52

AI & ML SIG: Artificial Intelligence updates and applications.

Sam Hadlington[1], Chris Harbron[2], Paola Berchialla[3], Danila Azzolina[4], Karl Koechert[5], Eliana Garcia-Cossio[6], Nils Ternes[7]

[1]Plus-Project Partnership, Hook, United Kingdom. [2]Roche, Welwyn Garden City, United Kingdom. [3]University of Torino, Turin, Italy. [4]University of Ferrara, Ferrara, Italy. [5]Sanofi R&D, Berlin, Germany. [6]Bayer, Berlin, Germany. [7]Sanofi R&D, Paris, France

Sam Hadlington
Please provide a brief biography for the Presenting author(s)
Sam Hadlington began his career with IQVIA, gaining experience in oncology among other indications. He later joined Plus-Project Partnership, focusing on post-marketing oncology immunology trials. Through PSI, he's contributed to events, career development, and networking initiatives for new statisticians as well as heading up the new AI & ML SIG.

Chris Harbron
Please provide a brief biography for the Presenting author(s)
Chris Harbron is an Expert Statistician leading capabilities in Advanced Analytics within the Data Sciences function at Roche. Through a variety of roles within the pharmaceutical industry Chris has worked in all stages of the drug development pipeline from drug discovery to early and late development. Chris has published and presented widely both within the statistical and the broader scientific literature.

Paola Berchialla
Please provide a brief biography for the Presenting author(s)
Paola Berchialla is an Associate Professor in Biostatistics at the Department of Clinical and Biological Sciences, University of Torino. Her research activity focuses on Bayesian Design for clinical trials and Machine Learning applied to epidemiological research and clinical decision support.
She has contributed her expertise to projects funded by the European Food Safety Authority, the European Commission's DG SANCO, and the European Space Agency. She has authored over 250 papers in international scientific journals.

Danila Azzolina
Please provide a brief biography for the Presenting author(s)
Danila Azzolina is an associate professor in biostatistics at the Department of Environmental and Preventive Science, University of Ferrara (Italy), and lead statistician at the Clinical Trial Biometry and Research Methodology Unit of the Ferrara University Hospital.

Karl Koechert
Please provide a brief biography for the Presenting author(s)
Since January 2025, Karl is a Statistical Project Leader at Sanofi's Statistical Innovation Hub. Prior to joining Sanofi, Karl was Head of Biomarker & Data Insights at Bayer AG (Berlin, Germany) leading a team of data scientists / statisticians. With a background in omics data science and precision medicine, his team's major objective is to advance drug development by enabling holistic understanding of complex biological systems - namely the patients in need. In this vein, their current endeavor is to understand how applied AI/ML can help to detect highly complex safety and efficacy signals in interventional clinical trials and how that can be utilized as a basis for creating virtual twins of specific disease indications.
Karl, being a Biochemist by training, discovered his passion for mathematical modelling of complex biological systems during his PhD at Humboldt University (Berlin, Germany) and subsequently devoted himself to applied machine learning during postdocs at TU-Dresden (Germany) and the Max-Delbrück-Center for Molecular Medicine (Berlin, Germany) before joining Bayer AG in 2014. At Bayer he has held positions of increasing responsibility as Study and Project Biomarker statistician for interventional trials of all phases in oncology.

Eliana Garcia-Cossio
Please provide a brief biography for the Presenting author(s)
Eliana Garcia-Cossio is a Senior Biomarker Data Scientist at Bayer's Data Science & Artificial Intelligence cluster, where she leverages her extensive expertise in both wet and digital biomarkers to drive data insights within the clinical development landscape. Her work is characterized by a strong emphasis on explainable artificial intelligence, enabling the translation of complex data into actionable insights that enhance decision-making processes.
Prior to her tenure at Bayer AG, which began in 2020, Eliana contributed her skills to a medical device company, where she played a pivotal role in the development of innovative applications for neuroscience-related products.
Eliana holds a PhD in Neuroscience and a degree in Biomedical Engineering from Colombia. She is also an active member of the PSI European Biomarker Special Interest Group, where she collaborates with fellow professionals to advance analytics in the biomarker domain, particularly through machine learning applications for biomarker identification.

