical tools for the asymptotic analysis of dynamical systems. The investigation concerns both linear and nonlinear models.

Decay of Linear Dynamical Systems

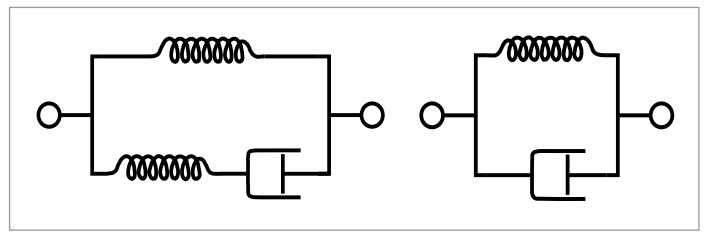
Concerning linear dynamical systems, we introduce new techniques allowing to analyze the decay properties of linear semigroups arising from systems where operators not admitting compact inverse are present. Indeed, the methods usually applied to perform stability analysis fit for systems with operators endowed with compact inverse, characterized by the crucial property of having a purely punctual spectrum. So far this issue seems not to have been considered in the literature, at least in the applications to PDEs. A further motivation is provided by our interest in linear evolution systems with memory, since in this situation operators not having compact inverse structurally appear. In order to understand the problem, we initially focus on an abstract system of Timoshenko type whose leading operator does not admit compact inverse. This model has an independent interest owing to its physical relevance and turns out to be nontrivial. At the same time, it does not reach the level of complexity generally shared by systems containing memory terms. As a result, we introduce a general technique to perform a complete stability analysis, which is subsequently applied to a linear model with memory.

Exponential Attractors for Abstract Equations with Memory

Concerning nonlinear dynamical systems, we investigate equations with memory, considering them from an abstract point of view and then focusing on specific concrete models. A common feature of equations arising from concrete physical models is the presence of a dissipation mechanism. In this perspective, here we are mostly interested in the longterm behavior of solutions. Since it is possible to translate a memory equation within a semigroup framework, the dissipativity properties of such an equation can be described in terms of "small" sets of the phase space able to eventually capture the trajectories of the related solution semigroup. Dealing with semigroups, an important object is the global attractor, whose existence has been proved for several models with memory. Instead, our main goal is to discuss the existence of exponential attractors, which have the advantage of being more stable than global attractors, and attract trajectories exponentially fast. Although the existence of global attractors for equations with memory has been investigated in several papers, there are considerably fewer results concerning exponential attractors. This is mainly due to the technical difficulties arising in the application of the classical techniques to this particular framework.
Here, we consider a memory equation in abstract form and we establish a general scheme to prove the existence of exponential attractors. With relatively little effort, we apply our abstract result to one of the most important models with memory: the equation of viscoelasticity. The existence of an exponential attractor for this equation was an open problem so far.

A Model of Viscoelasticity with Time-Dependent Memory Kernels

Finally, we address an innovative matter concerning the study of equations with time-dependent memory kernels. The equation of viscoelasticity mentioned above describes the behavior of viscoelastic materials whose properties remain constant over time. However, some viscoelastic materials undergo a process of aging, which corresponds to a change of the structural properties along the evolution, leading, possibly, to a different shape of the memory kernel. A simplified, yet very effective, way to represent linear viscoelastic materials is through rheological models, that is, by considering combinations of linear elastic springs and viscous dashpots. In particular, a standard viscoelastic solid is modeled as a Maxwell element, i.e. a Hookean spring and a Newtonian dashpot sequentially connected, which is in parallel with a lone spring (see fig. 1). As to the aging process of the material, there are several ways to reproduce this phenomenon within a rheological framework. Here, we propose to describe aging as a deterioration of the elastic response of the viscoelastic solid, translating into a progressive stiffening of the spring in the Maxwell element. In the limiting situation, when the spring becomes completely rigid, the outcome is the Kelvin-Voigt (solid) model, depicted by a damper and an elastic spring connected in parallel (see fig. 1).
In spite of a relatively vast literature concerning both the equation of viscoelasticity and the Kelvin-Voigt model, we are not aware of analytic studies which consider the possibility of including aging phenomena of the material within the dynamics. Therefore, we formalize in mathematical terms the modeling approach described above proposing a rheological model for aging viscoelastic materials. Such a model leads to a kinematic equation characterized by the presence of a time-dependent memory kernel. Owing to this feature, this model cannot be handled exploiting the classical tools for memory equations and new ideas are needed. Indeed, our model exhibits a structural nonautonomous character, in the sense that the leading differential operator depends explicitly on time. A much different situation than, say, having a time-dependent external force. In particular, the natural phase space turns out to be itself time-dependent, suggesting that the right strategy is to work within the theory of processes on time-dependent spaces. We provide a well-posedness result for the problem, with the purpose of laying the foundations for the study of the longterm behavior of the solutions.



