PAVIA Capitale della Cultura d'Impresa 2023

UNIVERSITÀ DI PAVIA

Università della Svizzera italiana

CompMat

Spring Workshop 2023

Joint PhD in

COMPUTATIONAL MATHEMATICS, LEARNING AND DATA SCIENCE

May 22nd, Università di Pavia

The Spring Workshop targets MSc graduates interested in pursuing doctoral studies in Computational Mathematics, Machine Learning, Statistics, and related fields. It aims to promote academic-industrial collaborations to create research and innovation opportunities.

PROGRAM
&
BOOK of ABSTRACT

Program

8:45 **Registration**

9:15 **Opening round table**

Chair: Prof. S. Figini (PhD Vice Coordinator, Dept. of Political and Social Sciences, University of Pavia)

Prof. G. De Nicolao (Direttore Scuola di Alta Formazione Dottorale, University of Pavia)

Prof. L. F. Pavarino (PhD Coordinator, Dept. of Mathematics, University of Pavia)

Prof. R. Krause (Coordinator, Università della Svizzera Italiana)

Dr. F. Caracciolo (Vice Direttore Generale Assolombarda)

Dr. A. Sassi (Partner, Federated Innovation Milano Innovation District (MIND))

9:45 **Spring Workshop 2023 - motivations**

Dr. E. Ballante (Post-doc, Dept. of Political and Social Sciences, University of Pavia)

Dr. N.M.M. Huynh (Post-doc, Dept. of Mathematics, University of Pavia)

Session 1: Digital technologies for Health: an institutional viewpoint

Chair: Prof. G. Toscani (Emeritus Professor, University of Pavia)

10:00 **Fondazione Bruno Kessler**, Dr. G. Jurman

10:30 **International Center for Advanced Computing in Medicine (ICAM)**

Prof. A. Lascialfari (Dept. of Physics, University of Pavia)

10:45 **Future4Health in Pavia**

Dr. G. Bonelli (IRCCS Mondino - Direttore Generale)

Dr. R. Bergamaschi (IRCCS Mondino - Direttore Scientifico)

Prof. A. Venturi (IRCCS Policlinico S. Matteo - Presidente)

Prof. V. Bellotti (IRCCS Policlinico S. Matteo - Direttore Scientifico)

11:00 **Coffee break**

Session 2: New frontiers in methodological and computational data analysis for neuroimaging, pharma and cardiology

Chair: Prof. A. Pichiecchio (Dept. of Brain and Behavioral Sciences, University of Pavia and IRCCS Mondino)

11:30 **IRCCS Mondino**, Prof. A. Pichiecchio
L. Barzaghi (CompMath PhD) and Dr. G. Colelli (Post-doc, IRCCS Mondino)

12:00 **Alumni**,
Dr. S. Botti (Post-doc, University of Pavia and Università della Svizzera Italiana)

12:20 **SEA Vision group**, Dr. A. Codegoni and Dr. G. Lombardi

12.40 **PhD candidate**, R. Cabini (CompMath PhD)

13:00 **Lunch break**

Session 3: Data driven approaches in health

Chair: Prof. L. Pavarino (PhD Coordinator, Dept. of Mathematics, University of Pavia)

14:10 **Medical Statistics and Genetic Epidemiology**
Prof. L. Bernardinelli (Dept. of Brain and Behavioral Sciences, University of Pavia)
Prof. D. Gentilini (Dept. of Brain and Behavioral Sciences, University of Pavia)
B. Tarantino and Prof. M. Grassi (Dept. of Brain and Behavioral Sciences, University of Pavia)

14:30 **Public Health,** Prof. M. Zanella (Dept. of Mathematics, University of Pavia)

14:50 **PhD candidate**, A. Medaglia (CompMath PhD)

15:10 **Quick break**

Session 4: Opportunity and challenges in real-world projects

Chair: Prof. S. Figini (PhD Vice Coordinator, Dept. of Political and Social Sciences, University of Pavia)

15:20 **Alumni**, Dr. C. Tomasi (Post-doc, Dept. of Mathematics, University of Pavia)

15:40 **RES group**, F. Bonelli

16:00 **Oracle Labs**, Dr. M. Arnaboldi

16:20 **Assicurazioni Generali**, M. Malosetti, Dr. M. Qyrana and A. Bonaita

16:40 **Istat, Centre for Trusted Smart Statistics**, Dr. A. Righi

17:00 **Closing remarks**

Our partners

(in alphabetic order)

