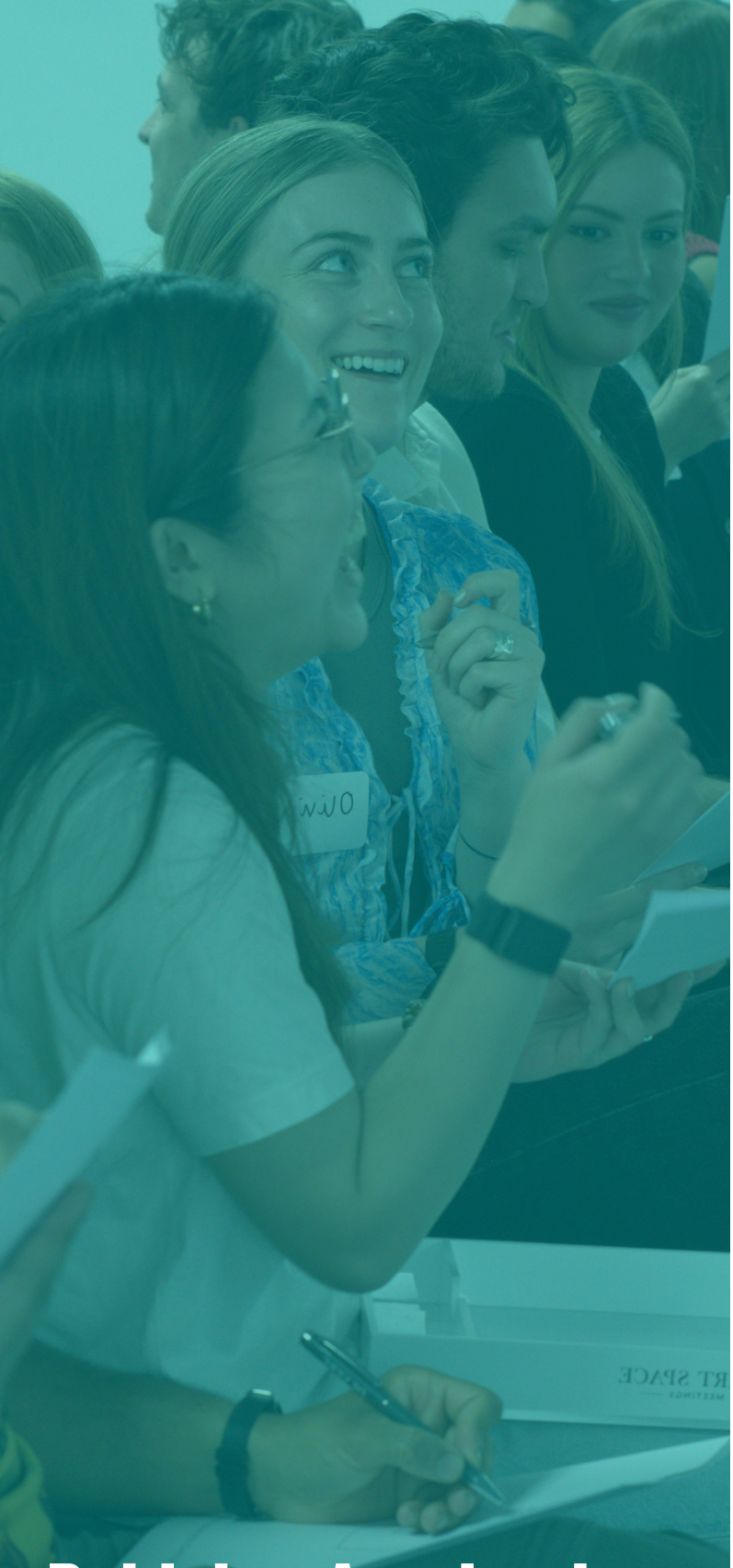

DRIVE-Health
EPSRC Centre for Doctoral Training in Data-Driven Health

UKRI Engineering and Physical Sciences Research Council

KING'S College LONDON

Symposium Booklet

Bridging Academia and Industry: Turning Health Data into Health Solutions

Agenda Thursday 11 June

DRIVE-Health
EPSRC Centre for Doctoral Training in Data-Driven Health
UKRI Engineering and Physical Sciences Research Council
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***Full day will take place in the Theatre**

09:15 **Registration**

10:00 **Welcome**

10:10 **Keynote Lecture: Dr. Luis Garcia-Gancedo, Executive Director and Head of Digital Medicine - Respiratory, Immunology and Inflammation, GSK**

Digital Medicine in Clinical Development: Innovation at the Industry-Academia Interface.

