The Cambridge Centre for AI in Medicine (CCAIM) is excited to host the world’s first Online Summer School exclusively focused on AI and Machine Learning for Healthcare, bringing together Students, Researchers, Clinicians, and Industry Experts.

Over five days, we will provide an intense dive into clinical problems which can benefit from the use of machine learning, machine learning for personalised therapeutics, next-generation clinical trials, building clinical risk scores using AutoML, clinical time-series forecasting, assessment of genetic risks, synthetic data, and much more…

This booklet will introduce all our speakers, explain how the sessions work, and what you can expect from our Summer School.

For more updates, please refer to the Summer School Website and have an eye on the emails and communications we put out during the event.
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We are delighted to welcome you all to this unique Summer School focused entirely on artificial intelligence and machine learning for healthcare.

Our vision was to create a diverse programme of talks aimed at (and accessible to) data scientists, clinicians, and industry experts that describe the existing domain challenges, showcase the remarkable advances in AI-ML for healthcare, and that will hopefully inspire participants to develop new methods and imagine novel applications of machine learning to improve patient care and re-think healthcare delivery.

We hope you find the Summer School enjoyable, informative, and inspiring!

With best wishes,

Prof Mihaela van der Schaar  
*Director*

Prof Andres Floto  
*Co-Director*
The Summer School in Numbers

300+ Participants

47% Students
53% Professionals

66% Academic
13% Clinician
21% Industry

A field as quickly developing and constantly changing as AI and machine learning for healthcare, continuous learning is of significant importance. We are proud to offer a program that is engaging for both students and established professionals alike.

Although CCAIM is based in Cambridge, our aim was to bring together visionaries from all over the world. For our first Summer School, we are joined by people from Institutions in 18 different countries.

Top International Institutions such as
- Technical University Munich
- The Chinese University of Hong Kong
- Politecnico di Milano
- Virginia Tech
- Karolinska Institute

Top Domestic Institutions such as
- University of Cambridge
- Imperial College London
- University College London
- King's College London
- University of Oxford
In the next few pages, we will present to you the program for the Summer School. The days will start at 9:00 am BST and last until 6:30 or 7:00 pm BST at the latest.

All of the sessions will follow a mostly similar format:

- Sessions start with a short 1-minute introduction of the speaker and topic
- 45 minutes are scheduled for the presentation/program
- This is followed by 14 minutes of Q&A

All sessions will only be available online and are accessible via the same Zoom every day. That link will be provided in a separate email.

Please note: To ensure that only participants who have correctly registered may attend the Summer School, you will be required to log into the Zoom call with the full name you used when registering for the course.

Unfortunately, we will not be able to record and then share the sessions afterwards. *Recording the sessions is not permitted at any time.*

If you would like to ask a question during the Q&A, either read out by the moderator or asked in person by yourself, kindly, at any point during the session, write down your question in the Zoom chat or simply mention your intent.

*Do not unmute or activate your camera without being instructed to.*
We believe that we have created a diverse and engaging program for our wide array of participants.

Lectures, Talks, and Masterclasses

Roundtables and Industry Representation
Mentorship

We offer the opportunity to enjoy a unique Mentorship program where you can ask our experts any questions you might have about methodology, career options, and their projects. We will set up dedicated breakout rooms in Zoom which you can enter to listen to/chat with the mentor of your choice.

The following table explains the colour coding of the individual sessions:

<table>
<thead>
<tr>
<th>Colour</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Green</td>
<td>Limited previous knowledge necessary</td>
</tr>
<tr>
<td>Yellow</td>
<td>Sessions aiming at an intermediate/more advanced level</td>
</tr>
<tr>
<td>Blue</td>
<td>Sessions with a clinical focus</td>
</tr>
<tr>
<td>Red</td>
<td>Keynote sessions and Roundtables</td>
</tr>
<tr>
<td>Purple</td>
<td>Additional topics, Participant Exhibition, and Outreach</td>
</tr>
<tr>
<td>Grey</td>
<td>Optional sessions such as Networking and Mentorship</td>
</tr>
</tbody>
</table>
During the daily breaks and in dedicated time slots, we offer the opportunity to connect with other participants, our speakers, and our industry representatives. For networking and our ‘Speed Dating’ sessions, we will use Wonder Space.

The Wonder Space is easy to use:

Let’s get started!

Summer School networking

First you need to permit the website to use your camera and microphone to be able to interact with other participants.
Then, you enter your full name and create an avatar which you can move around the screen. Overlapping your avatar with another person’s avatar will create a ‘circle’ in which you can talk with each other. Each circle can have a maximum number of 10 people at any time. Feel free to move around the space and chat with different people, just as you would do at an in-person conference.

Please note: this space is always open so feel free to head over at any time but will be busiest during the networking breaks at 12.30-13.30 BST and our Research Speed Dating sessions. We will announce the end of these sessions and when it is time to return to our conference space on Zoom.
09:00 – 09:30 Opening Welcome

Prof Mihaela van der Schaar and Prof Andres Floto

09:30 – 10:30 Clinical Problems and Demonstrators

Dr Eoin McKinney
10:30 – 11:30  ML meets Biostatistics I

Prof Angela Wood

This session will cover some fundamentals of developing and evaluating risk prediction tools, using both biostatistical principles and machine learning approaches. We will consider solutions for real clinical problems, such as handling missing data, “treatment drop-ins” during follow-up, very big datasets (e.g., > 1 million individuals), longitudinal measures of risk predictors and the use of developed polygenic risk scores. We will also discuss the issues around model performance, including which measures to use and how to ensure alignment with future clinical implementation. We will end by discussing how to make prediction models useful in clinical practice.

11:30 – 12:30  Healthcare Data Resources & UK Biobank

Prof Angela Wood and Dr Fergus Imrie

This session will provide an overview of some major healthcare data resources which have enabled discoveries that improve people’s lives. We will introduce the UK Biobank, OpenSAFELY, NHS Digital Trusted Research Environment for England, INTERVAL, as well as others, and illustrate important learnings from these data resources made by the machine learning community.
This session will cover the fundamentals of the Bayesian approach to learning from data, which provides a natural framework for uncertainty quantification in the predictions of machine learning methods. Bayesian methods often require computing intractable expectations with respect to complicated probability distributions. In this session, we will recover some of the basic methods for doing this, including 1) The Laplace approximation, 2) Variational inference and 3) Markov chain Monte Carlo methods. We will look at the advantages and disadvantages of these methods and we will see some real-world applications of these techniques.

