CompMat2022

SPRING WORKSHOP 2022

Joint PhD in
COMPUTATIONAL MATHEMATICS AND DECISION SCIENCES

March 16-17, Università di Pavia

PROGRAM

&

BOOK of ABSTRACT

Università della Svizzera italiana

UNIVERSITÀ DI PAVIA
Corso di Dottorato in Computational Mathematics and Decision Sciences

Program

	Wednesday 16	Thursday 17
8:30	Registration	
9:15	Opening	
9:30	Prof. Piernicola Oliva	Prof. Paola Causin
10:20	Andrea Medaglia	Alen Kushova
10:40	Raffaella Cabini	Silvia Caligari
11:00	Coffee break	
11:30	Lorenzo Zambon	Fabio Credali
11:50	Sergio A. Gomez	Eleonora Vercesi
12:10	Sofia Botti	Claudio Tomasi
12:30	Lunch break	
14:30	Giulia Colelli *with* Fondazione Mondino	Chiara Bardelli *with* Datev
15:30	Mishel Qyrana *with* Assicurazioni Generali	Andrea Codegoni *with* Sea Vision
16:30		Prof. Francesca Ieva

Our partners

(in alphabetic order)

- Assicurazioni Generali: www.generali.com

- Datev: www.datev.com

- Fondazione Mondino: www.mondino.it

- RES: www.res-group.eu

- Sea Vision: www.seavision.it

Contents

Presentation

The Spring Workshop is aimed for advanced MSc graduates interested in pursuing doctoral studies in Computational Mathematics, Decision Sciences, Machine Learning, Statistics and related areas.

It is also intended as a meeting opportunity between academia and industry, with the belief that the contamination of knowledge can lead to collaborative networks and to a fruitful ground for research and innovation.

Organising committee

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https://mate.unipv.it/matcomp22/

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Contacts

joint PhD program in
Computational Mathematics and Decision Sciences UniPV-USI

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Università di Pavia	Università di Pavia

Plenary talks

Prof. Paola CAUSIN

Università degli Studi di Milano

MATHEMATICAL AND NUMERICAL CHALLENGES IN OPTICAL TOMOGRAPHY

In this talk I will deal with optical tomography, an innovative technology which aims to perform medical imaging in a non invasive and non ionizing manner. This technology offers to mathematicians a wide and interesting field of research, both from the theoretical and computational viewpoints. Specifically, I will focus on Diffuse Optical Tomography (DOT), which employs light in the NIR band to estimate the spatial distribution of optical coefficients in a living being for diagnostic purposes. In the NIR band, light interacts with biological tissues mainly via absorption and elastic scattering. The difficulty in the reconstruction lays in the fact that scattering is highly prevalent on absorption: biological tissues behave indeed as turbid media, somewhat like a cloud of fog or a glass of milk, hindering the view of the internal structure. This, in turn, implies that from the mathematical viewpoint the related inverse problem for coefficient reconstruction is severely ill–conditioned and regularization procedures are mandatory. Regularization methods based on L_2, L_1 norms or Total Variation control have been classically used in literature [3], but they are not flawless. The paradigm shift which is taking place in imaging, from classical analytic to learning and data-based methods [1], opens new paths also for DOT reconstruction. With its severe ill–posedness, this is indeed a challenging candidate application to explore new automatized regularization procedures. I will refer about our work on both the regularization approaches, the data–driven one being the most recent. I will discuss about our research on using physics–driven and data-driven models [2], analyzing their respective pros and cons.

[1] S. Arridge and A. Hauptmann, *Networks for nonlinear diffusion problems in imaging*, Journal of mathematical imaging and vision, pp.1–17, (2019).

[2] A. Benfenati, G. Bisazza, P. Causin, *A Learned SVD approach for Inverse Problem Regularization in Diffuse Optical Tomography*, arXiv preprint arXiv:2111.13401, (2021).

[3] P. Causin, M. Lupieri, G. Naldi, R.M. Weishaeupl, *Mathematical and numerical challenges in optical screening of female breast*, International Journal for Numerical Methods in Biomedical Engineering, 36(2), e3286, (2020).