11:00 **Student Spotlight Presentations**

11:45 **Break**

12:00 **Student Lightning Talks**

13:15 **Light Lunch served in the foyer**

14:15 **Student Debate Session**

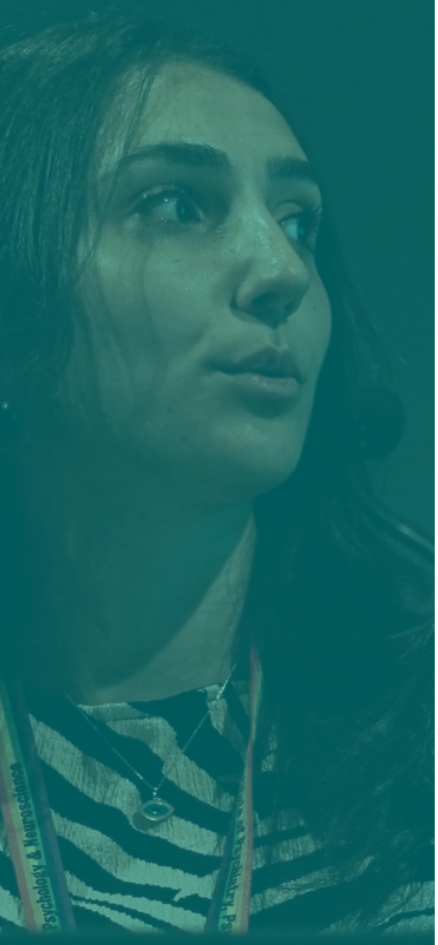
Debate Motion: This house believes that, as things stand, the risks of AI to healthcare outweigh its benefits.

Moderators:
Dr James Roberts, Deputy Chair of the RCGP Health Informatics Group and the Joint GP IT Committee
Marium Naqvi, NIHR Doctoral Clinical Academic Fellow

15:15 **Audience Vote and Chair's Summary**

16:00 **Acknowledgements and Closing Remarks**

Agenda Friday 12 June



***Morning session will take place in the Theatre, then move to the 1st floor Studio**

09:30 **Registration**

10:00 **Welcome**

10:05 **Keynote Lecture: Dr. Jake Taylor-King, Co-founder and Chief Innovation Officer, Relation Therapeutics**

Extracting cytokine perturbation signatures from full-length spatial transcriptomics using biophysical modelling.

10:50 **Panel Discussion:** What does industry actually need from health data PhDs, and how can industry partner with academia for maximum impact?

Panelists and Judges: Dr Jake Taylor-King (Relation), Dr Laura Acqualagna (GSK), Dr Chris Callaghan (Guy's Hospital), Dr Nina Sesto (MEGI Health), Dr Nicolas Huber (King's Innovation Catalyst), Dr Irena Brookes-Smith (AstraZeneca)

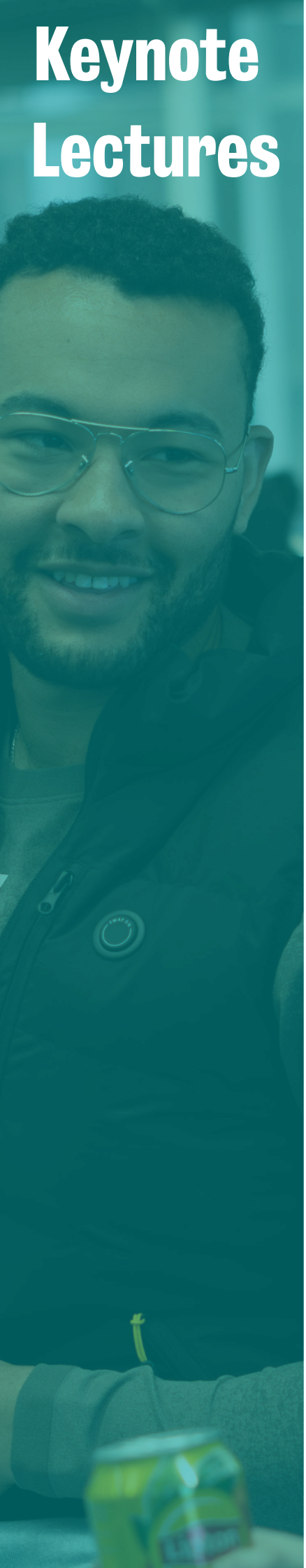
12:00 **Light lunch served in the 1st floor studio**