1. Mechanical schemes of the standard viscoelastic solid model (left) and the Kelvin-Voigt model (right).

NUMERICAL MODELING OF NANOPARTICLE TRANSPORT AND ABSORPTION

Elena Danesi - Supervisor: Dr. Carlo De Falco

Nanomedicine is the emerging medical research branch which employs nanotechnological devices to improve clinical diagnosis and to propose more effective therapeutic methodologies. In particular, functionalized nanoparticles have proved their clinical usefulness for cancer therapy, either as vectors for targeted drug delivery or for hyperthermia treatment. The effectiveness of such novel therapeutic strategies in nanomedicine results from the capability of the nanoparticles to penetrate into the living tissue through the vascular network and to reach the targeted site. Accordingly, their success is controlled by the multi-physics and multi-scale aspects governing the diffusion and transport properties of the nanoparticles, together with the geometrical and chemo-mechanical factors regulating the nanoparticles-tissue interactions. Indeed, the therapeutic effectiveness of earlier approaches was hindered by their limited ability in penetrating within the tumor tissue.
Mathematical modeling is often employed in nanomedicine to analyze *in silico* the key mechanisms acting at the different scales of investigations, providing useful guidelines for optimizing the novel experimental techniques. Many mathematical works have focused on studying the diffusion of nanoparticles in tumor tissue and their absorption by targeted cells in order to improve the effectiveness of their injection process. Since this whole process involves different characteristic time and length scales, a multi-scale modeling approach is mandatory. At the macroscopic scale, the living tissue is typically modeled as a homogenized, porous material of varying permeability, where the fluid flow is modeled by Darcy's equation and nanoparticle transport is described by a continuum Diffusion-Reaction-Advection equation. At the microscale, the fluid flow is modeled by Stokes' equation and the transport of nanoparticles is modeled either by the stochastic Langevin equation or by its continuous limit, considering in both cases short distance interaction forces such as Coulomb and van der Waals interactions between particles and collecting cells as well as disturbances of the fluid velocity field induced by the presence of the nanoparticles.
In this work we propose a *bottom-up* approach to study the transport and the diffusion of nanoparticles in living materials. Our multi-scale analysis starts at the smallest scale, whilst its results are used as input conditions for the largest scale. In particular, we determine the concentrated parameters regulating the nanoparticle transport equation at the tissue level by means of simulations at the microscale. In the following, we focus on two problems of clinical interests, mimicking both the particles' absorption into a regular packing of cellular aggregates and their extra-vasation through the surface of a pore of different geometries. We propose an original approach for determining particle diffusion and convection velocities as well as deposition rates by means either of Lattice Kinetic Monte Carlo (LKMC) microscale simulations or by Finite Volume Method (FVM) applied to continuum Partial Derivative Equation (PDE) models. We also derive macroscale equation coefficients from the results of microscale simulations by means of a suitable Upscaling technique.
In the first part of the thesis we explain the motivations of the work, related to recent development of tumor therapies involving the use of nanoparticles, and we make an overview of the mathematical models present in literature for the description of the diffusion in tissues of different types of particles applied for tumor treatment.
Then we discuss the mathematical models for the description of the problem under consideration. We study the equations which describe the problem at the different length-scales and then we relate them through a proper upscaling.
In particular, we focus our attention on the microscopic scale, investigating the physical phenomena which influence the motion of the nanoparticles in the extracellular space. We introduce Happel's sphere-in-cell model, which is a simplified model widely used in literature as a representation of the microscopic structure of a porous medium, and we highlight its weaknesses.
After that we describe the numerical methods applied to solve the equations involved in the description of the problem, that is a Lattice Kinetic Monte Carlo method and a stabilized Finite Volume Method.
At last we present the results of the numerical simulations of this multi-scale model. In particular, we investigate the effect of nanoparticles and tissue microscopic properties on the absorption efficiency, which represents the percentage of nanoparticles captured by the solid phase.