Prof. Francesca IEVA

Politecnico di Milano

HEALTH ANALYTICS:
HOW TO EXPLOIT COMPLEX DATA TO INFORM PRECISION MEDICINE AND SUPPORT CLINICAL DECISION MAKING

The medical practice is currently undergoing a transformative era, shifting the paradigm from the primarily reactive medicine of the past to a more proactive and predictive medicine, and trying to outdo the traditional "one-size-fits-all" approach designed for the average patient. This new paradigm takes the name of Precision Medicine. Rather than treating a disease, the attention now is moving toward streating the individual patients. In other words, this methodological framework seeks to include a range of complex personal data in order to build a Patient Representation, that combined with a tailored modelling can answer relevant clinical research questions and support clinical decisions. In fact, the power of precision medicine lies in its ability to guide healthcare decisions toward the most effective treatment for each individual, and thus, improve care quality, while reducing the need for unnecessary diagnostic testing and therapies.

In this talk we will explore situations where the use of advanced analytics designed on complex, multi-modal and multi-omics data allows for an effective support of clinical decision making in oncological setting and other relevant clinical scenarios (e.g. Covid-19). The first example concerns the use of Machine Learning techniques for predicting the development of toxicity adverse events due to radiotherapy in prostate cancer patients, starting from genomic information, then a case where graph theory is introduced in order to spot the high order genome interaction in determining the severity of Covid expressions. The second example regards the assessment of the potential of the virtualy biopsy in predicting the treatment response of Hodgkin Lymphoma patients.

Prof. Piernicola OLIVA

Università di Sassari - INFN

DEALING WITH CONFOUNDERS IN ML ANALYSES OF MULTICENTRIC DATASETS: A CASE STUDY FROM MRI

Machine learning (ML) techniques have been widely applied to medical data, due to their powerful, multivariate, data-driven approach. An expected outcome of these approaches, in particular in complex pathologies, is the identification possible reliable biomarkers of the disease.

However, ML findings can be misled by biases and outliers in the training set, which can be affected by sample-dependent patterns. This confounding aspect is often critical in biomedical applications in which heterogeneity of the data and of their acquisition process is often combined with a limited amount of collected samples.

The case of a publicly available dataset of magnetic resonance images (MRI) of the brain, devoted to the investigation of Autism Spectrum Disorders (ASD), will be discussed.

In particular, the data dependence on the acquisition center will be presented, for both structural and functional images, together with possible approaches on how to deal with it.

Industry sessions

Assicurazioni Generali

PhD candidate: *Mishel QYRANA*

DEEP LEARNING TECHNIQUES FOR IMAGE ANALYSIS

The past two years have been focused on Deep Learning techniques for Image Recognition, Classification and Segmentation, which have been applied to a phletora of tasks such as smartphone screen damage detection and car damage segmentation.
The activity was focused on both implementation and adaptation of models and on related literature deep review.
The last developments of my contribution are focusing on adapting and exploiting these techniques for financial markets applications, as for example Deep Learning Techniques for diversified portfolios construction.

Datev

Chiara BARDELLI

MACHINE LEARNING MODELS
FOR THE AUTOMATION OF ACCOUNTING PROCESS

In this presentation we will describe a methodological proposal to automate part of the business accounting process and integrate the prediction output of a Machine Learning classifier into a software for account officers.

Since the accounting profession often deals with repetitive and time-consuming tasks, Machine Learning models can be a useful tool to replace such monotonous activities and give the accountant the possibility to focus on more stimulating occupations such as decision-making, problem solving, advising and business strategy development. The opportunity of integrating Machine Learning techniques into the accounting business process motivated the collaboration with Datev, a software company which develops IT services for accounting systems.

The aim of this project is the design and implementation of an automatic intelligent system for the creation of a bookkeeping entry associated to an xml invoice document. The workflow proposed include different procedural steps ranging from the reconstruction of the training set, to the application of a word embedding to learn a representation for the textual part, to the development of a classification model. Our final aim is to provide an entire framework which can be easily integrated and deployed in an accounting software.