12:45 **Poster Session and Networking**

14:00 **Student Spotlight Presentations**

15:00 **Awards, Acknowledgments & Close**

Keynote Lectures



Dr. Luis Garcia-Gancedo
Executive Director and Head of Digital Medicine - Respiratory, Immunology and Inflammation, GSK

Talk: Digital Medicine in Clinical Development: Innovation at the Industry-Academia Interface.

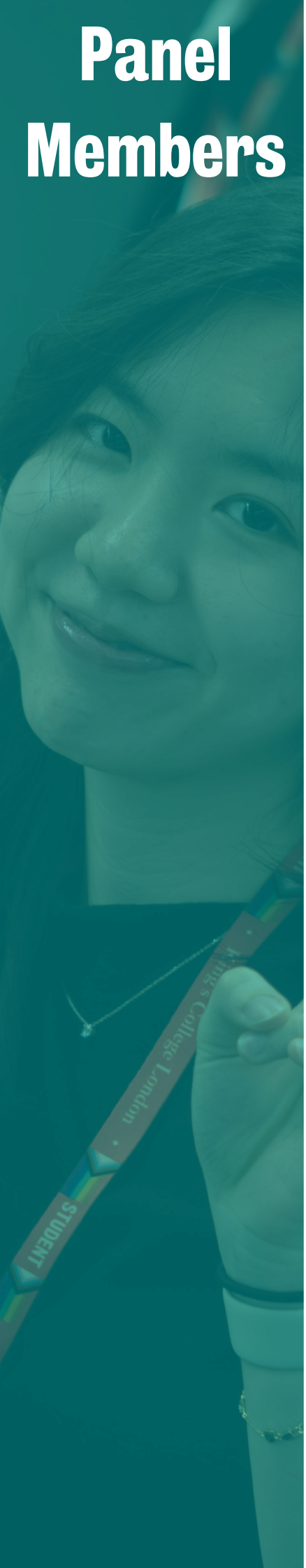
Digital Medicine is transforming clinical trials, with wearable devices, digital endpoints, decentralised trial technologies and AI-driven insights already integrated into many clinical development programmes. This presentation will provide an overview of the current landscape and will discuss the opportunity for industry-academia collaborations to overcome existing barriers (including evidence generation to support validation and regulatory acceptance) to propel the field forward for the benefit of patients.

Dr.Jake Taylor-King,
Co-founder and Chief Innovation Officer, Relation Therapeutics

Talk: Extracting cytokine perturbation signatures from full-length spatial transcriptomics using biophysical modelling.

Prior to co-founding Relation Therapeutics, Jake Taylor-King was an academic and industry researcher interested in company formation at the intersection of technology, computation, and the clinic. Previously an award-winning mathematician (G-Research prize, Lee Segel Prize), he has degrees from Bristol, Oxford, Cambridge, before later transitioning to biomedicine and genomics at ETH Zürich. Jake's role as Chief Innovation Officer at Relation cuts across many functions, including leading an experimental technology development group, engaging in ML research, and designing clinical studies for patient tissue access.

Panel Members



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Dr Laura Acqualagna
Director of AI/ML Engineering at GSK R&D

Laura Acqualagna, PhD, is Director of AI/ML Engineering at GSK R&D, where she leads the development of machine learning systems for computational pathology and multimodal data integration, driving precision medicine, translational research and clinical biomarker discovery. With over 15 years of experience in biomedical AI, she bridges cutting-edge research and real-world clinical impact. Previously, Laura was a Research Associate at Technische Universität Berlin, developing brain–computer interfaces and machine learning models to uncover neural correlates of cognition and motor imagery. She holds a PhD from TU Berlin and an MSc in Neuroengineering from the University of Genoa.