Assicurazioni Generali
www.generali.com

FernUniversität in Hagen
www.fernuni-hagen.de

Fedegari group
https://fedegari.com/

Fondazione Bruno Kessler
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International Center for Advanced Computing in Medicine
www.icam.unipv.it

IRCCS Mondino
www.mondino.it

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Istat
www.istat.it

Oracle Labs
www.labs.oracle.com

RES group
www.res-group.eu

SEA Vision group
www.seavision.it

Università della Svizzera Italiana
www.usi.ch

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/matcomp23/

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Computational Mathematics, Learning and Data Science UniPV-USI

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Companies and partners talks

Assicurazioni Generali

AI in Insurace: l'esperienza Generali e la partnership con Pavia

M. Malosetti, Dr. M. Qyrana and A. Bonaita

Our presentation focuses on the utilization of artificial intelligence in the insurance industry. We will describe how an insurance company harnesses AI and its applications, highlighting the research areas we plan to delve into in the upcoming years. Additionally, we will share the firsthand experience of a former doctoral student who has joined our team, bringing their expertise in AI. Our aim is to provide a comprehensive overview of the potential of AI in the insurance sector.

Fondazione Bruno Kessler

Data Science for Health @ Fondazione Bruno Kessler: methods, assets and projects

Dr. Giuseppe Jurmann

The world of Data Science applied to Life Sciences and Computational Biology is characterized by the need of dealing with a large number of heterogeneous situations, encompassing a widely diverse landscape of data, methods and results.

In this talk I will provide a brief overview of some of the arising challenges and opportunities, with a focus on the applications related to Artificial Intelligence in general and Machine/Deep Learning in particular.
Finally, I will conclude by showing a brief portfolio of some of the projects and activities my research unit DSH is currently involved in, together with the strategies used in their analysis.

IRCCS Mondino

Mathematical models and machine learning application on biomedical imaging

Prof. A. Pichiecchio (Dept. of Brain and Behavioral Sciences, University of Pavia and IRCCS Mondino)
L. Barzaghi (CompMath PhD, University of Pavia)
Dr. G. Colelli (Post-doctoral researcher, IRCCS Mondino)

The Advanced Imaging and Radiomics Center at IRCCS Mondino Foundation is promoting the application of mathematical and machine learning models for an ever-improving insight of various diseases affecting in particular the brain and the musculoskeletal tissue.

Muscoloskeletal tissue Quantitative muscle Magnetic Resonance Imaging (qmMRI) is considered an imaging biomarker in Neuromuscular disorders (NMDs) being able to quantitatively monitor muscle involvement through dedicated MRI sequences and post-processing software. For examples, Multi-echo Spin echo (MESE) sequence is sensitive to the relaxation time of water molecules (wT2) which is correlated to muscle edema [1], whereas Dixon Imaging is sensitive to the percentage of intramuscular fat (FF) [2]. The reconstruction of wT2 and FF maps, however, are time-consuming and require outdate computer architecture. Significant shortening of time in parameter extrapolation is desirable to accelerate the clinical investigation of NMDs. We propose a physics-informed encoder-decoder U-net Deep Learning architecture with Residual Block (Resnet [3]) for wT2 and FF regression task from an heterogenous cohort of NMDs. The proposed DL model predict wT2 with good accuracy and high time efficiency. We aim to extend the prediction to FF parameter to facilitate the quantitative approach in the diagnosis and in the clinical follow-up of NMDs.

Brain In the context of personalized medicine applied to neurology and neuroradiology, mathematical models have been introduced to describe the tumor growth[4] and a brain portion. In particular, the tumor growth was described using the statistical approach of many-agents systems, also taking into account the clinical uncertainties related to patient variability, whereas a brain portion was described with a quantum field theory and simulated through a feed-forward neural network.

[1] N. Locher et al. *Quantitative water T2 relaxometry in the early detection of neuromuscular diseases: a retrospective biopsy-controlled analysis.* Eur. Radiol. 32(11): pp. 7910–7917 (2022).

[2] P.G. Carlier et al. *Skeletal muscle quantitative nuclear magnetic resonance imaging and spectroscopy as an outcome measure for clinical trial.* J. Neuromuscul Dis. 3(1): pp. 1–28 (2016).