Suggested Reading:


AutoML is fundamental to the successful uptake of machine learning by non-expert end users because it will lower barriers to entry and unlock potent new capabilities that are out of reach when working with ad-hoc models. In healthcare, AutoML is already beginning to empower the clinical community by enabling the crafting of actionable analytics that can inform and improve decision-making by clinicians, administrators, researchers, policymakers, and beyond.

This talk presents state-of-the-art AutoML methods for healthcare which we have developed over the past years and how they have been applied in various clinical settings (including cancer, cardiovascular disease, cystic fibrosis, and recently Covid-19), and then introduces Adjutorium, an AutoML framework developed in our lab, for which the software will be made publicly available in the near future.

Suggested Reading:

AutoML: powering the new human-machine learning ecosystem

Million-patient study shows the strength of machine learning in recommending breast cancer therapies
Time series datasets such as electronic health records (EHR) and registries represent valuable (but imperfect) sources of information spanning a patient’s entire lifetime of care. While learning from temporal data is an established field, the healthcare domain raises unique problems and challenges that require new methodologies and ways of thinking.

Perhaps the most common application of time series is forecasting. While we will discuss state-of-the-art approaches for disease forecasting, we will also focus on other important problems in time series, such as time-to-event or survival analysis, personalized monitoring as well as uncertainty estimation, which is critical in high-stakes scenarios such as healthcare.

Suggested Reading:

Time series in healthcare: challenges and solutions
16:30 – 17:30 **Keynote: ML and Computer Vision for Developmental Disorders**

**Prof Guillermo Sapiro** (Duke University / Apple)

In this talk, I will describe how we are using computer vision and machine learning for addressing developmental disorders, ASD (Autism Spectrum Disorder) and ARFID (Avoidant/Restrictive Food Intake Disorder) in particular.

In ASD, I will describe how we developed and deployed a developmentally appropriate app, currently available in a number of pediatric and community clinics as well as for home use, and with it we collected and analyzed data from several thousand participants, leading to new scientific discoveries with significant impact in democratizing children’s health.

In the area of ARFID, I will also describe our work on quantifying the effects of interventions via computer vision and NLP.

17:30 – 18:00 Optional Mentoring Session
09:00 – 09:30 Introduction to the Day

09:30 – 10:30 Keynote: ML for Healthcare: Where are we on the Pathway to Personalisation

Dr Danielle Belgrave (DeepMind)
This session will cover the fundamentals of machine learning interpretability.

We will start by motivating interpretable machine learning with a special focus on medical applications.

Then, we will touch on several existing methods to increase the transparency of machine learning models, namely:

1. Feature-based explanations
2. Example-based explanations
3. Concept-based explanations
4. Hybrid methods

The session assumes no prior knowledge of interpretability, but the interested reader may refer to the following papers:

https://papers.nips.cc/paper/2021/hash/65658fde58ab3c2b6e5132a39fae7cb9-Abstract.html

https://arxiv.org/abs/1711.11279
11:30 – 12:30 Review of artificial intelligence for medical imaging and diagnosis

Prof Jong Chul Ye (Korea Advanced Institute of Science and Technology)

In recent years, artificial intelligence has become the main workhorse for radiology, from diagnosis to image processing. In this talk, I will review recent development in this field. First, from the basic CNN approaches, recent self-supervised learning approaches using a vision transformer will be reviewed for AI-based image diagnosis. Then, I will review the AI-based image enhancement techniques such as low-dose CT image enhancement and accelerated MRI that help radiologists to improve the diagnosis quality. Finally, the recent trend of vision-language pretraining and diffusion models will be explained as frontier research for AI-based image diagnostics and medical image processing.
This session will cover an introduction to the problem of estimating personalized treatment effects. We will highlight which machine learning problems arise in this context and cover some solutions that have been proposed in recent work.

Suggested Reading:


Multi-Armed Bandits in Healthcare

Prof Cem Tekin (Bilkent University)

This session will cover the fundamentals of multi-armed bandit algorithms and their application in healthcare. We will overview the multi-armed bandit problem and basic algorithms that trade-off exploration and exploitation. We will study several contextual bandit models and their healthcare applications, including (i) matching patients with clinicians/treatments in high-dimensional settings and (ii) ensuring the safety of recommendations.

Suggested Reading:


15:30 – 16:30 Clinical Trials: Current + NextGen

Alihan Hüyük

This session will explore how machine learning methods can empower clinical trials, from planning and conduct to analysis and clinical use (as we outline in our recent blog post: *Revolutionizing Clinical Trials using Machine Learning*).

Suggested Reading:

A. Hüyük, Z. Qian, E. McKinney, M. van der Schaar, “Revolutionizing clinical trials using machine learning.”


16:30 – 17:30 Roundtable with Pharma: Clinical Trials

Prof Richard Peck, Dr Eoin McKinney, Dr Graeme Archer (GSK),
Dr Megan Gibbs (AstraZeneca), and Alihan Hüyük

The session will begin with a short introduction by Prof Richard Peck, followed by opening remarks by all panellists, describing their views on key opportunities, challenges, and more. Then, the panel will turn to a discussion focused on the key questions previously established during the opening. An open Q&A will give the audience the chance to participate.

17:30 – 18:00 Research Speed Dating

18:00 – 18:30 Optional Mentoring Session
09:00 – 09:30 Introduction to the Day

09:30 – 10:30 Keynote: (Machine) Learnings from the Human Cell Atlas

Dr Sarah Teichman

10:30 – 11:30 Causal Deep Learning

Zhaozhi Qian and Jeroen Berrevoets

We will provide an overview of Causal Deep Learning (CDL), a new and emerging area in machine learning that builds on the strengths of causality and deep learning. We explain what we mean by CDL, which methods belong to this, and how they are situated within the larger field of machine learning. To illustrate, we will discuss some published works within CDL and explain why they are superior compared to other, standard, machine learning models. Furthermore, we will end our discussion with a look to the future; what can we expect from this new and exciting field?