Dr Nicolas Huber
Interim Director of King's Innovation Catalyst

Dr Nicolas Huber is interim Director of King's Innovation Catalyst, leading technology transfer across Translational Research, Industry Partnerships and IP & Licensing. He is also Director of Commercial Operations and Partnerships at the London Institute for Healthcare Engineering, driving LIHE's profile and ensuring its startup and partnership programmes deliver clinical impact.

He previously served as CEO of Cambridge spin-out ProteinLogic and held commercial roles in MedTech firms in Belgium and the UK. He mentors startups through major accelerators and sits on several biotech and medtech advisory boards. Dr Huber holds a PhD in Space Science and an MEng in Electronic Engineering from the University of Sussex.

Panel Members

Dr Nina Sesto
CEO of Megi Health

Nina Sesto, PhD, MBA is the Co-Founder and CEO of Megi Health, an AI-driven platform focused on improving cardiovascular outcomes for women, starting in pregnancy.

She holds a PhD in molecular biology from Institut Pasteur and an MBA from HEC Paris, and previously led digital health initiatives within a high-volume cardiovascular clinic. This experience shaped her focus on bridging the gap between clinical data, patient behavior, and real-world outcomes.

At Megi Health, Nina is building clinically grounded, AI-powered tools that turn health data into continuous, actionable care for patients and clinicians. Her work sits at the intersection of academia and industry, with a focus on translating research and large-scale datasets into solutions that can be deployed in everyday care.

Dr. Jake Taylor-King
Co-founder and Chief Innovation Officer, Relation Therapeutics

Prior to co-founding Relation Therapeutics, Jake Taylor-King was an academic and industry researcher interested in company formation at the intersection of technology, computation, and the clinic. Previously an award-winning mathematician (G-Research prize, Lee Segel Prize), he has degrees from Bristol, Oxford, Cambridge, before later transitioning to biomedicine and genomics at ETH Zürich. Jake's role as Chief Innovation Officer at Relation cuts across many functions, including leading an experimental technology development group, engaging in ML research, and designing clinical studies for patient tissue access.

Panel Members

Dr Irena Brookes-Smith
Head of Healthcare Analytics, AstraZeneca

Irena Brookes-Smith is a Real World Evidence leader with 15 years of experience in the pharmaceutical and healthcare sectors. She has deep expertise in utilising Real World Datasets (RWD) throughout drug development lifecycle and how to leverage data science and technology solutions to bridge the gap between research and clinical practice. Currently, she leads the Healthcare Analytics team in AstraZeneca's Biopharmaceutical R&D, where she focuses on utilizing RWD insights to optimise clinical development. Previously, she worked in Public Health, NHS and Deloitte consulting practice. She holds MSc from University of Pisa and an MPH from University of Birmingham.

Through her work, she has collaborated with academics, healthcare providers, and technology companies to develop analytical strategies aimed at accelerating clinical development and improving patient outcomes.

Dr Chris Callaghan
Consultant Transplant Surgeon, Guy's Hospital

Chris is a Consultant Transplant Surgeon at Guy's Hospital, and also works at the Evelina London Children's Hospital and Great Ormond Street Hospitals. He has research interests in the machine perfusion of organs, and the optimal use of higher risk deceased donor organs. Chris is an Honorary Senior Lecturer at King's.

Student Lightning Talks

Marium Naqvi - NIHR Doctoral Clinical Academic Fellow (Affiliate)

From Reactive to Predictive: AI-Enhanced Remote Monitoring in ILD

Interstitial lung disease (ILD) is characterised by unpredictable disease trajectories and periods of clinical deterioration that may not be identified promptly through traditional outpatient review. Advances in digital health technologies enable longitudinal home monitoring of physiological parameters and patient-reported outcomes, generating large volumes of real-world data with potential to transform ILD care.

AIRMILD is exploring the use of artificial intelligence (AI) to enhance remote monitoring in ILD. The project integrates home spirometry, pulse oximetry, symptom reporting and other digital biomarkers to investigate whether AI-driven approaches can identify clinically meaningful change earlier and support more proactive, personalised care pathways.

This lightning talk will provide an overview of AIRMILD, including the rationale for AI-enhanced monitoring, key methodological challenges, and opportunities for integrating predictive analytics into routine clinical practice. The talk will also explore wider considerations around implementation, patient acceptability, clinical workflow integration and the future role of AI in chronic respiratory disease management.