Fondazione Mondino

PhD candidate: *Giulia COLELLI*

MACHINE LEARNING AND DEEP LEARNING FOR QUANTITATIVE MRI IN FACIOSCAPULOHUMERAL MUSCULAR DYSTROPHY (FSHD) DISEASE

An increasing quantity and complexity of available clinical data has paved the way for the development of personalized and precision medicine. The latter helps the clinical decisional process through diagnosis and therapies optimization by taking advantage of patient specific characteristics and the associated morbidity. In this scenario, the possibility to extract quantitative information from biomedical images becomes very important.

In particular, quantitative Magnetic Resonance Imaging (qMRI) plays a crucial role for assessing diseases' diagnosis, progression and treatment response especially in the neurodegenerative diseases and neuromuscular disorders, such as FSHD [1]. However, the required MRI sequences are often not routinely available and also time consuming for the patient. The aim of this research at IRCCS Mondino is to combine AI [2] and texture analysis [3] in order to predict the qMRI values of Fat Fraction and water T2 biomarkers, indicators of neuromuscular involvement, starting from conventional MRI images.

[1] P.G. Carlier et al., *Skeletal Muscle Quantitative Nuclear Magnetic Resonance Imaging and Spectroscopy as an Outcome Measure for Clinical Trials*, J. Neuromusc. Dis. (2016), 3(1):1-28.

[2] G. James, D. Witten, T. Hastie, R. Tibshirani, *An Introduction to Statistical Learning with Application in R*, Springer (2013).

[3] M. Tuceryan and A.K. Jain, *Texture analysis*, Handbook of pattern recognition and computer vision (1993) 235-276.

Sea Vision

PhD candidate: *Andrea CODEGONI*

ONE-SHOT ANOMALY SEGMENTATION FOR LINE CLEARANCE

joint work with Luigi Carrioli, Alessandro Ferrari and Gabriele Lombardi

The problem of Line Clearance, that is to say whether a production line is in a state of cleanliness that does not have residues from previous processing, is a fundamental problem for all those companies that deal with production and packaging.

In particular, for pharmaceutical and cosmetic companies, in addition to checking that there are no production waste that could damage the machinery, it is also essential to check that there are no residues of old products to avoid the mixing of medicines.

Employing personnel to inspect long and complex production lines results in downtime for the production line. Thus arises the need to speed up the process by using cameras at strategic points and artificial vision algorithms to detect possible anomalies.

However, it is not an easy way to build a meaningful dataset that allows us to successfully use the tools of deep learning as it requires massive data acquisition. Furthermore, our aim is to detect anomalies not known a priori and also extreme situations that we cannot reproduce to avoid damaging the machinery during the acquisition phase.

Last but not least, we want to build a model that is able to autonomously generalize according to the customer's needs.

In this talk we will introduce all these issues related to Line Clearance and we will propose our solution based on a one shot learning model that allows us to obtain interesting results both in terms of accuracy and generalization using a small number of data and generating anomalies through the use of data augmentation only, thus avoiding any type of collateral damage during the construction of the dataset.

PhD presentations

Sofia BOTTI

XXXV cyle

From cardiac stem cell ionic models to isogeometric simulations of 3D cardiac tissue

Human induced pluripotent stem cells – derived cardiomyocytes (hiPSC-CMs) [3] are a promising in vitro tool for cardiac investigations, with the potential to eliminate interspecies and interpersonal variations though patient-specific derivation.

HiPSC-CMs are spontaneously beating cardiomyocytes. They express the main cardiac markers and ionic channels, they are functionally like adult human cardiomyocytes, but, unfortunately, they result in a mix of cells which can be classified as atrial-, ventricular- and sinoatrial-like CMs.

In the mathematical literature, the first work focusing on hiPSC-CMs modeling was published in 2013, then updated by a new publication in 2018 [1] for ventricular-like stem cells. In collaboration with the Cardiocentrum Ticino Institute, we are developing a new computational model for hiPSC-CMs with an atrial-like phenotype.

Using these cells in a totally different setting, laboratory studies have been able to reproduce a tissue engineered scale model of the human ventricle [2], in order to create a reliable substitute to animal models. An in silico replica of this engineered platform is useful for a number of reasons, such as fast preliminary tests and the quantification of non-experimentally measurable quantities. Isogeometric Analysis (IGA) is a recent effective alternative to Finite Element Methods, due to its higher accuracy per degree of freedom. In this setting, we build up a suitable IGA framework for modeling a monoventricular geometry and for simulating the cardiac monodomain equation coupled with a hiPSC-CM ionic model.