Suggested Reading:

Causal Deep Learning
11:30 – 12:30 Causality in the Era of Deep Learning  
Dr Cheng Zhang (Microsoft Research)

This session will cover fundamental causal discovery and inference concepts and provide an overview of recent advances considering real-world application needs.

Suggested Reading:

13:30 – 14:30 ML meets Biostatistics II  
Prof Qingyuan Zhao

This session will give a brief introduction to causal inference, an interdisciplinary area that seeks to obtain knowledge about causality from empirical (often observational) data. We will review the counterfactual (also called potential outcomes) and graphical approaches to theorise causality and point to connections to artificial intelligence and medicine.
14:30 – 16:30 Graph Neural Networks

Prof Pietro Liò, Emma Rocheteau, Andreea Deac, Paul Scherer, and Nikola Simidjievski

16:30 – 18:30 Genomics and Roundtable with Pharma

Prof Andres Floto, Dr Kim Branson (GSK), and Dr Slavé Petrovski (AstraZeneca)
Successful Organ Transplantation requires the matching of recipients with a donor in a high dimensional state which will optimise the outcome, whether that is defined as preventing deaths without a transplant, maximising post-transplant survival or net life years gained. We have shown that machine learning techniques of Individual Treatment Effects outperform standard Cox models. ML methodologies can also address counterfactual impacts of a decision to transplant a specific individual on all the other waiting list cases not transplanted.
Intensive care unit (ICU) admissions are the most data-dense hospital episodes since these patients are subject to continuous physiological monitoring, have numerous time-sensitive interventions and are extensively investigated with laboratory and imaging on a daily basis. Along with the time-criticality of decision-making and biological heterogeneity of intensive care patients, this makes the intensive care unit a fertile place for machine learning techniques. At the same time, open access intensive care databases such as MIMIC have provided a substrate for developing novel machine learning algorithms too. This talk will discuss opportunities for ML in the ICU but also explain how the way ICU data is collected means that the data has a particularly complex structure in terms of sampling behaviour, informative missingness and treatment effects which must be considered by researchers to avoid making false inferences.
Chronic health conditions place a huge and increasing burden on finite NHS resources. The cost of managing chronic respiratory conditions alone is estimated to be in excess of £4B pa. We believe that Machine Learning/Artificial Intelligence (ML/AI) can provide the safe, radical reform that is urgently needed to ensure the sustainability of high healthcare standards.

To accelerate the adoption of AI in clinical decision-making, some exemplar quick wins are needed for safe deployment, demonstration of improved healthcare while reducing the burden of care on users, providers, and payers and which can then be easily modified to encompass other chronic conditions facing similar challenges.

Cystic fibrosis (CF) is almost the perfect exemplar testbed for chronic respiratory conditions. CF is a genetic condition characterised by thick sticky mucus on epithelial surfaces. Diagnosis is made at birth and untreated the condition is fatal. In common with many other lung diseases (such as Asthma and smoking-related lung disease (COPD)), people with CF are medically relatively stable for long periods of time punctuated by abrupt clinical deterioration known as acute pulmonary exacerbations (APEs) which drive pulmonary inflammation, progressive lung damage, and premature death. Diagnosis of APEs is complex and currently relies on lung function measures which are late and blunt clinical markers.

We will discuss how machine learning methods can be applied to home monitoring data to build a robust predictor of acute clinical deteriorations that can (i) enable early medical and non-medical interventions to preserve long-term lung health, (ii) provide support to transform clinical care delivery, and (iii) accelerate biomarker discover.
In this tutorial, we provide an overview of state-of-the-art techniques for synthesizing the two most common types of clinical data; namely tabular (or multidimensional) data and time-series data. In particular, we discuss various generative modelling approaches based on generative adversarial networks (GANs) normalizing flows and state-space models for cross-sectional and time-series data demonstrating the use cases of such models in creating synthetic training data for machine learning algorithms and highlighting the comparative strengths and weaknesses of these different approaches. In addition, we discuss the issue of evaluating the quality of synthetic data and the performance of generative models; we highlight the challenges associated with evaluating generative models as compared to discriminative predictions and present various metrics that can be used to quantify different aspects of synthetic data quality.
Intelligent systems are continuously faced with the challenge of adapting their decisions and predictions to the particular environment in which they are deployed. For example, if the target environment is arbitrary, or substantially different from the study environment, transporting predictions is difficult or even impossible. In principle, however, whenever the causal mechanisms and qualitative differences between domains are understood, one may reason about how to optimally leverage prior information and data from related domains to make accurate decisions in the target domain. In this presentation, I will describe a causal perspective on the problem of transfer learning, and data fusion more generally, with the aim of introducing an overall framework and concrete solutions, as well as making contrasts with transfer learning as understood in the machine learning literature.
In the current data-rich healthcare environment, our capacity to collect vast amounts of longitudinal, multimodal data needs to be matched with a comparable ability to continuously learn from the data and tailor clinical decisions to an individual. Biomedical informatics is the study and application of computational methods to transform data into knowledge for problem-solving and clinical decision-making. This session will cover the fundamental concepts and approaches for evaluating and applying multimodal data integration and machine learning techniques in today’s healthcare environment. Through real-world examples drawn from literature and my research in cancer imaging, we will examine the promise and pitfalls of these approaches to inform and improve clinical practice, identifying opportunities for further advances.

Suggested Reading:


17:30 – 18:30 Software Resources

Evgeny Saveliev

In his talk, Evgeny will discuss the software for Machine Learning with medical time series, with a focus on the Clairvoyance library and individualised treatment effect inference.

Suggested Reading:

https://openreview.net/pdf?id=xnC8YWKUE3k
No one should be discouraged from pursuing AI and machine learning. Many of us have been told at some point that these areas are not for women, that they are dry and lack creativity, or that they don't offer a way to make an impact and change the world.

We want to explore these myths and prove them wrong. That's why, while our message is mainly aimed at women, all are welcome. All you need is curiosity and an open mind.