Student Lightning Talks

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Tomas Solomon - Cohort 2024

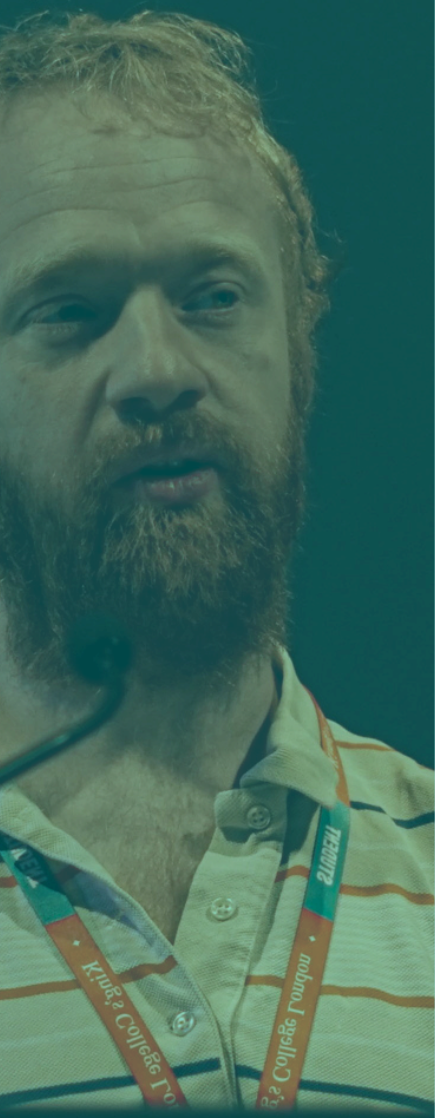
Low-dose chronic rotenone exposure alters transcriptomic and epigenetic signatures in a dopaminergic cell line

Chronic exposure to the mitochondrial complex I inhibitor rotenone is a well-established model for Parkinson's disease (PD), yet the long-term epigenetic mechanisms driving neuronal decline remain unclear. In this study, we assess the impact of chronic low-dose exposure to the pesticide rotenone on gene regulation of SH-SY5Y cells differentiated into dopaminergic neurons.

We performed RNA-seq and H3K27ac ChIP-seq to profile gene expression and active regulatory elements after 1, 5 and 30 days of exposure. We show coordinated suppression of gene expression and histone hypoacetylation in the mevalonate pathway, as well as in axonal and synaptic-neurotransmission genes over 30 days. Hypoacetylated regions associated with rate-limiting mevalonate pathway genes HMGCS1, FDFT1, and INSIG1 showed enrichment for master regulator transcription factor motifs of SREBP1a and SREBP2 motifs, indicating silencing of cholesterol homeostatic machinery. Furthermore, motif enrichment analysis of hypoacetylated regions identified a high prevalence of AP-1 (c-Jun/ATF) and C/EBP complexes important in cellular stress response. These are particularly enriched in hypoacetylated regions associated with axon maintenance, neurotransmission, and apoptotic genes.

Overall, our results demonstrate chronic rotenone exposure triggers transcriptomic and epigenomic changes in the dopaminergic cell model affecting cholesterol metabolism and neurite outgrowth genes.

Student Lightning Talks



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Ella Maunder - Cohort 2025

Cross-species single-cell atlas of cardiovascular diseases

"Ella J. Maunder1, Jirapath Thammaphet1, Catherine M. Shanahan1, and Konstantinos Theofilatos1

1 British Heart Foundation Centre for Research Excellence, School of Cardiovascular and Metabolic Medicine and Sciences, James Black Centre, King's College London, UK

Background

Cardiovascular diseases and conditions, including atherosclerosis, vascular ageing and vascular calcification, arise from age-driven vascular remodelling shaped by genetic and environmental factors. Single-cell RNA sequencing (scRNA-seq) has enabled high-resolution dissection of vascular cellular heterogeneity, but existing integrated atlases are limited by heterogeneous preprocessing and manual parameter tuning. In parallel, gene regulatory network (GRN) inference from scRNA-seq data remains constrained by reliance on curated interactions and known regulators.