[3] K. He et al. *Deep Residual Learning for image recognition.* IEEE Conference on Computer Vision and Pattern Recognition (CVPR), pp. 770–778 (2016).

[4] A. Medaglia et al. *Uncertainty quantification and control of kinetic models of tumour growth under clinical uncertainties.* Int. J. Non-Linear Mechs. 141, 103933 (2022).

Public Health

Mathematical models for vaccine hesitancy

*Prof. M. Zanella**

joint work with Prof. A. Odone**

*Department Mathematics, University of Pavia
**Department of Public Health, Experimental and Forensic Medicine, University of Pavia

In this talk, we introduce a mathematical description of the impact of opinion heterogeneity in the spread of infectious diseases by integrating an epidemiological compartmentalization with a kinetic model for population-based social features. The resulting set of Boltzmann-type equations models the evolution over time of the densities of opinions of compartmental models. Additionally, we examine the mathematical connection between these models and available data and NLP (Natural Language Processing) methods. By deriving the evolution of observable quantities from appropriate macroscopic limits of classical kinetic theory, we establish a foundation for comprehending the effects of vaccination campaigns in social systems.

This analysis provides valuable insights that can be applied to address important public health concerns, particularly those related to the impact of vaccination campaigns in social systems. By understanding the dynamics of opinion heterogeneity and its interplay with infectious disease transmission, we gain a deeper understanding of how vaccination efforts can be optimized and tailored to specific populations. This knowledge allows us to design more effective strategies for promoting vaccination acceptance, addressing vaccine hesitancy, and mitigating the spread of infectious diseases within communities. By bridging the gap between mathematical modeling, epidemiology, and social science, our findings contribute to the development of effective policies and interventions that can safeguard public health and enhance the overall well-being of society.

Medical Statistics and Genetic Epidemiology
University of Pavia

A Causal Inference Approach to the Genetic, Environmental and Phenotypic Determinants of Susceptibility to and (course of) Multiple Sclerosis

*Prof. L. Bernardinelli**

joint work with Prof. C. Berzuini**, Dr. T. Fazia*, Dr. A. Nova*

*Department of Brain and Behavioral Sciences, University of Pavia
** Center of Biostatistics, University of Manchester, UK

Multiple Sclerosis (MS) is a chronic autoimmune disease of the Central Nervous System (CNS), which involves demyelination of CNS cells. Its complex and largely unknown etiology involves genetic, environmental and lifestyle determinants. Its onset is typically, but not necessarily, observed during the 20–40 (years) age interval.

My research group has a 30-year long experience in the study of MS. We investigate the way genetic information penetrates the early layers of the biological cascade and, from them, it propagates along (yet unknown) molecular pathways that affect susceptibility to the disease, and its subsequent course. Discovery of these paths is the necessary first step toward our scientific objectives, that are explaining WHY we get the disease, and HOW we can cure it.

This enterprise has led us to develop and integrate diverse types of expertise, that range from genetics, informatics, data science and, importantly, causal inference. The framework we have developed is not specific to a particular disease... it is of broad relevance in the general field of health care. Data science methods, for example, help us perform an integrated analysis of data collected at different levels of the biological cascade... genetic... epigenetic... gene expression... protein concentration, up to more readily visible putative causal precursors of the disease, such as, for example, D vitamin and obesity. Part of the study data consists of patient-level longitudinal information about disease course extracted from the UK Biobank, allowing for censoring. An integrated analysis of these data, jointly with, say, genetic information, and the need to account for censoring invites the use of sophisticated modelling methods within the framework of causal inference theory. The latter is required to avoid or attenuate the typical biases encountered in the analysis of observational data, for example due to confounding and selection. An important class of methods in this context is based on principles of Mendelian Randomisation (MR), where genetic variation is used as an "instrument" to assess the putative causal effect of a phenotype of interest on disease, even in the presence of unobserved confounding between these. Methods of colocalization may be used in conjunction. Also part of our research is elucidation of gene environment interactions, where genes are seen as capable of modifying the effects of disease-inducing environmental or lifestyle factors.

Methodological refinements will be called for. One of these could be required to deal with situations where the effect of an exposure X on an outcome Y is investigated under conditioning on an event located along the causal path from X to Y. The problem being that in such situations, non-causal associations between X and Y will generally be induced. One example of this situation arises in the study of the causal effect of a gene X on course of the disease (eg in the search for new disease therapies), the conditioning here being on disease onset.