More info and engagement sessions here: WeCREATE is a community built to inspire female students and young professionals, dispelling myths, and highlighting the creative promise of AI and machine learning.
09:30 – 10:30 Roundtable: Ethical AI and ML

Prof Andres Floto, Dr Alexander Gimson, Prof Angela Wood, Prof Stefan Scholtes, Dr Lea Goetz (GSK)
Reliably estimating the individualized effects of treatments is crucial for decision-making in the healthcare setting. Machine learning methods for causal inference can be used to leverage the increasingly available patient observational data, such as electronic health records (EHRs), in order to estimate heterogeneous treatment effects. In this context, several causal inference methods have been developed to estimate the effects of treatments in the static, cross-sectional setting. Nevertheless, estimating the effects of treatments over time poses unique opportunities such as understanding how diseases evolve under different treatment plans, which are optimal timings for assigning treatments, but also how individual patients respond to medication over time.

This session will describe the main challenges that arise when using longitudinal patient observational data for causal inference. Then, it will introduce several methods that employ recent advances in representation learning to achieve state-of-the-art performance in estimating causal effects in the temporal setting. Finally, the session will outline the advantages and disadvantages of each method, but also highlight future research directions that could lead to achieving the full potential of utilising electronic health records and machine learning methods for causal inference to make personalised treatment recommendations.
Suggested Reading:


11:30 – 12:30 Advanced Time-Series

Dr Fergus Imrie, Prof Mihaela van der Schaar
Disease-associated variants lie primarily in non-coding regions, increasing the urgency of understanding how gene-regulatory circuitry impacts human disease. To address this challenge, we generate comparative genomics, epigenomic, and transcriptional maps, spanning 823 human tissues, 1500 individuals, and 20 million single cells. We link variants to target genes, upstream regulators, cell types of action, and perturbed pathways, and predict causal genes and regions to provide unbiased views of disease mechanisms, sometimes re-shaping our understanding.

We find that Alzheimer’s variants act primarily through immune processes, rather than neuronal processes, and the strongest genetic association with obesity acts via energy storage/dissipation rather than appetite/exercise decisions. We combine single-cell profiles, tissue-level variation, and genetic variation across healthy and diseased individuals to map genetic effects into epigenomic, transcriptional, and function changes at single-cell resolution, to recognize cell-type-specific disease-associated somatic mutations indicative of mosaicism, and to recognize multi-tissue single-cell effects of exercise and obesity.

We expand these methods to electronic health records to recognize the multi-phenotype effects of genetics, environment, and disease, combining clinical notes, lab tests, and diverse data modalities despite missing data.
We integrate large cohorts to factorize phenotype-genotype correlations to reveal distinct biological contributors to complex diseases and traits, partition disease complexity, and stratify patients for pathway-matched treatments.

Lastly, we develop massively parallel, programmable and modular technologies for manipulating these pathways by high-throughput reporter assays, genome editing, and gene targeting in human cells and mice, to propose new therapeutic hypotheses in Alzheimer’s, obesity, and cancer. These results provide a roadmap for translating genetic findings into mechanistic insights and ultimately new therapeutic avenues for complex disease and cancer.

14:30 – 15:00 Get involved in CCAIM

Prof Andres Floto, Prof Mihaela van der Schaar,

Prof José Miguel Hernández-Lobato, Femke Cole

15:00 – 17:30 Exhibition Highlights

Summer School participants will present their research projects and ideas to the community.
Prof Guillermo Sapiro

Guillermo Sapiro is a James B. Duke Professor at Duke University and a Distinguished Engineer leading the Health AI team at Apple. He has published over 500 peer-reviewed papers in the areas of computer vision, machine learning, and their applications to health. He received the Test-of-Time Award twice, once in ML (ICML) and once in computer vision (ICCV). His awards include the NSF CAREER, ONR Young Investigator, and the Presidential Early Career Award for Scientists and Engineers. He is a Member of the National Academy of Engineering and a Fellow of IEEE, SIAM, and the American Academy of Arts and Sciences.

Dr Danielle Belgrave

Danielle Belgrave is a senior staff research scientist at DeepMind. Prior to joining DeepMind, she worked in the Healthcare Intelligence group at Microsoft Research and was a tenured research fellow at Imperial College London. Her research focuses on integrating medical domain knowledge, machine learning and causal modelling frameworks to understand health. She obtained a BSc in Mathematics and Statistics from the London School of Economics, an MSc in Statistics from University College London, and a PhD in the area of machine learning in health applications from the University of Manchester.
Dr Sarah Teichmann

Sarah Teichmann is interested in global principles of regulation of gene expression and protein complexes, specifically in the context of immunity. Sarah did her PhD at the MRC Laboratory of Molecular Biology, Cambridge, UK and was a Beit Memorial Fellow at University College London. She started her group at the MRC Laboratory of Molecular Biology in 2001. In 2013, she moved to the Wellcome Genome Campus in Hinxton/Cambridge, jointly with the EMBL-European Bioinformatics Institute and the Wellcome Sanger Institute (WSI). In January 2016 she became Head of the Cellular Genetics Programme at the WSI. Sarah co-founded and is co-leader of the “Human Cell Atlas” (HCA) international consortium. She is an EMBO member, a Fellow of the Academy of Medical Sciences and a Fellow of the Royal Society. Her work has been recognized by a number of prizes, including the Lister Prize, Biochemical Society Colworth Medal, Royal Society Crick Lecture, EMBO Gold Medal and the Mary Lyon Medal.

Prof Manolis Kellis

Manolis Kellis is a professor of computer science at MIT, a member of the Broad Institute of MIT and Harvard, a principal investigator of the Computer Science and Artificial Intelligence Lab at MIT, and head of the MIT Computational Biology Group (compbio.mit.edu). His research includes disease circuitry, genetics, genomics, epigenomics, coding genes, non-coding RNAs, regulatory genomics, and comparative genomics, applied to Alzheimer's Disease, Obesity, Schizophrenia, Cardiac Disorders, Cancer, Immune Disorders, and multiple other disorders. He has led several large-scale genomics projects, including the Roadmap Epigenomics project,
the ENCODE project, the Genotype Tissue-Expression (GTEx) project, and comparative genomics projects in mammals, flies, and yeasts. He received the US Presidential Early Career Award in Science and Engineering (PECASE) by US President Barack Obama, the Mendel Medal for Outstanding Achievements in Science, the NIH Director’s Transformative Research Award, the Boston Patent Law Association award, the NSF CAREER award, the Alfred P. Sloan Fellowship, the Technology Review TR35 recognition, the AIT Niki Award, and the Sprowls award for the best PhD thesis in computer science at MIT. He has authored over 245 journal publications cited more than 125,000 times. He has obtained more than 20 multi-year grants from the NIH, and his trainees hold faculty positions at Stanford, Harvard, CMU, McGill, Johns Hopkins, UCLA, and other top universities. He lived in Greece and France before moving to the US, and he studied and conducted research at MIT, the Xerox Palo Alto Research Center, and the Cold Spring Harbor Lab. For more info, see: compbio.mit.edu
Prof Mihaela van der Schaar

Mihaela van der Schaar is the John Humphrey Plummer Professor of Machine Learning, Artificial Intelligence and Medicine at the University of Cambridge and a Fellow at The Alan Turing Institute in London. In addition to leading the van der Schaar Lab, Mihaela is founder and director of the Cambridge Centre for AI in Medicine (CCAIM).