[1] M. Paci et al., *Automatic optimization of an in silico model of human ipsc derived cardiomyocytes recapitulating calcium handling abnormalities*, Frontiers in physiology (2018) 709.

[2] L.A. MacQueen et al., *A tissue-engineered scale model of the heart ventricle*, Nature biomedical engineering 2 (12) (2018) 930-941.

[3] K. Takahashi et al., *Induction of pluripotent stem cells from adult human fibroblasts by defined factors*, Cell 131 (5) (2007) 861-872.

Raffaella F. CABINI

XXXVI cycle

APPLICATION OF MEAN FIELD INTERACTION ALGORITHM TO MEDICAL IMAGE SEGMENTATION

joint work with Silvia Figini, Anna Pichiecchio, Alessandro Lascialfari and Mattia Zanella

Image segmentation is an important task in the field of image processing and computer vision and it is widely used in several application areas, including the field of medical imaging. Several widely studied approaches to image segmentation are based on clustering techniques such as the k-means method, the c-means method and the hierarchical clustering method. Indeed, image segmentation may be considered a clustering process where the pixels are classified into the attribute regions based on a vector of features calculated around the pixel local neighborhood.

The purpose of this work is to generalize the Hegselmann-Krause (HK) aggregation model to solve data-clustering problems and apply it to image segmentation. The key idea of this approach is to associate to each particle a time-dependent state vector and features representing static characteristics of the system, i.e. the position and the gray level of the pixel (Herty et al., 2020). Particles interact according to the generalized HK equation and, in a finite time, the system converges to a stable configuration where the initial states are grouped in a finite number of clusters.

The corresponding Boltzmann formulation is derived and the agreement with the Fokker Planck equation is proved. In particular, the Boltzmann formulation allows the use of a direct Monte Carlo simulation based on the Nanbu-Babovsky scheme for efficient computation of the final configuration of the clusters. Applications to image segmentation are presented, particularly for the research context of Magnetic Resonance Images of thigh muscles.

Silvia CALIGARI

XXXV cycle

AN ELECTRO FLUID STRUCTURE MODEL
BASED ON AN EMBEDDED STRATEGY
WITH APPLICATION TO CARDIAC SIMULATIONS

joint work with Maria Giuseppina Chiara Nestola, Marco Favino and Rolf Krause

Computing a fully coupled cardiac model consists in connecting electrophysiology, active and passive mechanics and fluido dynamics.

We start from the electrophysiological environment, where transmembrane electric potential is described by the Monodomain system coupled with Luo-Rudy model for ionic currents. In this work it is used a space discretization based on finite elements method and a combination of an implicit scheme and Rush-Larsen method.
Then we introduce a novel framework inspired by the Immersed Boundary Method for predicting the fluid-structure interaction of complex structures immersed in laminar, transitional and turbulent flows.

The dynamic behavior of a deformable structure is simulated in a finite element framework by adopting a fully implicit scheme for its temporal integration, while the Navier-Stokes equations for the incompressible flow are discretized with high-order finite difference.
The structure and the flow solvers are coupled by using an L^2-projection method for the transfer of velocities and forces between the fluid grid and the solid mesh.
Lastly we insert into the structure's behavior an active force, which would represent muscle contraction in order to create an embryonal connection between the FSI environment end the electrophysiological one.

All numerical simulations are implemented using the open source framework Moose.

Fabio CREDALI

XXXVI cycle

MODEL ORDER REDUCTION
IN SUPPORT OF THE VIRTUAL ELEMENT METHOD

The Virtual Element Method allows us to solve PDEs on complex geometries without limitations on the degree of the polynomial contribution to the approximation.

An important aspect of this method is that we are not required to compute explicitly the basis functions of the VEM space because they are themselves solutions of PDEs. However, not computing the basis functions implies that several quantities are not computed exactly.
Two of these quantities are the bilinear form (for which the action of the non polynomial part is handled by a stabilization term) and the error, where the contribution of the non polynomial part is neglected.