DISCONTINUOUS GALERKIN REDUCED BASIS ELEMENT METHODS FOR PARAMETRIZED PARTIAL DIFFERENTIAL EQUATIONS IN PARTITIONED DOMAINS

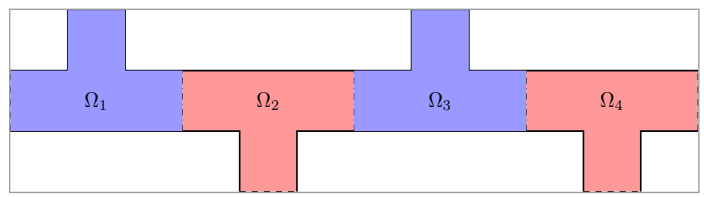
Paolo Pacciarini

The numerical approximation of Parametrized Partial Differential Equations (PPDEs) is a challenging task, especially when a rapid computation of the solution is required for a new given value of the parameter. In many applications, for instance real-time simulations, resorting to approximation methods like the Finite Element Method (FEM) or the Spectral Element Method (SEM) can be too computationally demanding. To face this problem, a wide range of model order reduction techniques have been proposed in the past two decades. An important approach is represented by the Reduced Basis (RB) method, that approximates the solution of the PPDE through a Galerkin projection on a suitably built low-dimensional space, providing significant computational savings. There are several possibilities for the construction of such a low-dimensional space. A possible strategy is the Proper Orthogonal Decomposition (POD), which is based on a singular value decomposition of a set of high-fidelity approximations of the solution computed on a large set of parameters. An alternative approach is represented by the use of a Greedy algorithm, driven by an error estimator. In this case, a small set of parameter values is selected and then, for each chosen parameter value, a high-fidelity approximation of the solution is computed. The latter is usually provided by a Galerkin method like FEM, that is the most common approach, but also SEM, typically featuring a very large number of degrees of freedom. The main advantage of the Greedy approach is that the number of high-fidelity approximations required is much smaller than that needed by the POD.
In recent years, the RB method has been successfully applied to several problems, such as heat transfer, diffusion of pollutants in the atmosphere, fluid mechanics, wave problems and linear elasticity.

When the domain of the PPDE is partitioned into several subdomains, a convenient numerical approach is provided by the so-called Reduced Basis Element method, first introduced in 2002 by Maday and Rønquist, in which local (i.e., defined on each subdomain) reduced bases are built by restriction of global solutions *high-fidelity* approximations, while the global continuity of the RB solution is guaranteed by the introduction of suitable Lagrange multipliers.

In this thesis we propose a discontinuous Galerkin Reduced Basis Element Method (DGRBE) method which is based upon the construction of a set of local basis functions that features non-homogeneous Neumann conditions on the interfaces.
As most of the model order reduction techniques, our method is built upon two computational stages: the "offline stage" (expensive and to be performed only once) and the "online stage" (inexpensive and to be performed as many times as needed). In the offline stage a non-conforming (discontinuous) global reduced space is built as a direct sum of local basis functions generated independently on each subdomain. However, only local problems are actually solved to generate the basis functions.
In the online stage, for any given value of the parameter, the global reduced solution is obtained by (weakly) ensuring the continuity properties across the interfaces thanks to a discontinuous Galerkin approach. The latter allows also to weakly recover the continuity of the fluxes (in elliptic problems) or of the normal component of the Cauchy stress tensor (in Stokes problems). Another advantage guaranteed by the use of DG interface conditions is that we can deal with mesh that are non-conforming at the interfaces. This feature makes the DGRBE method particularly well suited for problems defined on ``modular" domains, namely composed by an arbitrary number of subdomains that can be obtained by geometrical transformation of few parameter-independent building blocks, as depicted in Figure 1