Mihaela was elected IEEE Fellow in 2009. She has received numerous awards, including the Oon Prize on Preventative Medicine from the University of Cambridge (2018), a National Science Foundation CAREER Award (2004), 3 IBM Faculty Awards, the IBM Exploratory Stream Analytics Innovation Award, the Philips Make a Difference Award and several best paper awards, including the IEEE Darlington Award.

Mihaela is personally credited as inventor on 35 USA patents (the majority of which are listed here), many of which are still frequently cited and adopted in standards. She has made over 45 contributions to international standards for which she received 3 ISO Awards. In 2019, a Nesta report determined that Mihaela was the most-cited female AI researcher in the U.K.
Prof Andres Floto

Andres Floto is Professor of Respiratory Biology at the University of Cambridge, a Wellcome Trust Senior Investigator, and Research Director of the Cambridge Centre for Lung Infection at Papworth Hospital, Cambridge.

His research is focused on understanding how immune cells interact with bacteria, how intracellular killing and inflammation are regulated and sometimes subverted during infection, how population-level whole genome sequencing can be used to reveal the biology of bacterial infection, and how the therapeutic enhancement of cell-autonomous immunity may provide novel strategies to treat multi drug-resistant pathogens.

Clinically, he specialises in the treatment of patients with Cystic Fibrosis (CF), non-CF bronchiectasis, and infections with Nontuberculous Mycobacteria (NTM). He is co-chair of the British Thoracic Society NTM guidelines committee, the joint US CF Foundation-European CF Society (ECFS) NTM Guidelines Group and the ECFS working group on NTM.
Dr Ari Ecole

Ari Ercole is a consultant in intensive care medicine and deputy chief clinical informatics officer at Cambridge University Hospitals NHS Foundation Trust. He holds a PhD in physics and is an expert in intensive care data science, signal processing and computational representation of complex critical illnesses. He is the Chair of the European Society of Intensive Care Medicine data science scientific section and a founding fellow of the Faculty of Clinical Informatics. He has published extensively on applications of machine learning in intensive care.

Prof Stefan Scholtes

Stefan Scholtes is Dennis Gillings Professor of Health Management at the Cambridge Judge Business School, and Director of the Centre for Health Leadership & Enterprise. His research is strongly practice-based and embedded in close collaborations with the Cambridge University Hospitals NHS Foundation Trust, Cambridgeshire and Peterborough Foundation Trust, and Public Health England. He also engages closely with local GP practices and has co-founded the Primary Care Innovation Academy at the Cambridge Judge Business School to support the transformation of out-of-hospital services.
Dr Eoin McKinney

Eoin McKinney is University Lecturer in Renal medicine at the University of Cambridge, and Honorary consultant in nephrology and transplantation at the Cambridge University Hospitals NHS Foundation Trust. Dr McKinney’s research explores the interface between immune responses to infection and those driving inflammatory pathology, applying machine learning methods to the integration of multi-omics data, building interpretable predictive models for rapid translation into clinical practice while informing underlying disease biology and identifying novel therapeutic strategies.

Dr Alexander Gimson

Alexander Gimson is Consultant Transplant Hepatologist at the Cambridge University Hospitals NHS Foundation Trust, and Chair of the Care Advisory Group at the Cambridgeshire & Peterborough Sustainability and Transformation Partnership. Dr Gimson led the national team which developed a new organ allocation offering scheme whereby organs are offered to the person on a national waiting list who has the greatest calculated net life years gained from the particular donor organ.

He is running a project which aims to discover if an AI/machine learning model can beat existing models, to make that organ offering even more equitable.
Dr Angela Wood

Angela Wood is Professor of Health Data Science at the University of Cambridge and Turing Fellow. Dr Wood’s research interests are centred on the development and application of statistical methods for advancing epidemiological research. She has focused on developing statistical methodology for handling measurement error, using repeated measures of risk factors, missing data problems, multiple imputation, risk prediction and meta-analysis.

Prof Pietro Liò

Pietro Liò is Professor of Computational Biology in the Department of Computer Science at the University of Cambridge, and Member of the Artificial Intelligence group of the Computer Laboratory.

Professor Liò has PhDs in Complex Systems and Non-Linear Dynamics and in Theoretical Genetics. He is the author of over 400 papers. His specialities include bioinformatics algorithms, predictive models in personalised medicine, modelling comorbidity and ageing, methods for combining multi-scale biological processes, statistics of multi-omics and multi-physics modelling of molecules-cell-tissue-organ interactions.
Dr José Miguel Hernández-Lobato

José Miguel is Associate Professor in Machine Learning at the Department of Engineering at the University of Cambridge, UK. Before this, he was a postdoctoral fellow in the Harvard Intelligent Probabilistic Systems group at Harvard University, working with Ryan Adams, and a postdoctoral research associate in the Machine Learning Group at the University of Cambridge (UK), working with Zoubin Ghahramani. José Miguel completed his PhD and M.Phil. in Computer Science at the Computer Science Department in Universidad Autónoma de Madrid (Spain), where he also obtained a B.Sc. in Computer Science from this institution, with a special prize for the best academic record on graduation. José Miguel's research focuses on probabilistic machine learning, with a particular interest in deep generative models, Bayesian optimization, approximate inference and Bayesian neural networks and applications of these methods to real-world problems.