We investigated different techniques for the explicit computation of (more or less rough approximations of) the basis functions of the VEM space, to be used in support of the Virtual Element Method (for instance, for the design of the stabilization term or for the post-processing of the solution).

To this aim, we resorted to the Reduced Basis Method. For the sake of comparison and for the offline step of the Reduced Basis Method, we also implemented a finite element solution of the appropriate PDEs for each degree of freedom of each element of the polygonal mesh.

Sergio A. GOMEZ
XXXVI cycle

A space–time Trefftz discontinuous Galerkin method for the linear Schrödinger equation

A space–time Trefftz discontinuous Galerkin method for the Schrödinger equation with piecewise-constant potential is proposed and analyzed.

Following the spirit of Trefftz methods, trial and test spaces are spanned by non-polynomial complex wave functions that satisfy the Schrödinger equation locally on each element of the space–time mesh. This allows for a significant reduction in the number of degrees of freedom in comparison with full polynomial spaces.

We prove well-posedness and stability of the method, and, for the one- and two-dimensional cases, optimal, high-order, h-convergence error estimates in a skeleton norm. Some numerical experiments validate the theoretical results presented.

Alen KUSHOVA

XXXVI cycle

ON A CONSERVATIVE ISOGEOMETRIC SCHEME FOR THE WAVE EQUATION

We consider the wave equation as a model problem for hyperbolic differential equations. The domain in which it is defined is a two-dimensional quarter of a ring, and the propagation coefficient may depend on the spatial variable.

The problem is completed with mixed Dirichlet/periodic boundary conditions, and suitable initial data.

We propose to tackle the problem in mixed form and a discretization based on isogeometric techniques, combined with the Crank-Nicolson method in time.

The aim is to conserve the total Energy of the system for long-time simulations.

The proposed results are compared with those obtained by solving the same problem with a method of Galerkin in space and Crank-Nicolson in time.

Some future perspectives will be discussed as a possible development of the proposed discretization.

Andrea MEDAGLIA

XXXVI cycle

Uncertainty quantification and control of kinetic models of tumour growth under clinical uncertainties

The processes of tumour formation are highly complex phenomena involving different stages starting from damages in the DNA molecules leading to harmful mutations in the cell's genome that are not repaired in absence of cellular apoptosis. This mechanism leads to an unregulated mitosis and then to the formation of tumours. These mutations may be triggered by many aspects, including both environmental and genetic factors.

In the last decades, extensive research efforts have been devoted to the mathematical formalisation of tumour growth dynamics and to the formalisation of growth factors. Among the easiest way to describe these biological phenomena can be found in the literature of population dynamics to describe the evolution in time of the volume of a tumour, based on first order ODEs.

In particular, in [11, 8] the authors proposed a statistical approach based on kinetic theory to describe the growth of tumour cells in terms of the evolution of a distribution function. The temporal variation of such distribution is considered as a result of elementary transitions occurring at the cellular level which takes environmental cues and random fluctuations into account. The expected cellular variations are coherent with the mentioned ODE-based models in suitable limits. Furthermore, through the explicit computation of the equilibrium states of the resulting Fokker-Planck-type equation, we get additional information on the decay of the tails.

Following the afore-mentioned works, in this talk we will develop a kinetic model of tumour growth taking into account also the effects of clinical uncertainties characterising the tumours' progression. The action of therapeutic protocols trying to steer the tumours' volume towards a target size will be investigated by means of suitable selective-type controls acting at the level of cellular dynamics [1, 2, 3, 4]. By means of classical tools of statistical mechanics for many-agent systems [7, 9], we will prove that it is possible to dampen clinical uncertainties across the scales [12].

To take into account the scarcity of clinical data and the possible source of error in the image segmentation of tumours' evolution, we will estimate empirical distributions of relevant parameters that are considered to calibrate the resulting model obtained from real cases of primary glioblastoma. Suitable numerical methods for uncertainty quantification (see, e.g. [5, 6, 10, 13]) of the resulting kinetic equations will be used, in the last part of the talk, to compare the effectiveness of the introduced control approaches in reducing the variability in tumours' size due to the presence of uncertain quantities.

[1] G. Albi, M. Fornasier, D. Kalise. *A Boltzmann approach to mean-field sparse feedback control.* IFAC PapersOnLine, 50(1): 2898–2903.