In the first chapter of the thesis the DGRBE method is presented in an abstract way, starting from the continuous formulation of a general second order PPDE defined on a partitioned domain, highlighting the proper interface matching conditions. We show how a DG approach allows to obtain a variational formulation of the problem which is suitable to perform a Galerkin projection onto the space spanned by the local reduced basis built separately on each subdomain.
I show in detail how the general formulation can be set in the case of diffusion-reaction equations and of Stokes equations.
In second chapter we present and analyse in detail the DGRBE method for elliptic problems. We describe two strategies to build the local reduced bases and we analyse the approximation properties of the global reduced space obtained. We also provide results about the conditioning of the DGRBE problem and we propose a two-level preconditioning strategy based on the introduction of a global coarse space. The preconditioner turns out to be convenient when the global domain is partitioned in a large number of subdomain, as we show through numerical tests. In third chapter we extend the analysis of the DGRBE method for elliptic problems and we introduce an *a posteriori* error estimation technique which allows to estimate the error committed by the DGRBE (inexpensive) approximation, with respect to a high-fidelity (expensive) approximation on the whole domain (without solving the latter). We provide a detailed theoretical analysis of the error estimator and we assess its performance through numerical experiments. In the fourth chapter we present the DGRBE method for the approximation of a parametrized Stokes problem. Here we discuss how the techniques used to build the local spaces presented in the previous chapters can be extended to the Stokes case. We then show theoretically that the method proposed guarantees the inf-sup stability of the DGRBE problem.
In the fifth hapter, differently from the other chapters, in which I used FEM techniques to build the local bases, here I resort to a SEM approach. The goal is to understand the performance of the DGRBE method when compared with high-order approximation methods. In the numerical experiments I investigate in detail the approximation properties of the local bases obtained using SEM.



1. Here we show a global domain Ω that is assembled using two types of building blocks: the blue one and the red one.

DISCONTINUOUS GALERKIN REDUCED BASIS ELEMENT METHODS FOR PARAMETRIZED PARTIAL DIFFERENTIAL EQUATIONS IN PARTITIONED DOMAINS

Silvia Maria Carla Pagani - Advisor: Paolo Dulio

Tomography is a powerful technique to retrieve information about objects that are not directly accessible. Tomographic reconstructions have a wide range of applications, such as in medicine, industry, crystallography, and several other areas of research.
Tomography was born thanks to the early work of Johann Radon, who published in 1917 a theoretical paper concerning the reconstruction of a function from the knowledge of its line integrals. The result was later exploited by Allan McLeod Cormack and Godfrey Newbold Hounsfield, who designed and invented the first scanner, based on the use of X-ray radiation along a number of directions. This allowed them to share the 1979 Nobel Prize in Medicine, and represented the beginning of Computerized Axial Tomography (CAT) as a powerful diagnostic method in Medicine.
When trying to adapt the theory to real applications, one needs to change the continuous model into several critical items, which are obtained by introducing different discretization steps. This leads to discrete tomography, where the word ``discrete'' refers both to the discretization of the image, which is seen as a collection of pixels, and the discrete (and finite) number of admissible directions and densities. Discrete tomography is the topic of the present thesis.
One of the main goals of tomography is uniqueness of reconstruction. In fact, the tomographic problem is ill-posed, due to the presence of the so-called ghosts. These are non-null functions having zero line sums along the considered directions, and consequently they can be added to a solution in order to obtain other admissible solutions. Some prior knowledge is exploited to lower the number of possible solutions. For instance, one can assume to know in advance the number of the grey levels in the object to be reconstructed (the limit case is represented by binary, i.e., black-and-white, images). Further, one can set the tomographic problem inside a finite grid of known size, or, also, the knowledge of some features of the object can be added, such as convexity, or the particular geometric class it belongs to.
The present thesis focuses both on theoretical and algorithmic aspects of discrete tomography, mainly related to the uniqueness issue, to reconstruction and to characterization algorithms.
Reconstruction algorithms are performed on binary images, with no other features (by employing special sets of four directions), and in the case of hv-convex polyominoes, for whom special frameworks are considered, namely, noisy projections and a blocking component. In the last case, a reconstruction algorithm is provided also for the subclass of L-convex polyominoes.
On the other side, we characterize a subset of the set of uniquely determined pixels of an integer-valued function, depending only on the set of chosen directions.
For both kinds of algorithms, simulations and experiments are provided.