The questions we address are relevant from a scientific point of view, as they improve our insight into the mechanisms of the disease, and they may, in addition, lead to the identification of pharmacological targets toward the development of advanced therapies for MS.

Whole-genoMe epIgenetic aNalysis and deep phenotyping: a combined approach to disentangle the aUtism SpeCtrUm compLExity

*Prof. D. Gentilini**

joint work with R. Cavagnola*, Prof. N. Brondino*

*Department of Brain and Behavioral Sciences, University of Pavia

Autism Spectrum Disorders (ASD) pose a significant challenge in the classification and diagnosis of patients. One main problem that can arise from misclassification of ASD patients is that they may receive inappropriate treatment or interventions that do not address their specific needs. This can result in poor outcomes for the patient, including decreased quality of life and limited social and cognitive development. Misclassification can also affect research studies and clinical trials by including patients who do not actually have ASD, leading to inaccurate results. Therefore, accurate and reliable classification of ASD patients is essential for effective treatment and research. It has been described that the condition arises from a combination of genetic, epigenetic, and environmental factors. While each of these factors is recognized as a main player in the development of ASD, it is not yet clear how they interact to produce the phenotype.

The goal of this project is to enhance the classification of individuals with ASD by combining genetic and epigenetic data with in-depth phenotyping information. This two-step approach involves detailed phenotyping of individuals with ASD and the genomic and epigenomic characterization of these individuals to identify and describe genetic variations and incorporate epigenomic data. Novel analysis methods, such as Stochastic Epigenetic Mutation (SEMs) analysis, will be used to identify rare epigenomic changes that could contribute to the development of ASD. Moreover stochastic epigenetic changes could serve as an indicator of epigenetic drift, allowing the study of environmental factors on ASD.

SEMgraph: An R package for casual network inference of high-throughput data with structural equation models

B. Tarantino and Prof. M. Grassi**

**Department of Brain and Behavioral Sciences, University of Pavia*

With the advent of high-throughput sequencing (HTS) in molecular biology and medicine, the need for scalable statistical solutions for modeling complex biological systems has become of critical importance.

Combining network analysis and causal inference within the framework of Structural Equation Modelling (SEM), we developed the R package `SEMgraph`.
It provides a fully automated toolkit, managing complex biological systems as multivariate networks, ensuring robustness and reproducibility through data-driven evaluation of model architecture and perturbation, that is readily interpretable in terms of causal effects among sys- tem components.
Moreover, `SEMgraph` offers the possibility to predict the output value for new cases for whom we have scores on the genes/predictors using the model estimated from the current sample, taking into account the structure defined in the SEM.

We will illustrate the utility of our `SEMgraph` package in an empirical example with a Coronavirus disease (COVID-19) RNA-seq dataset (GEO accession: GSE172114).

`SEMgraph` is available on https://cran.r-project.org/web/packages/SEMgraph.

Istat

The Istat path to Trusted Smart statistics

Dr. A. Righi

This presentation is aimed at describing the role that Istat is called to play in the transformation into official statistics of the amount of data that derives from the digitalization and datafication of society. We explain what the so-called Trusted Smart Statistics are, what they are for, and the criteria used by Istat in the production of new outputs. We describe also the path that began almost 10 years ago and led from the first trials to the set of a dedicated production process.

We then show an overview of new outputs made using Big Data sources and innovative methods, the collaborations undertaken and some of the methodologies used. These outputs derive from a plurality of sources ranging from scanner data to textual data from social networks and the Internet, from mobile phone data to financial transaction data.
The experiments launched have produced very encouraging results and Istat have now some outputs integrated into the official production besides experimental statistics and other research projects.

The effort to innovate methods has involved the entire Institute and has required innovative organizational solutions. However, Istat collaborated a lot at the EU or UN level, with other statistical institutes, universities, and private partners.

We conclude with a brief assessment of the benefits and challenges that the new sources pose to official statistics. As the future of the development of these TSSs lies in the increasingly broad access to privately-held data, this poses some issues related to the considerable costs for the Official statistics that this entails and to the not-foreseeable risks that company changes bring and which can jeopardize statistical productions. Moreover, the ongoing transformation process also raises the issue of the acquisition of new skills for the staff and/or new data scientists to cope with the new types of statistical treatment of large databases.