Prof Qingyuan Zhao

Qingyuan Zhao is a University Assistant Professor in the Statistical Laboratory, Department of Pure Mathematics and Mathematical Statistics (DPMMS) at University of Cambridge and a Turing Fellow at the Alan Turing Institute. He is interested in improving the quality and appraisal of statistical research, including new methodology and a better understanding of causal inference, novel study designs, sensitivity analysis, multiple testing, and selective inference. His substantive research focuses on causal inference problems arising in genetics and epidemiology.
Richard Peck spent over 30 years as a clinical pharmacologist in the pharmaceutical industry and was Global head of Clinical Pharmacology at Roche for the last thirteen of these. Since retiring from Roche, he has been appointed Honorary Professor of Pharmacology & Therapeutics at the University of Liverpool.

His research interests include understanding and utilising variability in drug response to enable precision dosing; applying clinical pharmacology to enable the development of personalised/stratified medicines and the use of model-based drug development strategies.
Prof Jong Chul Ye

Jong Chul Ye is IEEE Fellow and Endowed Chair Professor at the Kim Jaechul Graduate School of AI of the Korea Advanced Institute of Science & Technology (KAIST). His research interests include deep learning, computer vision, generative models, computational imaging, MRI signal processing, super-resolution microscopy, and statistical signal processing.

Prof Cem Tekin

Cem Tekin is an Associate Professor in the Department of Electrical and Electronics Engineering and Head of Cognitive Systems, Bandits and Optimization Research Group (CYBORG) at Bilkent University.

From February 2013 to January 2015, he was a postdoctoral scholar in Electrical Engineering Department, UCLA (advisor: Mihaela van der Schaar). He received the Fred W. Ellersick award for the best paper in MILCOM 2009, the Science Academy Association of Turkey Distinguished Young Scientist (BAGEP) Award in 2019, Parlar Foundation Research Incentive Award in 2019, and IEEE Turkey Chapter Research Incentive Award in 2020. He is a Senior Member of IEEE. Cem has authored or co-authored over 60 research papers, 5 book chapters and a research monograph.
Dr Cheng Zhang

Cheng Zhang is a principal researcher at Microsoft Research Cambridge, where she leads the project Azua: Efficient Decision Making. Before joining Microsoft Research, Dr Zhang was at Disney Research Pittsburgh located at Carnegie Mellon University. She received her PhD from the Department of Robotics, Perception and Learning (RPL/ former CVAP), KTH Royal Institute of Technology. Her general interests are causal machine learning, deep generative models and approximate inference.

Dr Kim Branson

Kim Branson is SVP, Global Head, AI/ML at GSK, based in San Francisco. Kim leads the GSK.ai team, a global organization of nearly 100 machine learning researchers and engineers who are pioneering the application of AI to drug discovery and development. Kim brings deep expertise in modelling and machine learning to drug and vaccine discovery, combining perspectives spanning academia to a technology start-up. Under his leadership, GSK has built one of the industry’s few completely in-house AI efforts to unlock the potential of complex genetic data and leverage GSK’s industry-leading collaborations. Kim joined GSK in 2019 from Genentech where he was Head of AI, Early Clinical Development. Kim has been involved in large-scale machine learning and medical informatics initiatives for more than 20 years over a range of ventures from computational drug design to disease risk prediction. Previously Kim helped found several Silicon Valley start-ups, including Discovery Engine (acquired by Twitter in 2009), Glimpse as Chief Scientist (acquired by Apple in 2017), and Lumiata, a predictive health analytics company. Kim received degrees from the University of Adelaide and a PhD from the University of Melbourne. He was a Peter Doherty fellow and received postdoctoral training at Stanford University.
Dr Slavé Petrovski

Slavé Petrovski is Vice President, Head of Genome Analytics and Bioinformatics, R&D at AstraZeneca. His background is in human genomics, population genetics, precision medicine and leading large-scale human genomics studies. He joined AstraZeneca in August 2017 and his role as Vice President and Head of Genome Analytics and Bioinformatics for AstraZeneca’s Centre for Genomics Research (CGR) involves leading the design and implementation of human genomic studies as part of AstraZeneca’s Genomics Initiative. His team applies human genetics to inform and drive novel target discovery, target validation, target safety, precision medicine and late-stage support.

Prior to this, Dr Petrovski was a Senior Research Fellow and Group Leader in Computational Genomics within the Department of Medicine at the University of Melbourne, Australia. He was awarded a PhD in Bioinformatics and Biostatistics from the Faculty of Medicine, Dentistry & Health Sciences at the University of Melbourne in 2011.

Dr John Winn

John Winn is a Principal Researcher at Microsoft Research Cambridge, in the Machine Learning and Perception group. His main research interests are machine learning, machine vision, ML for healthcare and information extraction. Previously, he was a PhD. student in the Inference Group at the Cavendish Laboratory, supervised by Chris Bishop and David MacKay. He has also been a member of the Signal Processing Group at the Engineering Department and the Learning and Vision Group at the MIT AI Lab. His undergraduate degree was in Electrical and Information Sciences at Cambridge University.
Dr Alexis Bellot

Alexis Bellot is a research scientist at DeepMind in London, UK. He was previously a postdoctoral scholar at Columbia University sponsored by Professor Elias Bareinboim. Prior to Columbia, he graduated with a PhD in Applied Mathematics from the University of Cambridge under the supervision of Professor Mihaela van der Schaar. Alexis works on the study of causality from data and its applications, with an emphasis on methods and theory that combine causality and machine learning to both improve the robustness of machine learning algorithms and improve causal discovery and causal inference methods.