Materials and Methods

We analysed an integrated scRNA-seq atlas of human vascular cells alongside two independent mouse scRNA-seq datasets from novel models of vascular ageing and calcification, each spanning multiple timepoints. The two in vivo mouse models are a vascular smooth muscle cell (SMC)-specific Zmpste24 knockout that induces prelamin A accumulation (vascular ageing) and a SMC-specific Zmpste24/Runx2 double knockout (vascular calcification). We are developing an optimised scRNA-seq processing and integration framework to allow more reproducible preprocessing of the data and better within and cross-species integration and comparability, removing technical biases and retaining biological variability. In parallel, we are constructing an unbiased GRN inference workflow to identify regulatory interactions de novo across conditions.

Results

Integrated analysis resolved conserved vascular cell populations across human and mouse datasets. Level 1 clustering identified major vascular cell types, while level 2 SMC analysis revealed distinct transcriptional substates associated with ageing and calcification. Preliminary cross-condition integration demonstrates robust alignment of cellular states across species and disease models. Ongoing work extends these analyses toward a unified cross-species vascular atlas.

Discussion

These data support the feasibility of a unified cross-species vascular single-cell atlas capturing cellular and transcriptional diversity across ageing and disease. Coupling optimised integration with high-resolution cell-state decomposition and unbiased GRN inference provides a framework to resolve regulatory mechanisms underlying vascular remodelling and identify candidate therapeutic targets in atherosclerosis and vascular calcification."

Student Lightning Talks

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Akshit Achara - Cohort 2024

Localising Shortcut Learning in Pixel Space via Ordinal Scoring Correlations for Attribution Representations (OSCAR)

Deep neural networks often exploit shortcuts. These are spurious cues which are associated with output labels in the training data but are unrelated to task semantics. When the shortcut features are associated with sensitive attributes, shortcut learning can lead to biased model performance. Existing methods for localising and understanding shortcut learning are mostly based upon qualitative, image-level inspection and assume cues are human-visible, limiting their use in domains such as medical imaging.

We introduce OSCAR (Ordinal Scoring Correlations for Attribution Representations), a model-agnostic framework for quantifying shortcut learning and localising shortcut features. OSCAR converts image-level task attribution maps into dataset-level rank profiles of image regions and compares them across three models: a balanced baseline model (BA), a test model (TS), and a sensitive attribute predictor (SA). By computing pairwise, partial, and deviation-based correlations on these rank profiles, we produce a set of quantitative metrics that characterise the degree of shortcut reliance for TS, together with a ranking of image-level regions that contribute most to it. Experiments on CelebA, CheXpert, and ADNI show that our correlations are (i) stable across seeds and partitions, (ii) sensitive to the level of association between shortcut features and output labels in the training data, and (iii) able to distinguish localised from diffuse shortcut features.

As an illustration of the utility of our method, we show how worst-group performance disparities can be reduced using a simple test-time attenuation approach based on the identified shortcut regions. OSCAR provides a lightweight, pixel-space audit that yields statistical decision rules and spatial maps, enabling users to test, localise, and mitigate shortcut reliance.

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Saif Latifi - Cohort 2024

Workflow-Aware Interaction Detection: Integrating Clinical Workflows with Treatment Effect Reasoning

Introduction

Clinical Practice Guidelines (CPGs) frequently struggle to accommodate the complexities of multimorbidity [1]. To automate decision support, these narrative documents are often translated into Computer-Interpretable Guidelines (CIGs) [2]. Whilst the Transition-based Medical Recommendations (TMR) model effectively identifies treatment interactions within CIGs by analysing intended physiological effects rather than using static rules [3], previous implementations have functioned primarily as static analysis tools. Crucially, by representing guidelines as a flat set of recommendations, they failed to capture the inherent hierarchical and temporal structures commonly found in real-world guidelines. This structural limitation not only rendered them unsuitable for accurate, patient-specific interaction detection but also resulted in falsely flagged conflicts between treatments that would never clinically co-occur. Therefore, this work aims to extend the TMR framework by integrating a clinical workflow representation, accurately reflecting CPG architecture to enable dynamic execution, longitudinal care modelling, and context-aware conflict detection.