Oracle Labs

How do you feel?

Dr. M. Arnaboldi

A story about questioning yourself. In particular, a story about how I questioned myself during my career so far. The turning points that lead me from academia to industrial research at Oracle Labs.

SEA Vision group

A Change Detection approach for Line Clearance

Dr. A. Codegoni and Dr. G. Lombardi

Ensuring Line Clearance is a vital concern for production and packaging companies, especially for pharmaceutical and cosmetic businesses to prevent product contamination and machinery damage from remnants of previous processes.
Manual inspection of complex production lines results in significant downtime, which can be reduced by utilizing cameras and artificial vision algorithms to identify anomalies at strategic locations. However, several challenges must be addressed, such as developing a scalable model capable of identifying unseen objects during training and avoiding false positives caused by moving machinery parts.
A flexible model adaptable to various machines is required to meet customer requirements.

Our model's efficacy was validated on our industrial dataset and also by comparing it to existing literature in remote sensing change detection.
Despite being significantly smaller (13 to 140 times) and more computationally efficient (at least 1/3 GFlops) than comparable models, our model outperforms the state-of-the-art by at least 1% on both F1 score and IoU on the LEVIR-CD dataset and more than 8% on the WHU-CD dataset.

PhD candidates and Alumni presentations

Alumni

Mathematical and numerical modelling of cardiac stem cells and regenerative medicine

Dr. S. Botti

Post-doctoral researcher, University of Pavia and Università della Svizzera Italiana

The discovery of induced pluripotent stem cells in 2006 has transformed the field of Regenerative Medicine, specifically Regenerative Cardiology, through the development of induced pluripotent stem cells-derived cardiomyocytes (hiPSC-CMs), [1]. Mathematical models of the ionic currents through hiPSC-CM's membrane have been developed for the immature ventricular-like phenotype using systems of stiff ordinary differential equations. However, recent experimental techniques enable the growth of hiPSC-CMs towards a more adult cardiac phenotype, [2], which necessitates the development of novel, phenotype-specific in-silico models of hiPSC-CM ionic currents. The first part of this talk will focus on recent research on these new ionic models, which are critical for creating accurate cardiac in-silico simulations based on biophysically detailed representations of regenerated heart tissue.

The second part of the talk will focus on recent research in Computational Cardiology aimed at overcoming the limitations of current computational models, which approximate the cardiac tissue using a spatial scale that is several times larger than the actual cell size. Novel cardiac cell-by-cell mathematical formulations that can represent the interaction of many cardiac cells, the extracellular space, and the cell membrane at a microscopic scale have been constructed and analyzed. However, numerical simulation of these novel cell-by-cell models is challenging due to their increased space resolution and heterogeneous cellular structure. Therefore, proper numerical methods and high-performance solvers are necessary to obtain efficient numerical simulations of these cardiac microscopic models, [3]. Ongoing research work is also exploiting the use of deep learning techniques for cardiac ionic models, in particular using Physics-Informed Neural Networks and Deep Operator Networks. The outcomes of these new models and numerical methods are expected to significantly contribute to advancing the understanding and treatment of cardiac diseases.

[1] K. Takahashi, S. Yamanaka (2006). *Induction of Pluripotent Stem Cells from Mouse Embryonic and Adult Fibroblast Cultures by Defined Factors.* Cell 126.4, 663–676 (2006).

[2] S. Botti et al. *An in silico Study of Cardiac hiPSC Electronic Maturation by Dynamic Clamp.* In Functional Imaging and Modeling of the Heart - FIMH 2023, eds.: O. Bernard, P. Clarysse, N. Duchateau, J. Ohayon, M. Viallon, to appear (2023).

[3] N.M.M. Huynh et al. *Convergence analysis of BDDC preconditioners for hybrid DG discretizations of the cardiac cell-by-cell model.* arXiv preprint arXiv:2212.12295 (2022).

Evaluating Public Transport by Multimodal Schedule-based Routing

Dr. C. Tomasi

Post-doctoral researcher, University of Pavia

One of the main EU policy priorities under the European Green Deal is to achieve climate neutrality by 2050, and transport is a key sector in this effort due to its significant contribution to greenhouse gas emissions. To monitor the performance of public transport in the EU, the European Commission uses comprehensive data to compute accessibility-to-opportunities measures related to public transport.
These measures are based on various Operations Research challenges, such as the schedule-based time-dependent all-pairs scheduling problem of calculating accessibility measures across Europe. While previous methods have considered multiple modes of transport for this problem, they have not been able to effectively handle large in- stances, such as entire European countries.