Dr Greg Pottie

Gregory J. Pottie has been a faculty member of the UCLA Electrical and Computer Engineering Department since 1991, serving in vice-chair roles from 1999-2003 and as Chair from 2015-2020. From 2003-2009, 2022-23 he served as the Associate Dean for Research and Physical Resources of the Henry Samueli School of Engineering and Applied Science. From 2002-2012 he was deputy director of the NSF-funded Center for Embedded Networked Sensing. His research interests have included wireless communication systems, sensor networks and interactive educational systems. His current focus is on causal modelling of interactive systems. From 1997 to 1999 he was secretary to the board of governors for the IEEE Information Theory Society. In 1998 he received the Allied Signal Award for outstanding faculty research for UCLA engineering. In 2005 he became a Fellow of the IEEE for contributions to the modelling and applications of sensor networks. In 2009 he received a Fulbright Senior Scholar award. He is a Senior Member of the National Academy of Inventors.
Prof William Hsu

William Hsu is an Associate Professor in the Department of Radiological Sciences and a member of the Medical Imaging & Informatics group. He received his PhD in Biomedical Engineering with an emphasis in Medical Imaging Informatics from the University of California, Los Angeles in 2009 and a BS degree in Biomedical Engineering from Johns Hopkins University in 2004. His research interests include data integration, predictive modelling, population health management, and imaging informatics. He is an active member of the American Medical Informatics Association, serving on the Working Group Steering Committee and as a leader in the Biomedical Imaging Informatics Working Group.

Dr Ioana Bica

Ioana Bica has just joined DeepMind as Research Scientist. Previously, she received her PhD from the University of Oxford and Alan Turing Institute, advised by Prof Mihaela van der Schaar. Her PhD research has focused on building causal inference methods for supporting, understanding, and improving decision-making. Dr Bica has been working on building methods for causal inference to estimate the effects of treatments from observational data in the healthcare setting. Prior to her PhD, she completed a Bachelor’s degree and a Master’s degree in Computer Science at the University of Cambridge where she worked with Prof. Pietro Liò on multi-modal data integration and unsupervised learning for genomics data. Dr Bica is also Board Member at Women in Machine Learning.
Andreea Deac

Andreea Deac is a PhD student in Machine Learning at Mila and the University of Montreal, with Prof Jian Tang. She is broadly interested in how learning can be improved through the use of graph representations, having previously worked on neural algorithmic reasoners for implicit planning and applications to biotechnology, focusing on drug discovery.

Dr Emma Slade

Emma Slade is an AI/ML Engineer at GSK. She previously completed a DPhil at the University of Oxford in Theoretical Physics, specialising in computational particle theory.

Dr Lea Goetz

Lea Goetz is a Senior AI/ML Engineer at GSK. Previously, she was a doctoral researcher and associate faculty member at the Wolfson Institute for Biomedical Research at UCL, where she also received her PhD.
Dr Fergus Imrie

Fergus Imrie is a postdoc at the ECE Department, University of California, Los Angeles (UCLA), and member of the van der Schaar Lab. Prior to joining the lab, Fergus completed his DPhil (PhD) at the University of Oxford in the Department of Statistics, developing deep learning approaches for drug discovery. Dr Imrie is interested in self-supervised learning and methods for understanding clinical decision-making.

Bogdan Cebere

Bogdan Cebere has been a research engineer at the van der Schaar Lab since 2021. He received his bachelor’s degree in computer science in 2012 and his master’s degree in distributed systems in 2014, both from the University of Bucharest. Prior to joining the van der Schaar Lab, Bogdan worked for roughly 10 years at a cybersecurity company. During this time, he contributed to a range of research projects related to network security, cryptography, and data privacy, which required high-performance solutions in embedded or cloud environments.
Jonathan Crabbé

Jonathan Crabbé is a PhD student at the van der Schaar Lab. He joins the lab following a MASt in theoretical physics and applied mathematics at Cambridge, which he passed with distinction, receiving the Wolfson College Jennings Price. Before this, he received an M.Sc. from Ecole Normale Superieure of Paris’ Department of Physics, with his studies fully funded under the LABEX-ICFP Scholarship. Jonathan’s work focuses on the development of explainable artificial intelligence (XAI), which he believes to be one of the biggest challenges in machine learning.

Alicia Curth

Alicia Curth is a PhD student at the van der Schaar Lab. She recently completed an MSc in Statistical Science at the University of Oxford, where she graduated with distinction and was awarded the Gutiérrez Toscano Prize (awarded to the best-performing MSc candidates in Statistical Science each year). Her previous professional experience includes a data science role for Media Analytics, and a research internship at Pacmed, a healthcare tech start-up. Alicia also holds a BSc in Econometrics and Operations Research and a BSc in Economics and Business Economics from Erasmus University Rotterdam. Alicia is interested in building a better understanding of which algorithms work when and why and aims to contribute to bridging the gap between theory and practice in machine learning. She is particularly interested in building decision support systems for doctors and aiding knowledge discovery through next-generation clinical trials as well as analyses of genomics (and other omics) data.
Alihan Hüyük

Alihan is a PhD student in the Department of Applied Mathematics and Theoretical Physics at the University of Cambridge. He is supervised by Professor Mihaela van der Schaar. Prior to attending Cambridge, he completed a BSc in Electrical and Electronics Engineering at Bilkent University, Turkey. Alihan’s current research revolves around decision-making problems encountered in clinical development. He is also interested in developing interpretable machine learning methods with the purpose of understanding the decision-making process of clinicians. Previously, he worked on multi-armed bandit problems in combinatorial and multi-objective settings.

Zhaozhi Qian

Zhaozhi Qian is a PhD student at the van der Schaar Lab. After obtaining an MSc in Machine Learning at UCL, Zhaozhi Qian started his career as a data scientist in the largest mobile gaming company in Europe. He joined the group in 2019 as a PhD student focusing on robust and interpretable learning for longitudinal data. So far, his work has included inferring latent disease interaction networks from Electronic Health Records, uncovering the causal structure between events that unfold over time and calibrating the predictive uncertainty under domain shift. Zhaozhi also worked as a contractor in the NHS during the COVID-19 pandemic contributing his analytical skills to the national response to the pandemic.
Jeroen Berrevoets

Jeroen Berrevoets is a PhD student at the van der Schaar Lab. He joined from the Vrije Universiteit Brussel (VUB). Prior to this, he analysed traffic data at 4 of Belgium’s largest media outlets and performed structural dynamics analysis at BMW Group in Munich. Jeroen plans to explore the potential of machine learning in aiding medical discovery, rather than simply applying it to non-obvious predictions. His main research interests involve using machine learning and causal inference to gain an understanding of various diseases and medications.