Methods

We expanded the TMR ontology to support executable clinical workflows structured via distinct node types: Recommendation nodes (which start, stop, or give treatments), Decision nodes (XOR logic automating workflow traversal via patient data, including SNOMED codes, numeric measurements, and age thresholds), Choice nodes (facilitating clinician preference), and Pause nodes (suspending execution to evaluate treatment efficacy over time). To accommodate this dynamic structure, the reasoning engine was upgraded with workflow-aware predicates, ensuring that the Z3 theorem prover only flags conflicts within concurrent, realistically co-occurring workflow branches. Finally, the formalised workflows are automatically translated (transpiled) into Business Process Model and Notation (BPMN) for execution via the Camunda engine.

Student Lightning Talks

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Results

The introduction of workflow semantics successfully transitions the TMR platform from a static knowledge acquisition environment into a dynamic framework for patient-specific interaction detection. By actively evaluating patient data to navigate decision nodes, the system filters out irrelevant recommendations. Consequently, workflow-aware reasoning significantly reduces false-positive conflict alerts by recognising that treatments in mutually exclusive branches do not contradict one another. Furthermore, the inclusion of pause nodes natively supports longitudinal management, allowing workflows to resume and adapt if a patient's condition remains uncontrolled. While a full clinical and performance evaluation is currently pending, initial case studies have shown strong results demonstrating the soundness and expressiveness of the new formalism. The automatic conversion to BPMN effectively translates formal logical verification into executable process models.

Conclusions

Integrating workflow mechanisms with physiological effect-based reasoning provides a robust, scalable foundation for multimorbidity management. This advancement empowers healthcare systems to model complex, patient-specific CIGs with higher fidelity, enabling rigorous, automated auditing of treatment conflicts as a crucial step towards fully realised clinical decision support.

Student Posters

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Anna Redly - Cohort 2025
Intentional ADHD medication non-adherence in the first year following adult ADHD diagnosis: the role of ADHD symptom severity, impairment and employment

Alexander Anderson - Cohort 2025
Multimodal AI to predict Cardiovascular disease

Ao Zhang - Cohort 2025
Latent Behavioural States from Passive Digital Phenotyping in Depression

Wenqi Zhu - Cohort 2025
Understanding and Designing Technologies to Support People with Communication Difficulties Through Healthcare Journeys

Kanyakorn Veerakanjana - Cohort 2022
Wearable-derived cardiovascular and autonomic changes associated with ADHD stimulant medication: A remote monitoring study of adults with ADHD

Arman Orbeladze - Cohort 2025
Multi-omics analysis of ageing heart

Patrick Campbell - Cohort 2024
The contribution of rare genetic variation and prenatal & perinatal factors to rare developmental disorders

Ella Maunder - Cohort 2025
Cross-species single-cell atlas of cardiovascular diseases

Saif Latifi - Cohort 2024
Workflow-Aware Interaction Detection: Integrating Clinical Workflows with Treatment Effect Reasoning

Olivia Dann - Cohort 2024
Gender disparities in neurodevelopmental identification: evidence from a linked health visiting and primary care cohort in South London

Student Posters

Akshit Achara - Cohort 2024
Localising Shortcut Learning in Pixel Space via Ordinal Scoring Correlations for Attribution Representations (OSCAR)

Yusuf Abdulle - Cohort 2024
Symptom-based phenotype discovery in motor neuron disease using natural language processing of electronic health records

Idris Matine - Cohort 2024
Transcription Factor Binding Site Prediction in Biosynthetic Gene Cluster Families

Abed Alah Mosa Al Refaee - Cohort 2024
Microsecond molecular dynamics of SOD1 variants suggest a structural basis for divergent ALS clinical outcomes

Emily Gillings - Cohort 2024
The role of digital phenotyping in monitoring stress and trauma-related mental health disorders: A systematic review on the feasibility of passive sensing for symptom prediction

Agathe Zecevic - Cohort 2024
Uncertainty-Aware Multi-Label Routing of Clinical Text to Surveillance Pathways

Yigit Avci - Cohort 2024
Metadata-Aligned 3D MRI Representations for Contrast Understanding and Quality Control

Marium Naqvi - NIHR Doctoral Clinical Academic Fellow (Affiliate)
AIRMILD: Artificial Intelligence enhanced Remote Monitoring in Interstitial Lung Disease

Narges Matinazad - Cohort 2024
Evaluating HTT Repeat Length As A Potential Genetic Modifier Of Disease Susceptibility And Onset Timing In ALS Cases

