M4H 2026

Mathematics for our Health Workshop

Second edition

Book of Abstracts

November 11–13, 2026

Politecnico di Milano, Milan, Italy

Aula Rogers, Building 11, Via Ampère 2, Milano

https://www.mate.polimi.it/events/M4H26/

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About the workshop

The second edition of the *Mathematics for our Health* (M4H) Workshop brings together leading experts working at the intersection of mathematics, data science and medical sciences, to explore innovative mathematical and computational models for improving medical care.

Presentations and posters highlight how mathematical models, numerical and statistical methods, and machine learning techniques can support the development of precision medicine, optimise the allocation of healthcare resources, and enhance the analysis and management of multimodal patient data. The workshop also showcases some results of Line 2 (*Mathematics for Sustainable Development*) of the Department of Excellence grant funded by the Italian Ministry of University and Research.

This activity promotes interdisciplinary collaboration to strengthen the role of mathematics in addressing major medical and societal challenges.

This booklet collects the abstracts of the keynote lectures and of the invited talks of the workshop, listed in alphabetical order of the speaker, together with the programme of the discussion sessions.

Dates	November 11–13, 2026
Venue	Aula Rogers, Building 11, Via Ampère 2, Milano (Piola station, metro line MM2)
Posters	Aula Vetrata – Trifoglio, Building 13, Via Bonardi 9, Milano
Website	`https://www.mate.polimi.it/events/M4H26/`
Contact	math4health-dmat@polimi.it

Committees

Scientific Committee

- Luca Dede' (chair)
- Pasquale Ciarletta
- Francesca Ieva
- Laura Maria Sangalli
- Paolo Zunino

Organizing Committee

- Francesco Regazzoni (chair)
- Francesca Bonizzoni
- Ivan Fumagalli
- Stefano Pagani
- Andrea Signori

All the members of both committees are members of the Department of Mathematics, Politecnico di Milano.

The scientific coordinator of Line 2 (*Mathematics for Sustainable Development*) of the Department of Excellence grant is Luca Formaggia.

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Keynote lectures

Alexander R. A. Anderson

Director, Center of Excellence in Evolutionary Therapy, Richard O. Jacobson Distinguished Endowed Chair, Integrated Mathematical Oncology Department, H. Lee Moffitt Cancer Center & Research Institute

Phase I trials in cancer: from board to bench to bedside and back again

Cancers are complex evolving systems that adapt to therapeutic intervention through a suite of resistance mechanisms, therefore whilst the maximum tolerated dose (MTD) therapies generally achieve impressive short-term responses, they unfortunately give way to treatment resistance and tumor relapse. The importance of evolution during cancer treatment is becoming more widely accepted. However, MTD treatment strategies continue to dominate precision oncology. Adaptive therapy is an evolutionary therapy that aims to slow down the emergence of drug resistance by controlling tumor burden through competition between drug sensitive and resistant cell populations. This approach was developed through mathematical model driven insights and has been shown to work in preclinical animal models (prostate, ovarian, melanoma, breast) and in pilot clinical trials (NCT02415621; NCT05189457; NCT03543969). In this talk we will discuss how mathematical models and machine learning can be used to optimize treatment strategies, including adaptive therapy, and drive Phase i (imaginary) trials. We will highlight how mathematical model driven digital twins can: (i) Integrate patient variability; (ii) Bridge between bench and bedside; (iii) Be calibrated from historic clinical data; (iv) Drive Phase i trials; (v) Stratify and optimize treatment; (vi) Predict novel trial outcomes.

Jessica Barrett

Research Professor at MRC Biostatistics Unit, University of Cambridge

Using electronic health records for healthcare research: potentials and pitfalls

Routinely collected healthcare data is becoming more commonly used for healthcare research. The increasing availability of such data promises advantages in the shape of largescale, representative data, but also brings many challenges which require statistical innovation. I will highlight some of these promises and challenges using three examples illustrating the use of routinely collected data, including modelling lung function trajectories of cystic fibrosis patients, dynamic prediction of rehospitalization risk for patients admitted to hospital with heart failure and the use of multi-state modelling to characterize disease transitions for patients with multimorbidity.