CUSTOMIZED FINITE ELEMENT MODELS OF THE HUMAN CORNEA FROM IMAGING AND BIO-MECHANICAL CONTACTLESS TESTS

Irene Simonini - Advisor: Prof. Anna Marina Pandolfi

Patient-specific geometry and material parameters are fundamental in the view of obtaining predictive numerical models of the anterior segment of the eye. Diagnostic devices adopted in the modern optometric practice acquire the tridimensional geometry of the whole anterior chamber of eye. Through these instruments it is possible to acquire individual geometrical data which can be used to obtain accurate quantitative information on the optical properties of the cornea, and estimate the biomechanical changes due to refractive surgery. In this thesis we aimed at developing and validating an advanced numerical procedure that, starting from images of the anterior chamber of the eye, builds accurate, patient-specific geometrical models of the human cornea. The cornea geometry is achieved through a sophisticated interpolation procedure of the surface points provided by the Sirius (CSO, Scandicci, Italy) topographer apparatus. Regrettably, owing to the impossibility to obtain in-vivo data on the mechanical properties of the various parts of the eye, customized models of the anterior chamber are not available yet. Indeed, also for the cornea, most of the available mechanical data have been obtained ex-vivo through experiments on bovine, porcine, or rabbit eye samples. The use of the results of such tests on animals is always of concern for the potential differences in the material properties. Research is moving fast in view of tackling this missing point, and a promising testing procedure is the air-puff tonometry. Since at the moment experimental techniques are not ready, in this study we used patient-specific geometries of the cornea to estimate the material properties corresponding to an individual in the cases when preoperative and postoperative geometries of the human cornea were available. Once the material properties have been identified, the model has been used to perform quasi-static analyses of corneas undergoing laser refractive surgery to treat myopia or astigmatism, and of corneas affected by keratoconus. The analyses provided a wealth of numerical results, in terms of displacements, strains and stresses.

In view of the future use of non-invasive dynamic testing to estimate the material properties of the cornea, we have also investigated the dynamical behavior of healthy corneas undergoing the air puff test. In particular, we aimed at understanding the influence of elasticity and viscosity on the results of the test and at analyzing how geometrical changes due to corneal reprofiling may affect the results of the test. We adopted and compared two different approaches. The first one is an analytical approach, based on a simple one-degree-of-freedom model characterized by a mass, a spring and a dashpot. The displacement and velocity of the mass are obtained in closed-form, and the results are useful to distinguish the effects of viscosity and elasticity. The second approach is based on the FE patient-specific model described above, that allows to simulate accurately the dynamic response of the cornea to the air puff tests. The numerical results compared well with the experimental data provided by two different clinical ocular instruments.

The thesis is organized as follows. Firstly we describe the anatomy and the most common pathologies of the human cornea, the techniques of refractive surgery, the ocular instruments used to perform our analysis and we discuss the state of the art in the theoretical and computational ophthalmology. Then we examine the analytical, the material and patient-specific finite element models, used in our work. Results of the numerical investigations are collected. Finally we compare numerical and experimental results (taken from the literature) and discuss the consequences of surgical procedures and the possibility to use the air-puff test for the characterization of the corneal material properties.