[2] G. Albi, L. Pareschi. *Selective model-predictive control for flocking systems*, Commun. Appl. Ind. Math. 9(2):4–21.

[3] G. Albi, M. Herty, L. Pareschi. *Kinetic description of optimal control problems and applications to opinion consensus.* Commun. Math. Sci., 13(6): 1407–1429, 2015.

[4] G. Albi, L. Pareschi, M. Zanella. *Boltzmann-type control of opinion consensus through leaders.* Phil. Trans. R. Soc. A, 372: 20140138, 2014.

[5] J. A. Carrillo, M. Zanella. *Monte Carlo gPC methods for diffusive kinetic flocking models with uncertainties.* Viet. J. Math., 47(4): 931-954, 2019.

[6] J. A. Carrillo, L. Pareschi, M. Zanella. *Particle based gPC methods for mean-field models of swarming with uncertainty.* Commun. Comput. Phys., 25(2): 508-531, 2019.

[7] C. Cercignani. *The Boltzmann Equation and its Applications.* Springer Series in Applied Mathematical Sciences, vol. 67. Springer-Verlag, New York.

[8] A. Medaglia, G. Colelli, L. Farina, A. Bacila, P. Bini, E. Marchioni, S. Figini, A. Pichiecchio, M. Zanella. *Uncertainty quantification and control of kinetic models of tumour growth under clinical uncertainties, International journal of non-linear mechanics.* In press.

[9] L. Pareschi, G. Toscani. *Interacting Multiagent Systems: Kinetic Equations and Monte Carlo Methods.* Oxford University Press, 2013.

[10] L. Pareschi, M. Zanella. *Monte Carlo stochastic Galerkin methods for the Boltzmann equation with uncertainties: space-homogeneous case.* J. Comput. Phys., 423: 109822, 2020.

[11] L. Preziosi, G. Toscani, and M. Zanella. *Control of tumour growth distributions through kinetic methods.* J. Theor. Biol., 514: 110579, 2021.

[12] A. Tosin, M. Zanella. *Uncertainty damping in kinetic traffic models by driver-assist controls.* Math. Contr. Relat Fields, 11(3): 681–713, 2021.

[13] D. Xiu. N*umerical Methods for Stochastic Computations.* Princeton University Press, 2010

Claudio TOMASI

XXXIV cycle

Multimodal route planning

Designing efficient multimodal route planning algorithms has been an active area of research in recent years, with focus on the computation of both road networks and public transportation networks.

The main challenge consists in finding a smart combination of the two kinds of networks, to quickly solve queries regarding journeys computation.

While road networks can be modeled as graphs, transportation networks are restricted by timetables, and therefore their structures can change depending on the time of the day.

In this talk, we start from notions of graph theory to introduce the common Dijkstra's algorithm, used to find shortest paths between points, to then extend the argument of routing on restricted networks.

We will approach recent algorithms which forget the notion of graph to only working on public transportation data, for then looking at their performance on case studies of metropolitan scales.

Eleonora VERCESI
XXXVI cycle

HARDNESS OF METRIC TSP INSTANCES:
A COMPUTATIONAL STUDY

In this talk, we investigate the difficulty of the metric Traveling Salesman Problem (TSP). Starting from the instances proposed in Benoit and Boyd [2008], we perform parameter tuning to make such instances hard-to-solve for concorde [Applegate et al., 2003], the state-of-art metric TSP solver. We compare the difficulty of such instances with other families appeared in the literature [Benoit and Boyd, 2008, Hougardy and Zhong, 2020, Zhong, 2021, Vercesi et al., 2021, Hougardy, 2014, Reinelt, 1991]. For each of these families, we analyze features computed from instances to investigate if it is possible to predict the hardness of an instance without effectively solving it. Some features, such as the variance of the cost matrix, have already been studied in the literature [Cheeseman et al., 1991]. Furthermore, we introduce new features that depend only on the cost vector of the TSP instance. We note that none of these parameters is completely able to predict the difficulty of an instance by itself. Thus, we combine such parameters by training a decision tree. The training set consists of instances from the families available in the literature with less than 80 nodes. We complete the dataset with random-easy instances to make it balanced. Preliminary tests show that the tree can predict easy and hard instances with an average accuracy higher than 92% both on the train and on the validation set.