Kathryn Hess Bellwald

Full Professor, Brain Mind Institute and Mathematics Institute, EPFL

A topological and geometric pipeline for detecting and analyzing cyclic cell processes

In this talk I will introduce CocycleHunter, a pipeline for identifying and analyzing circular structure in gene expression data, which integrates methods from topological data analysis with geometric lead-lag analysis. Our method provides a powerful, cohomology-based technique for estimating the phase of genes exhibiting cyclic expression patterns (gene cascades), which has been validated on synthetic RNA transcription models, as well as on real datasets. I'll explain the math behind the pipeline and illustrate its application to gene expression data, providing novel insights into how cell processes intertwine. This is joint work, led by Kelly Maggs and Markus Youssef, with the collaboration of Cyril Pulver, Jovan Isa, Tâm Nguyên, Wouter Karthaus, Heather Harrington, and Paolo Dotto.

Andre Marquand

Professor - Donders Institute / Radboud University Medical Centre, Nijmegen, the Netherlands.

Combining statistical and machine learning innovations with big data for predicting mental health

Neuroscience and mental health science has now transitioned into the era of big data and is witnessing an explosion of the number and types of measures that are measured in clinical populations. This has given rise to the emerging field of population neuroscience, which holds potential to improve prediction of disease states in many clinical conditions. However, achieving this objective places increasing demands on the statistical and machine learning methodology that are used to analyse these cohorts, namely to understand population variation in imaging derived markers and their relationship between environmental and behavioural factors. In this talk I will describe statistical innovations that enable us to make progress in this domain, including brain charting techniques that allow us to chart variability at the level of each individual, techniques rooted in the statistics of extremes that allow us to reconceptualise pathology as extreme deviations from an expected pattern and innovative timeseries analysis methods for quantifying behaviour and environment based on passive smartphone monitoring and remote sensing satellite data. I will illustrate this discussion by showing applications of these methods to cross-diagnostic psychiatric cohorts and I will argue that these innovations provide a principled method to move beyond simple statements about group averages and can provide a way to dissect the inherent heterogeneity in mental disorders, ultimately paving the way to earlier and personalised interventions.

Charles Taylor

Professor, Department of Internal Medicine, W.A. "Tex" Moncrief, Jr., Chair in Computational Medicine, Oden Institute for Computational Engineering & Sciences, Director, Center for Computational Medicine, Dell Medical School

Patient-specific modeling of blood flow in arteries: from the academy to the clinic

Patient-specific computational models of blood flow in arteries derived from medical imaging data have generated significant interest since they were introduced 30 years ago. This is a new approach in medicine whereby predictive computational models can be used to evaluate and select alternate treatment strategies. Patient-specific models of coronary artery blood flow constructed from coronary CT angiography (cCTA) images leveraging deep learning A.I. methods and using computational fluid dynamics have transformed the diagnosis of heart disease. Such noninvasive, computational models have provided safer, less expensive and more efficient procedures as compared to the standard of care that often involves nuclear imaging and invasive cardiac catheterizations. Such image-based computations require an accurate segmentation of the coronary artery lumen from cCTA images and employ biologic principles relating form (anatomy) to function (physiology). HeartFlow developed a non-invasive test, FFRCT, based on computing flow and pressure in the coronary arteries. FFRCT has been validated against invasive pressure measurements in more than 1000 patients and demonstrated to improve care in over 100 clinical studies enrolling more than 100,000 patients. At present, FFRCT has been used for routine clinical decision making in more than 1500 hospitals that have served over 600,000 patients in the United States, Europe, and Japan. In the United States, the American College of Cardiology and the American Heart Association guidelines include FFRCT in the recommended diagnostic pathway for heart disease. New products including AI-enabled software for quantifying coronary anatomic narrowings, quantifying coronary atherosclerotic plaque, and predicting changes in blood flow arising from alternate treatment plans will be discussed. Future opportunities for research in developing and applying cardiac digital twins for diagnosing and treating cardiovascular diseases will be presented.