Emma Rocheteau

Emma Rocheteau is a PhD student at the University of Cambridge working on machine learning problems for healthcare, supervised by Pietro Liò. She is part of the AI group in the computer science and technology department, but she is originally from a medical background. After completing parts IA and IB (years 1 and 2) of the pre-clinical medical and veterinary sciences tripos, part IIA (intercalation year) of the engineering tripos and one year of clinical medicine (on the wards in the hospital setting), she has now paused her medical studies to pursue her PhD. Her interests include deep learning, graph neural networks, electronic health records, and AI/ML in medicine.
Paul Scherer

Paul Scherer is a PhD student at the University of Cambridge Computer Laboratory under the supervision of Prof. Pietro Lio' and Prof. Mateja Jamnik as part of the Artificial Intelligence Group and the Computational Biology Group. He is funded by the W.D Armstrong Fund.

His research interests lie within the fields of information theory, machine learning, and biomedical informatics. His current research looks into developing learning algorithms applicable to irregularly structured data such as graphs and domain-specific applications in precision oncology. His general interest lies in the design of useful inductive biases for representation learning that goes beyond graph contexts. In previous years his research has focused on developing clustering algorithms on graphs, heterogeneous data integration, and data harmonization techniques.

Dr Nikola Simidjievski

Nikola Simidjievski is a Senior Research Associate at the Department of Computer Science and Technology at the University of Cambridge. He is also Co-Founder of Bias Variance Labs and a Research Associate at the Jozef Stefan Institute in Ljubljana. His research interests are at the intersection of machine learning and natural sciences (medicine, biology and neuroscience). More specifically, he is interested in different machine learning topics for data integrations and their application in oncology. He has experience in computational scientific discovery, and he is also quite keen on machine learning for modelling dynamic systems. More broadly, he is interested in applications of machine learning applications for space research.
Evgeny Saveliev is a PhD Student and Research Engineer at the van der Schaar Lab since 2021. He has previously studied Natural Sciences at the University of Cambridge followed by postgraduate study in Computer Science at the University of Southampton. Evgeny was an AI Resident at Microsoft Research Cambridge before joining the lab, where he worked on projects covering meta-learning and reinforcement learning as applied to recommender systems. He also has experience in computational finance, having worked in a fintech start-up and commodities trading. He is particularly interested in working on AutoML and time-series modelling, as well as machine learning for time series, and synthetic data.
Femke Cole

Femke Cole is the CCAIM Centre Coordinator and acts as intermediary between all parties involved in CCAIM. She oversees the development, delivery and evaluation of the Centre’s projects. She has worked in different parts of the University of Cambridge, supporting a range of projects, and is passionate about bringing people together to achieve the best possible outcome and impact for CCAIM. Femke has a background in Art and Cinematography, and still works as a printmaker and filmmaking educator in her spare time.

Andreas Bedorf

Andreas Bedorf is the CCAIM Communications Manager. He leads the Centre’s creative strategy. He is responsible for the development of digital content, a brand strategy, and relationships with academic researchers, clinicians, and industry partners. Andreas studied Biology, Evolutionary Biology, and Biological Anthropology, in which he is currently pursuing a PhD.
We want to thank all our participants and speakers for their involvement in our first Summer School. A special thanks go out to our industry sponsors and the University of Cambridge for hosting this event. We are proud to collaborate with some of the biggest companies in AI and machine learning research, as well as representatives of the healthcare industry.

Feedback

To improve our Summer School for future iterations, we would be very thankful if you could fill in a very short feedback form and share your experiences with us. This will be provided to you in a separate email.
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<thead>
<tr>
<th>Time</th>
<th>Monday 5th</th>
<th>Tuesday</th>
<th>Wednesday</th>
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<tr>
<td>09:00</td>
<td>Opening welcome</td>
<td>Introduction to the Day</td>
<td>Introduction to the Day</td>
<td>Research Speed Dating</td>
<td>Women in ML</td>
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<tr>
<td>09:30</td>
<td>Clinical Problems and Demonstrators</td>
<td>Dr Eoin McKinney</td>
<td>ML for Healthcare: Where are we on the Pathway to Personalisation</td>
<td>Dr Sarah Teichman</td>
<td>Dr Alexander Gimson</td>
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<td>10:15</td>
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<td>10:30</td>
<td>ML meets Biostatistics 1</td>
<td>Dr Angela Wood</td>
<td>ML interpretability in Healthcare</td>
<td>Dr Ari Ercole</td>
<td>&quot;Advanced&quot; Individualised Treatment Effects</td>
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<td>11:15</td>
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<td>11:30</td>
<td>Healthcare Data Resources &amp; UK Biobank</td>
<td>Dr Angela Wood</td>
<td>Review of AI for medical imaging and diagnosis</td>
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<td>Dr Ioana Bica (DeepMind)</td>
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<td>12:15</td>
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<td>13:00</td>
<td>Uncertainty in Healthcare</td>
<td>Prof José Miguel Hernández-Lobato</td>
<td>Personalised Treatment Effects</td>
<td>Prof Qingyujuan Zhao</td>
<td>From Genomics to Therapeutics</td>
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<td>14:30</td>
<td>AutoML in Healthcare</td>
<td>Prof Mihaela van der Schaar, Dr Fergus Imrie</td>
<td>Multi-Armed Bandits in Healthcare</td>
<td>Prof Cem Tekin (Bilkent University)</td>
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<td>15:15</td>
<td>Q&amp;A</td>
<td>Q&amp;A</td>
<td>Graph Neural Networks</td>
<td>Q &amp; A</td>
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<td>15:30</td>
<td>Time-Series to Forecast Patient Trajectories</td>
<td>Prof Mihaela van der Schaar, Dr Fergus Imrie</td>
<td>Clinical Trials: Current + NextGen</td>
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<td>Q&amp;A</td>
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<td>16:30</td>
<td>ML and Computer Vision for Developmental Disorders</td>
<td>Dr Guillermo Sapio (Duke University/Apple)</td>
<td>Round Table: Pharma Clinical Trials</td>
<td>Prof William Hsu (UCLA)</td>
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<td>17:15</td>
<td>Q&amp;A</td>
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<td>Genomics</td>
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<td>17:30</td>
<td>Optional 1 on 1 Mentoring</td>
<td>Research Speed Dating</td>
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<td>Q&amp;A</td>
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<td>18:00</td>
<td>Optional 1 on 1 Mentoring</td>
<td>Q&amp;A</td>
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