[1] G. Benoit and S. Boyd. *Finding the exact integrality gap for small traveling salesman problems.* Mathematics of Operations Research, 33(4):921– 931, 2008.

[2] D. Applegate, R. Bixby, V. Chvátal, and W. Cook. *Implement- ing the Dantzig-Fulkerson-Johnson algorithm for large traveling salesman problems.* Mathematical programming, 97(1):91–153, 2003.

[3] S. Hougardy and X. Zhong. *Hard to solve instances of the Euclidean Traveling Salesman Problem.* Mathematical Programming Computation, pages 1–24, 2020.

[4] X. Zhong. *Lower bounds on the integraliy ratio of the subtour lp for the traveling salesman problem.* arXiv preprint arXiv:2102.04765, 2021.

[5] E. Vercesi, S. Gualandi, M. Mastrolilli, and L.M. Gambardella. *On the generation of Metric TSP instances with a large integrality gap by branch-and-cut.* arXiv preprint arXiv:2109.02454, 2021.

[6] S. Hougardy. *On the integrality ratio of the subtour LP for Euclidean TSP.* Operations Research Letters, 42(8):495 – 499, 2014.

[7] G. Reinelt. *TSPLIB—A Traveling Salesman Problem Library.* INFORMS Journal on Computing, 3(4):376–384, November 1991.

[8] Peter C Cheeseman, Bob Kanefsky, W.M. Taylor, et al. *Where the really hard problems are.* In IJCAI, volume 91, pages 331–337, 1991.

Lorenzo ZAMBON

XXXV cycle

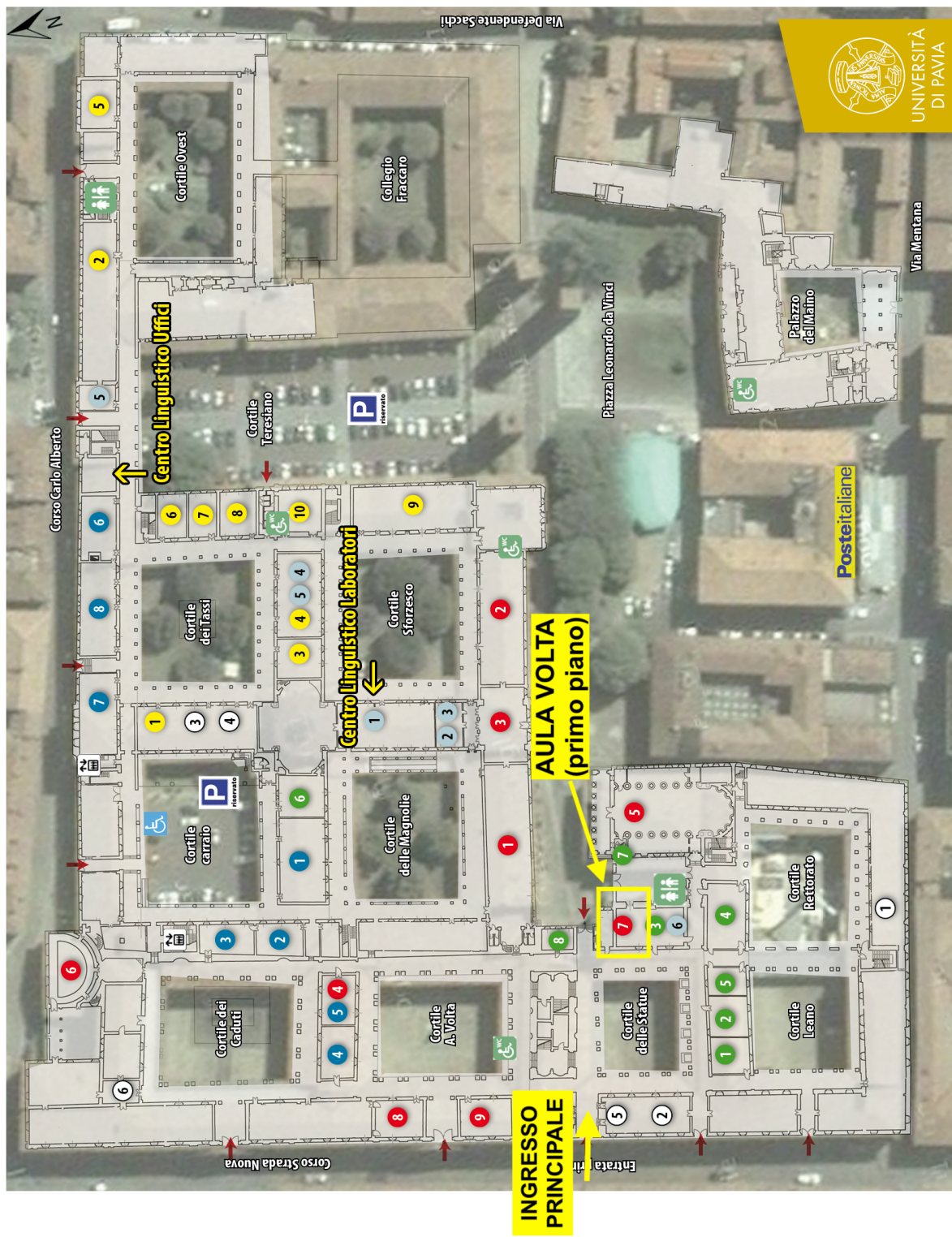## Probabilistic Reconciliation of Hierarchical Forecasts