Invited talks

Sarah Brüningk

Center for AI in Radiation Oncology, University of Bern

Towards Mechanistically Informed Treatment Response Prediction: Bridging Data, Biology and Dynamics

Reliable tumor treatment-response prediction is challenged by several factors, including how treatment response itself is represented, the amount and nature of available data, and the ability of predictive models to generalize beyond the settings in which they were trained. In oncology, response is observed at different biological scales, from molecular perturbations and cell-state changes to tumor growth dynamics and radiological phenotypes, yet these measurements are rarely connected within a common predictive framework. At the same time, predicting response from patient- or sample-specific characteristics is complicated by small and heterogeneous datasets, treatment-specific effects, and limited opportunities for external validation. Using pediatric diffuse midline glioma as a motivating example, this lecture will explore how mechanistic knowledge can complement data-driven modelling at both ends of this problem: in defining biologically meaningful response phenotypes and in predicting them from characteristics such as transcriptomic profiles or imaging data. Particular emphasis will be placed on approaches that incorporate biological structure into predictive models, exploit prior knowledge when data are limited, and move beyond static response labels through longitudinal experimental measurements. Examples will include mechanistically informed and foundation-model-based prediction, knowledge-guided representations, dynamic spheroid imaging, and knowledge graphs for generating treatment-combination hypotheses. The broader goal is to move from statistical associations between baseline features and treatment outcomes towards integrated models that connect patient state, mechanism of action and dynamic response across biological scales.

Aldo Clemente

MOX – Department of Mathematics, Politecnico di Milano

Modeling Spatio-Temporal Smoothness using Nonlinear Differential Operators

This work introduces a novel smoothing technique for data observed over space and time, based on a regularization term defined through a time-dependent nonlinear Partial Differential Equation (PDE). The proposed approach extends physics-informed statistical models, which have so far primarily relied on linear PDE-based penalties. By incorporating nonlinear PDEs into the regularization term, the method substantially broadens the applicability of smoothing models, while introducing new theoretical and computational challenges. Simulation studies illustrate the benefits of integrating physical knowledge into statistical modeling, with promising implications for real-world applications. The methodology is further demonstrated in a neuroimaging application, where nonlinear PDE regularization is used to model the progression of Alzheimer's disease from longitudinal Positron Emission Tomography data.

Sara Gazzoni

MOX – Department of Mathematics, Politecnico di Milano

Patient-specific Prediction of Glioblastoma Growth via Reduced Order Modeling and Neural Networks

Glioblastoma (GBL) is among the most aggressive brain tumors in adults, characterized by patient-specific invasion patterns driven by the underlying brain microstructure. In this work, we present a proof-of-concept for a mechanistic learning framework for patient-specific prediction of GBL growth. The approach integrates a diffuse-interface mathematical model to describe the tumor evolution with machine learning techniques to enable real-time prediction and parameter identification from longitudinal neuroimaging data. A reduced-order modeling strategy, based on proper orthogonal decomposition (POD), is trained on synthetic data generated from patient-specific brain anatomies reconstructed from magnetic resonance imaging (MRI) and diffusion tensor imaging (DTI). A neural network surrogate learns the inverse mapping from tumor evolution to model parameters, achieving a computational speed-up of 99% while maintaining an accuracy of 96% in forecasting tumor volume. This hybrid methodology bridges mechanistic modeling and data-driven learning, addressing both the direct and inverse problems of GBL evolution and offering a practical solution for time-sensitive clinical scenarios. The current contribution focuses on methodological innovation, providing a rigorous computational foundation for the future clinical deployment of patient-specific digital twins in neuro-oncology.

Giulia Luraghi

LaBS, Department of Chemistry, Materials and Chemical Engineering "Giulio Natta", Politecnico di Milano

Digital Twins for Pre-operative Planning: From Research Promise to Clinical Reality

Over the past decade, digital twins have evolved from a visionary concept to one of the most promising tools for personalized healthcare. By combining medical imaging, computational modeling, and data-driven approaches, digital twins aim to predict patient-specific responses to treatment before intervention. Applications of digital twins in cardiovascular medicine, focusing on transcatheter aortic valve implantation (TAVI) and thoracic and abdominal endovascular aortic repair (TEVAR and EVAR) will be presented. These clinical applications are characterized by different standards of care, methodological approaches, and levels of technological readiness.