Student Posters

Robert Manschke - Cohort 2025
Probabilistic Uncertainty-aware Longitudinal Simulation of EHR-trajectories

Jona Flavier - Cohort 2025
Developing a Multimodal Data Infrastructure and Biomarker Pipeline for Wearable Opioid Overdose Detection

Renato Dos Santos - Cohort 2024
Characterising the Metagenomic Landscape of Amyotrophic Lateral Sclerosis from Unmapped Whole Genome Sequencing Data

Tomas Solomon - Cohort 2024
Low-dose chronic rotenone exposure alters transcriptomic and epigenetic signatures in a dopaminergic cell line

Aleksandra Korbacz - Cohort 2024
Clinical Practice Research Datalink 2010-2024 cohort description – epidemiology of cancer in the United Kingdom

Michal Aleksandrowicz - Cohort 2025
Engagement with an AI-driven cardiovascular monitoring platform and blood pressure trajectories: a multi-stage analysis of 8,000 users

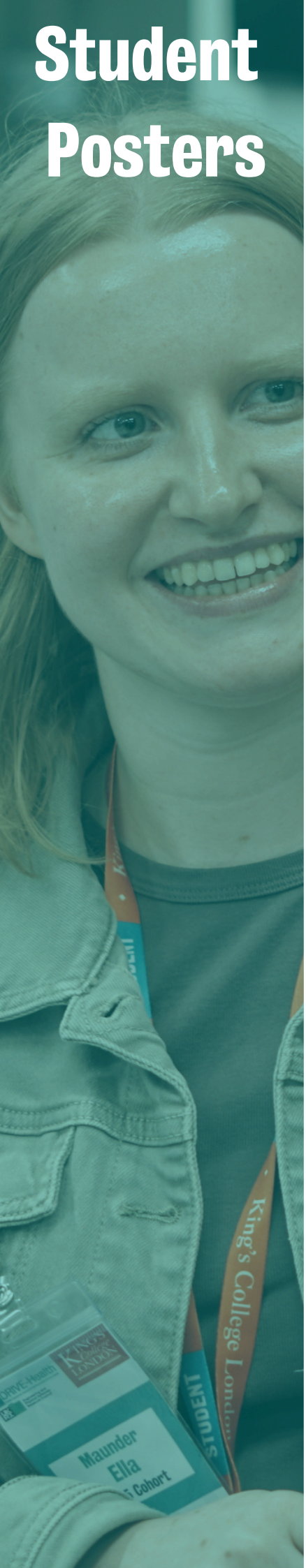
Binh Vu - Cohort 2024
Minimax Rates and Spectral Distillation for Tree Ensembles

Niko Moëller-Grell - Cohort 2024
Extending FastOMOP to the OHDSI Application Layer: MCP Servers for Vocabulary, Cohort Definition, and Statistical Profiling

Aditya Borakati - Cohort 2025
imProvIng Outcomes iN livEr transplantation with data warEhousing and natural language pRocessing (PIONEER)

Ziyuan Cai - Cohort 2024
Trial-level decomposition of remote cognitive tasks

Student Posters



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Kamara McLeish-Evoloko - Cohort 2024
Development and feasibility of the Community Ageing Research Across Ethnicities (CARE) Network APP for diverse communities and faith groups

Christopher Spence - 2025 Cohort
Data-Driven Neurorehabilitation with Machine Vision

Yuju Ahn - 2025 Cohort
Identification of Genetic and Environmental Drivers of Skin Ageing with AI and Multi-omics Analyses in TwinsUK

Acknowledgements

We would like to thank our Symposium Committee members for their contributions to the planning and delivery of this fantastic event. In particular, we would like to acknowledge those who played key roles in shaping the programme:

- **Aleksandra** – Planning and Delivery
- **Niko** – Panel Planning and Chairing
- **Anna, Robert, Michal, Renato, Tomas, Marium, Ao, Aleksandra, and Niko** – Debate Planning and Delivery

We would also like to thank all of our students for their enthusiastic involvement, as well as our keynote speakers, debate moderators, panel members, and judges for their time and expertise. Our appreciation also goes to the EPSRC DRIVE-Health team for their ongoing support and contributions.

Finally, we are grateful to all of our collaborators and partners for their continued engagement and support of our CDT.