MATHEMATICAL AND NUMERICAL MODELING OF BLOOD FLOW IN AN IDEALIZED LEFT VENTRICLE

Anna Tagliabue - Supervisor: Prof. A. Quarteroni

Nowadays, there is a growing interest in developing physical and computational models applied to the cardiovascular system, mainly motivated by the fact that computational models could offer a powerful and non-invasive tool to perform an accurate investigation of the physiology characterizing the cardiovascular system, both in healthy and pathological conditions. However, the computational modeling of cardiac hemodynamic is still away from clinical application and represents an active field for current research. Indeed, the modeling accounting for the whole heart physiology with the aim of performing a rigorous investigation of the flow represents a very challenging topic, due to several aspects. Among these we mention the complex electrical-fluid-structure interaction mechanism regulating the heart functioning and determining significant deformation of the structure, the flow regimes which varies during the heartbeat from laminar to nearly turbulent, the difficulty in obtaining accurate clinical data and the need to provide results in a clinically reasonable time frame. Moreover, even if one only focuses on the left ventricle which plays a fundamental role in distributing oxygenated blood to the body, carrying out a workload particularly heavy, still these complex features remain.
The reason which motivates the particular interest in the analysis of the blood flow pattern inside the left ventricular cavity is dual, on the one hand blood flow patterns represent useful indicators of heart dysfunctions and can be critical for the diagnosis, e.g. in dilated cardiomyopathy, on the other hand, intraventricular flow and hemodynamics visualizations currently rely mostly on synthetic quantities and global variables and are significantly dependent on the temporal and spatial resolutions and on the post processing procedures used. Conversely, computational fluid dynamics is able to provide a detailed description of both instantaneous and average quantities of interests. With this aim simulations in either realistic or idealized left ventricles have been performed in the last years. While the former case represents a powerful tool in view of patient-specific applications, it presents still some drawbacks as the need to have accurate clinical data and efficient procedures to extract the required informations to provide a computation-ready model, which result anyway in geometrical simplifications. The latter, instead, is more suitable to understand phenomena with a certain degree of generality, since the idealized geometry considered usually can be regarded as the average endocardial shape of different human subjects. Moreover, the idealized geometry is usually associated to a self-contained model and it has been noticed that, by setting all the geometric parameters to physiologically compatible values, some details of the actual geometry have little influence on the flow patterns.
In this thesis, I mathematically describe the blood flow in an idealized left ventricle by means of the Navier-Stokes equations in Arbitrary Lagrangian-Eulerian formulation by assuming a Newtonian rheological behaviour for the blood. Since the flow is mainly regulated by the action of the valves, which also force a one-way direction of the blood in the heart, the accurate valve modeling is crucial for obtaining meaningful results. However, a general lack of detailed clinical data describing the blood flow profile through the valves leads to formulate mathematical models accounting for their action.
In this respect, in this thesis, I propose a simplified but realistic treatment of the valves functioning as boundary conditions (BCs) for the Navier-Stokes equations, even if some mathematical and numerical challenges arise.
Indeed, the open and closed configurations of the valves, which cyclically occur during the heartbeat, are naturally associated to BCs of different nature, namely natural and essential BCs. From the numerical point of view, a standard numerical method based on a Galerkin method would require the definition of time varying function spaces depending on the location and the measure of the boundary where the essential BCs are applied, which varies in time. In order to face this issue, which could considerably affect the computational performances, I introduce mixed time varying BCs. In order to solve such problem, I propose a new numerical approach with time independent function spaces based on the Extended Nitsche's method with spatial discretization based on the Galerkin method, using either Isogeometric Analysis (IGA) or Finite Element (FE) methods.
I propose a theoretical analysis of the scheme in the context of the FE method, which, however, can be easily re-adapted for NURBS-based IGA. Specifically, in this thesis, I show the existence and the numerical stability of the solution for a simplified problem, namely a parabolic Partial Differential Equation endowed with mixed time varying BCs. Then, the proposed methodology is adapted and extended to model the open and closed configurations of the valves through mixed time varying BCs for the Navier-Stokes equations, which are weakly enforced at the numerical level by means of the Extended Nitsche's method.
In addition, in view of the improvements in both accuracy and efficiency of IGA compared to the FE method for the spatial approximation of hemodynamics problems, I used IGA for the intraventricular fluid dynamics study.
Since the mitral and aortic valves show an analogous behaviour, I use the same mathematical and numerical model for the treatment of the associated mixed time varying BCs, for which the valves are modelled as orifices of infinitesimal thickness located at the upper equatorial diameter of the idealized left ventricle. However, the sensitivity of the intraventricular flow patterns with respect to the inflow condition at the mitral valve suggests further improvements in the formulation of the BC at the mitral orifice, for which I specifically propose a regularizing high order penalty term to obtain more realistic inflow velocity profiles.
I perform an extensive study of the blood flow in two- and three-dimensional idealized left ventricles obtained by means of numerical simulations in an High Performance Computing framework. Several quantities of interest in hemodynamics and cardiac fluid dynamics are computed, evaluated, and analyzed, including instantaneous and phase-averaged quantities over multiple heartbeats. The numerical results, compared against those available in literature, both computational and experimental, highlight the validity and accuracy of the proposed mathematical and numerical models for blood flow in idealized left ventricles. Particular emphasis is put on the capability of the formulation in preventing the insurgency of backflow instabilities at the outflow boundary represented by the aortic valve orifice. Moreover, I consider left ventricles affected by cardiomyopathy, to highlight the versatility and clinical relevance of the proposed mathematical and computational model.
Finally, since the numerical solution of the intraventricular flow represents an example of flows in closed cavities, I further investigate this problem by considering the solution of the two-dimensional Navier-Stokes equations in stream function formulation for the benchmark lid-driven cavity problem in a semi-circular domain. Furthermore, I perform a theoretical analysis for the NURBS-based IGA approximation of the steady Navier-Stokes equations in stream function formulation, by providing a priori error estimates under h-refinement, including those in lower order norms.
This thesis have been developed under the supervision of Prof. A. Quarteroni at MOX-Modeling and Scientific Computing, Politecnico di Milano, and, during a six months visit, at the Chair of Modeling and Scientific Computing (CMCS), MATHICSE, École Polytechnique Fédérale de Lausanne (EPFL).