Stefano Pagani

MOX – Department of Mathematics, Politecnico di Milano

Modelling Neurological Disorders Across Spatial and Temporal Scales

Understanding the mechanisms underlying the onset and progression of neurological disorders is a pressing societal challenge. Early diagnosis, disease monitoring, and care planning are limited by heterogeneous clinical manifestations and by the sparsity and irregular acquisition of patient data. Mathematical models can help bridge this gap by providing quantitative frameworks that integrate physical knowledge across scales with patient-specific information extracted from multimodal data. This talk will present some examples from the BraiNum project in which high-order multiscale computational models are used to investigate neurodegenerative processes and alterations in brain electrical activity, together with their interactions with metabolic and vascular mechanisms. We will then discuss how scientific machine learning can complement physics-based modelling to infer patient's current state from sparse past examinations and forecast its progression, illustrating how clinically relevant biomarkers evolve over time Together, these approaches aim to improve clinical understanding of neurological disorders by uncovering underlying mechanisms and disease patterns, while providing new tools to support personalized medicine.

Francesco Regazzoni

MOX – Department of Mathematics, Politecnico di Milano

Understanding the heart, scaling its simulation

Mathematical models of the heart can serve both as virtual laboratories for understanding cardiac function and as predictive tools for patient-specific applications. As virtual laboratories, they allow us to formulate and test mechanistic hypotheses, disentangle the contribution of interacting processes, and connect phenomena across scales, thereby improving our understanding of cardiac physiology and pathophysiology. The talk will present examples in which multiscale computational models provide mechanistic insight into how myocardial structure, cellular contractile mechanisms, and organ-level function interact. It will then discuss how scientific machine learning can help overcome one of the main limitations of high-fidelity cardiac models, namely their computational cost, by enabling efficient simulations across different anatomies. Learned representations of cardiac anatomy, generative modeling, and shape-informed surrogate models will be presented as key tools toward scalable patient-specific computational cardiology.

Giorgio Scita

IFOM ETS - The AIRC Institute of Molecular Oncology, and Department of Oncology and Hematology-Oncology, Università degli Studi di Milano

Controlling Tissue Mechanics and Viscosity in Cancer Progression

Cancer progression depends not only on the forces that cells generate and encounter, but also on how readily a tissue deforms and flows. Yet the molecular control of tissue viscosity remains poorly understood. We find that IRSp53 restrains the spreading of epithelial and breast cancer spheroids by maintaining their mechanical cohesion. Loss of IRSp53 accelerates spheroid wetting and fusion, increases deformability, and reduces cortical stiffness and junctional tension, without a detectable increase in traction forces. Mechanistically, IRSp53 binds Afadin and supports its localization at cell–cell junctions, linking junctional architecture to the collective response to mechanical stress. These findings suggest that reduced viscosity can make a tumor collective more capable of remodeling its shape and spreading. They also raise a question for metastatic dormancy: could a highly cohesive, viscous state help maintain growth arrest, while fluidification permits awakening? Consistent with this possibility, dormant D2.0R breast cancer spheroids fuse less readily and resist deformation more than aggressive D2A1 spheroids. Whether changing viscosity is sufficient to alter dormant cell fate remains to be tested. Together, these observations place the regulation of tissue viscosity alongside stiffness and force generation as a potentially important mechanical dimension of cancer progression.

Andrea Sottoriva

Computational Biology Research Centre, Human Technopole

Mathematical modelling and Machine Learning in cancer

Cancer cells, like species, evolve over time following the laws of Darwin. Evolutionary theory offers the mathematical foundation to understand cancer molecular data, with the aim of identifying cancer vulnerabilities and predict the trajectory of the disease. We will discuss the use of mathematical modelling and Machine Learning approaches in cancer data that aid the discovery of new instruments for oncologists to contrast, control and prevent cancer.

Vittorio Torri

MOX – Department of Mathematics, Politecnico di Milano

Anchoring LLM Representations to Clinical Concepts: An Interpretability Framework for Clinical Text Classification

Clinical text classification is a relevant application of Artificial Intelligence in healthcare, since much of a patient's information is recorded as free text rather than structured data. Large Language Models (LLMs) achieve strong performance on these tasks, but their internal representations are difficult to interpret, making it hard to establish when and why a prediction should be trusted, which is a central concern for the safe adoption of Natural Language Processing (NLP) systems in clinical practice. In this talk, after a brief introduction to clinical NLP, we propose a novel interpretability framework built around the Variational Concept-Anchored Autoencoder (VCAE). This bottleneck module can be inserted into both encoder-only and decoder-only LLMs, constraining a subset of latent dimensions to represent specific clinical concepts mentioned in the documents. To assess and reinforce the semantics of these anchored dimensions, we train the model on pairs of original and counterfactual documents using a preference-based loss function that encourages a consistent directional response. We evaluate the resulting explanations in terms of directional consistency, monotonicity, and correlation with the expected clinical effect. We illustrate the approach on in-hospital mortality prediction from MIMIC-IV ICU admission notes, showing substantially higher fidelity according to these criteria than post-hoc interpretability methods, with a limited cost in predictive performance.