We propose a new method, based on the RAPTOR algorithm [1], that addresses this limitation by considering multiple modes of transport for large instances.
Our tool aims to support the design and implementation of policies promoting equitable access to public transport, and we apply it to a specific set of European countries with varying characteristics in terms of public transport coverage and population density.

The goal is to assess the number of relevant opportunities, or essential services, that are accessible through the transport network.

[1] D. Delling, T. Pajor, and R.F. Werneck. *Round-based public transit routing.* Transp. Sci. 49, 591–604 (2015).

PhD candidates

Integration of a Deep Learning-based method into a Magnetic Resonance Fingerprinting protocol for quantifying T_1 and T_2 maps.

R. F. Cabini

CompMath PhD candidate, University of Pavia

joint work with L. Barzaghi[1], D. Cicolari[2,3,4,5], S. Figini[1], M. Filibian[6,7], A. Pichiecchio[8,9], A. Lascialfari[2]

[1] Department of Political and Social Sciences, University of Pavia
[2] Department of Physics, University of Pavia
[3] Department of Physics, University of Milano
[4] INFN National Institute for Nuclear Physics, Milano
[5] Department of Medical Physics, ASST GOM Niguarda Milano
[6] Centro Grandi Strumenti, University of Pavia
[7] INFN National Institute for Nuclear Physics, Pavia
[8] Department of Brain and Behavioral Sciences, University of Pavia
[9] IRCCS Mondino, Pavia

Magnetic Resonance Fingerprinting (MRF) simultaneously measures multiple tissue properties through a more time-efficient acquisition routine than standard mapping techniques [1]. MRF post-processing methods based on dictionaries require significant computational time and storage capacity.
Hence, we propose a Deep Learning (DL) model and a hyperparameter optimization strategy to reconstruct T_1 and T_2 maps acquired with the MRF methodology. We applied two different MRF sequence routines [2, 3] to acquire images of ex vivo rat brain phantoms using a 7 Tesla preclinical scanner. We trained the DL model using experimental data, completely excluding the use of any theoretical MRI signal simulator. To select the best combination of the DL parameters we implemented an automatic hyperparameter optimization strategy. The key aspect of this technique is to include all the parameters to the fit, allowing the simultaneous optimization of the Neural Network (NN) architecture, the structure of the DL model and the supervised learning algorithm.
We compared the reconstruction performances of the DL technique with those achieved from the traditional dictionary-based method on an independent dataset. The DL approach improved the estimation of T_1 and T_2 maps for both the MRF sequences and the computational time required for the estimation. We analyzed the reconstruction performance as a function of different acquisition sequence lengths and k-space sampling percentages. The proposed DL method reached good results even with a lower number of MRF images and a reduced k-space sampling percentage compared to the dictionary-based method. These results suggest that this DL methodology may offer an improvement in reconstruction accuracy as well as a speed up of MRF for preclinical investigations.

[1] Ma et al. *Magnetic resonance fingerprinting.* Nature 495.7440, 187-192 (2013).

[2] Y. Gao, et al. NMR in Biomedicine 28.3, 384-394 (2015).

[3] Zhao et al. IEEE transactions on medical imaging 38.3, 844-861 (2018).

Kinetic models in mathematical epidemiology: optimal control in the presence of behavioural uncertainties

A. Medaglia

CompMath PhD candidate, University of Pavia

Kinetic equations have been recently employed to mimic the emergence of collective phenomena in life sciences. In this direction, during the COVID-19 pandemic, compartmental models describing the spreading of an infectious disease coupled with a kinetic-type description of the distribution of social contacts among the population have been developed [1]. In fact, it has been widely recognized that social structures can play an important role in the spreading of an epidemic, being a potential cause of pathogen transmission.

In more detail, the microscopic model describing the contact evolution is based on a simple transition operator with uncertain parameters [3]. At the kinetic level, this model can produce a range of equilibrium distributions, ranging from slim-tailed Gamma-type distributions to power-law-type distributions, depending on the introduced uncertainties. These equilibrium distributions are crucial for closing the hierarchy of moments that define the macroscopic observable trends of the infection, taking into account the incomplete knowledge of the actual contact distribution.