In time series forecasting, we often deal with the problem of forecasting quantities that are subject to some linear constraints. Indeed, in many cases time series are organized in hierarchies: for instance, sales data of a given product may be aggregated at different levels, such as sub-region, region, and country levels. Hierarchies may also be temporal: forecasts of a single time series may be done at different frequencies, such as daily, weekly, or monthly. In both cases, we would like our forecasts to be coherent, that is, to satisfy the constraints given by the hierarchy. For example, the sum of the daily predictions of a week should equal the weekly prediction. In general, this does not happen, since most models compute the forecasts independently for each time series. The problem of finding coherent predictions starting from the base forecasts is called reconciliation.

In this talk, I will focus on the probabilistic case, in which forecasts are in the form of a probability distribution. The reconciled distribution is obtained by conditioning on the set of constraints. However, in most cases, it is not available in closed form. I will present some techniques to sample from the reconciled distribution and show some numerical results.

Venue

ALL EVENTS TAKE PLACE IN THE HISTORICAL AULA VOLTA OF UNIVERSITÀ DI PAVIA

(see map in next page)

UNIVERSITÀ DI PAVIA

Via Defendente Sacchi

Cortile Ovest

Collegio Fraccaro

Centro Linguistico Uffici

Corso Carlo Alberto

Cortile Teresiano

P riservato

Via Mentana

Palazzo del Maino

Centro Linguistico Laboratori

Cortile dei Tassi

Cortile Sforzesco

Piazza Leonardo da Vinci

Posteitaliane

AULA VOLTA (primo piano)

Cortile carraio

P riservato

Cortile delle Magnolie

Cortile Rettorato

Cortile dei Caduti

Cortile A. Volta

Cortile delle Statue

Cortile Leano

Corso Strada Nuova

Entrata

INGRESSO PRINCIPALE

(1) Rettorato (1° piano) - (2) Biblioteca Centrale (1° piano) - (3) Shop-Up - (4) Bar - (5) Bidellato - (6) Museo della Storia - (7) URP

Aule di Giurisprudenza
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- 6 Aula 6
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- 8 Aula informatica

Aule di Scienze Politiche
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Aule di Lettere
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- 6 Aula Archeologia
- 7 Aula Magna sotterranea
- 8 Aula Storia della Musica

Aule Centro Linguistico
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- 3 Aula Marconi 2
- 4 CL3 e Auletta CLA
- 5 Aula 7 Sc. Politiche
- 6 Aula VI Lettere

Aule CIM
- 5 Aula CIM

Aule Storiche
- 1 Aula del '400
- 2 Aula di Disegno
- 3 Aula Forlanini
- 4 Aula Foscolo (1° piano)
- 5 Aula Magna
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Corso di Dottorato in Computational Mathematics and Decision Sciences