SOME FOURTH ORDER DIFFERENTIAL EQUATIONS MODELING SUSPENSION BRIDGES

Wang Yongda - Supervisor: Prof. Filippo Gazzola

Nowadays, the complicated oscillations of modern suspension bridges are still not completely understood. Moreover, most of the existing mathematical models in literature fail to describe the static or dynamic behavior of the suspension bridges. In this thesis, we suggest several reasonable new mathematical models including one beam model and two plate models, which may help to describe the oscillation behavior appearing in the actual suspension bridges.

Usually, the length of the deck of the bridge is much larger than its width. Hence, it is natural to view the deck as an elastic beam which is suspended to a flexible sustaining string, where the beam and the string are connected by a large number of inextensible hangers. We analyze the potential energies in the system (the suspension bridge) after the deformation of the system from the rest position to a new position due to a live load. The Euler-Lagrange equation is obtained by taking the critical points of the total energy in the bridge. Together with the hinged boundary conditions, we deduce a nonlinear nonlocal problem and we prove that it admits at least one weak solution whereas the uniqueness result seems to depend on the parameters involved in the equation.

Since the beam model cannot describe the torsional oscillation appearing in the suspension bridge, one should consider the deck of the bridge as a long-narrow thin rectangular plate. We first recall the plate model suggested by Ferrero-Gazzola for describing dynamical suspension bridge. Based on the linear Kirchhoff-Love plate theory, a semi-linear evolution problem which admits a unique solution is deduced. Then we consider a non-coercive problem corresponding to the plate model and this problem also has a unique local solution. We analyze the asymptotic behavior of the unique local solution of the problem for different initial conditions. Finally, in order to describe the boundary behavior of the plate (deck), we set up a kind of dynamical boundary conditions that reflect the physical constraints on the boundaries. Assume that the restoring force due to the hangers is in a linear regime, we obtain a linear evolution problem with the dynamical boundary conditions. We then prove that this evolution problem admits a unique explicit solution.

The previous plate model is correct adequately if the deformations of the plate are small. However, when large deformations appear in the plate, the linear Kirchhoff-Love plate theory cannot describe the behavior of the oscillations. Hence, one needs to consider the geometric nonlinearities of the plate due to the wide oscillations and the interaction with the stretching behavior of the plate should be analyzed. In this case, we suggest a quasilinear plate model based on the von Kármán plate equations. Two fourth order differential equations are deduced by applying variational principles to the energy functional, where we introduce the so-called Airy stress function. By adding the restoring force due to the hangers and cables to the equations, we obtain a system coupled by two fourth order differential equations. We prove existence and multiplicity results of the system with suitable boundary conditions which describe the situation of the suspension bridge.

Certainly, we do not claim that our mathematical models are perfect. This is just the beginning in order to reach more challenging results in this field and much more work (both mathematical and engineering) is still necessary. But we do hope that these models might induce some researcher, both mathematicians and engineers, to investigate more deeply into these fascinating challenges.