Furthermore, the presence of available data permits to investigate such models quantitatively. However, their statistical description does not possess universal patterns and may vary spatially and temporally. It is therefore essential to design optimal control strategies at the level of the agents [2], mimicking the effects of non-pharmaceutical interventions (NPIs) to limit efficiently the number of infected cases in the presence of uncertainties.

The epidemiological parameters are then calibrated on real-world data and, thanks to a retrospective analysis, it is possible to study the effects of a minimal lockdown strategy achieved by reducing the sociality of the agents with a large number of daily contacts.

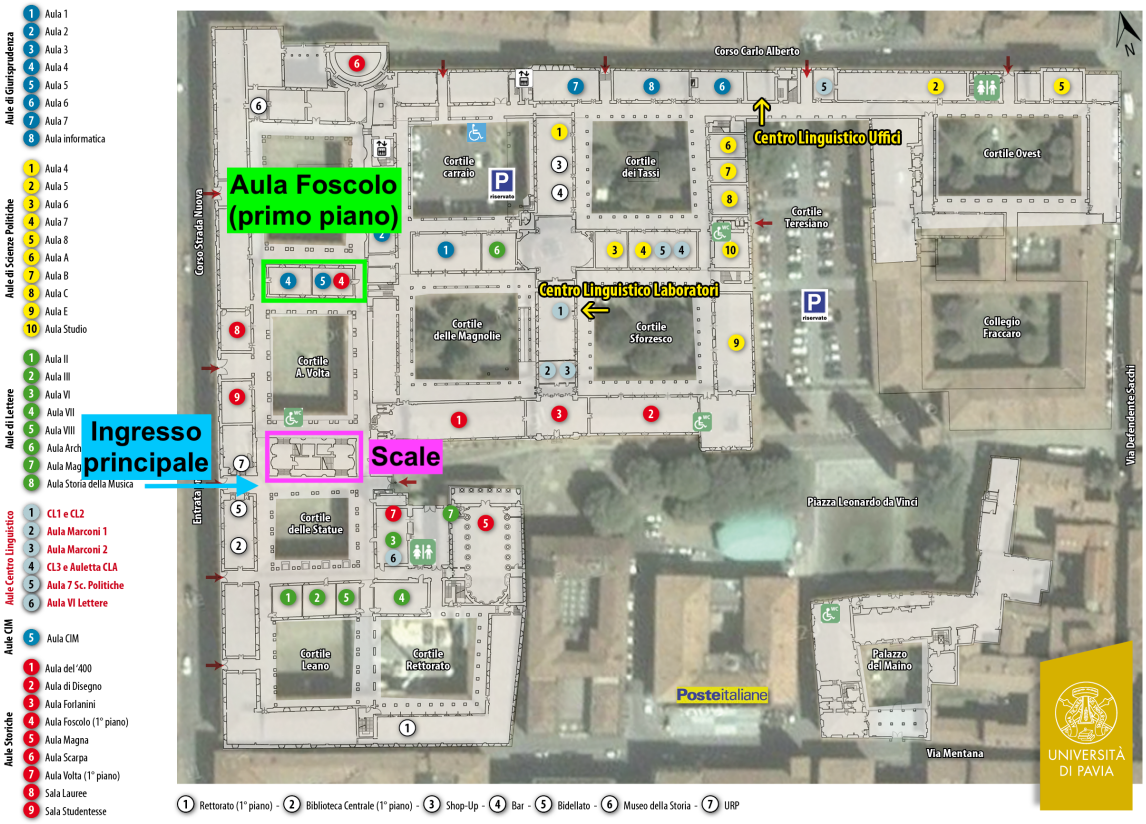
[1] G. Dimarco, B. Perthame, G. Toscani, and M. Zanella. *Kinetic models for epidemic dynamics with social heterogeneity.* J. Math. Biol., 83(1):1-32 (2021).

[2] G. Dimarco, G. Toscani, and M. Zanella. Optimal control of epidemic spreading in the presence of social heterogeneity. Phil. Trans. R. Soc. A., 380(2224):20210160 (2022).

[3] J. Franceschi, A. Medaglia, M. Zanella. *On the optimal control of kinetic epidemic models with uncertain social features.* arXiv preprint arXiv:2210.09201 (2022).

Venue

All events take place in the historical Aula Foscolo of University of Pavia



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