Johannes Weickenmeier

Department of Engineering Science, University of Oxford

Validation of Multiphysics Brain Aging Models Against UK Biobank Imaging Data

Abstract: The brain is our most complex organ and undergoes biomechanical changes with age, including during healthy aging. In this talk, I will describe our multiphysics models of brain aging and how we validate them against population-level imaging data from the UK Biobank. Because our models simulate changes over decades, longitudinal data from the same individuals across the full period are not available. Instead, we use cross-sectional imaging to calibrate model parameters and assess whether simulations reproduce observed age-related patterns of brain structure. Our models represent the brain's anatomy and couple mechanical response with biological processes that drive tissue change. They reproduce hallmark features of cerebral atrophy during aging, as observed in imaging data. This allows us to systematically investigate possible mechanisms of tissue damage, including those associated with prevalent neurodegenerative diseases such as Alzheimer's disease. Ultimately, validated models may help clarify how aging alters the brain and support the development of tools for personalized monitoring and informed prognoses of brain health later in life.

Discussion sessions and round table

Discussion session 1 *(Wednesday, November 11, 17:30–18:30)*

The Future of Cardiovascular Medicine: Integrating Mathematics, Engineering, AI, and Clinical Expertise

Chair: Paolo Zunino

Panelists:

- **Daniele Andreini**
  Division of University Cardiology and Cardiac Imaging – IRCCS Galeazzi Sant'Ambrogio Hospital; Department of Biomedical and Clinical Sciences – Università degli Studi di Milano
- **Bianca Maria Colosimo**
  Department of Mechanical Engineering – Politecnico di Milano
- **Giulia Luraghi**
  LaBS – Department of Chemistry, Materials and Chemical Engineering "Giulio Natta" – Politecnico di Milano
- **Gianluca Pontone**
  Department of Perioperative Cardiology and Cardiovascular Imaging – Centro Cardiologico Monzino IRCCS
- **Alfio M. Quarteroni**
  MOX – Department of Mathematics – Politecnico di Milano; Institute of Mathematics – École Polytechnique Fédérale de Lausanne, Professor Emeritus
- **Charles Taylor**
  Department of Internal Medicine W.A. "Tex" Moncrief Jr. – Oden Institute for Computational Engineering & Sciences; Center for Computational Medicine – Dell Medical School

Discussion session 2 *(Thursday, November 12, 16:30–17:30)*

Bridging Data, Mathematics and Discovery: the $1B Challenges in Health Data Science

Chair: Francesca Ieva

Panelists:

- **Alexander R. A. Anderson**
  Richard O. Jacobson Chair – Integrated Mathematical Oncology Department, Center of Excellence for Evolutionary Therapy – Moffitt Cancer Center
- **Jessica Barrett**
  MRC Biostatistics Unit – University of Cambridge
- **Antonio Esposito**
  Advanced Imaging for Personalized Medicine – San Raffaele Hospital; School of Medicine – Vita-Salute San Raffaele University
- **Andrea Sottoriva**
  Computational Biology Research Centre, Human Technopole

Round table *(Friday, November 13, 14:50–15:50)*

Mathematics for Sustainable Brain Health

Chair: Paola F. Antonietti

Panelists:

- **Carmen Giordano**
  Department of Chemistry, Materials and Chemical Engineering "Giulio Natta" – Politecnico di Milano
- **Andre Marquand**
  Donders Institute – Radboud University Medical Centre
- **Franco Molteni**
  Villa Beretta Rehabilitation Center – Valduce Hospital
- **Federico Pessina**
  Department of Neurosurgery – Humanitas Research Hospital; Department of Biomedical Sciences – Humanitas University
- **Alessandra Pedrocchi**
  NearLab – Department of Electronics, Computer Science, and Bioengineering – Politecnico di Milano
- **Laura Sangalli**
  MOX – Department of Mathematics – Politecnico di Milano

Acknowledgments

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