Nils Ternes
Please provide a brief biography for the Presenting author(s)
Nils Ternès is a statistical biomarker leader at Sanofi R&D in France where he leads the biomarker-related statistical activities on several compounds in clinical development across all phases in Oncology, Immunology and Neurology. With this position, Nils is continuously looking for data and analytical methods innovations as well as operational efficiency to ensure effective decision making, generate translational medicine insights and increase the productivity of drug development. Before joining Sanofi, Nils studied statistics applied to public health at Paris-Saclay University (MSc) and holds a PhD in Biostatistics (2016) at Gustave Roussy cancer institute on advanced penalized regression techniques for the identification of prognostic and predictive biomarkers in high-dimensional settings. With a constant interest in learning and promoting the use of ML/AI techniques to support clinical development, he is now co-leading the Machine Learning workstream from the Biomarkers ESIG.

Single topic, multi-speaker session, Workshop or Single presentation submission

A single topic, mutli-speaker session/workshop

Single topic session or workshop abstracts

Introduction to AI & ML SIG: Introducing the new artificial intelligence and machine learning special interest group. In this section we will give a brief overview of the SIG and discuss some of our goals for the future.

Predicting with uncertainty:

Predictive models are widely being developed and proving useful across a range of applications in pharmaceutical development and healthcare more generally. However, as good statisticians, we recognise that for a point prediction to be useful in decision making it needs to be put into context with an estimate of the uncertainty associated with that prediction, typically with some sort of prediction interval.

With standard statistical models such as linear regression, it is well known how to generate prediction intervals and their properties are well understood. However for more modern machine learning or artificial intelligence models, involving a greater degree of model selection or adaptability, these approaches don't naturally translate.

Conformal prediction is an emerging approach for generating prediction intervals with the minimal assumptions of exchangeability. Conformal prediction intervals can be calculated for predictive models generated using any statistical, ML or AI algorithm and don't make any distributional assumptions. In this talk I'll introduce two flavours of conformal prediction and compare their behaviour with that of standard statistical prediction intervals.

(also submitted as individual presentation)

AI Generated Synthetic Control Arms to optimize Clinical Trials:

Background. Clinical trials are lengthy, expensive, and frequently fail to demonstrate the expected treatment benefits. While Randomized Clinical Trials have been the gold standard, a surge in non-randomized evidence is reshaping evaluation methods. Regulatory bodies have increasingly recognized the value of incorporating external data in control arms to accelerate the approval of innovative therapies while maintaining rigorous standards for evidence quality.

Objective. The objective of this work is developing advanced AI algorithms to generate synthetic patients to augment control arms and design effective methods for treatment estimation that address challenges associated with non-randomized trials.

Methods. The methodology employs data from three studies conducted under the Multicentre Italian Trials in Ovarian Cancer aimed at assessing whether carboplatin combined with pegylated liposomal doxorubicin was more effective than standard chemotherapy. AI-based algorithms based on Variational Autoencorders Generative Adversarial Network VariationaAutoencoder (VAE-GANs) were utilized to generate patients data to be included in the control arm. Effect estimation methods incorporated machine learning causal inference models and Bayesian frameworks. Sensitivity analyses were conducted to evaluate the robustness of treatment effect estimates.

Results. Preliminary results indicate that the VAE-GANs model generates data with clinical variable distributions closely aligned with those of the original dataset. The autoencoder algorithm was employed to estimate the progression-free survival, yielding HR: 0.98 (95% CI: 0.81–1.19), comparable to estimates obtained from the pooled database.

Conclusions. The findings demonstrate the potential of VAE-GAN and autoencoders to generate reliable synthetic data suggesting more efficient clinical trial designs while maintaining robust validity.

(also submitted as individual presentation)

Explainable AI for Causal Inference and Heterogeneous Treatment Effect Estimation via AI/ML – a conceptual framework for late phase clinical trials:

Recent advancements in machine learning (ML)-based causal inference enable the estimation of treatment effects tailored to individual patients based on complex covariate profiles. These methods facilitate further analysis, allowing researchers to evaluate covariates driving treatment effect heterogeneity and predict individual treatment effects for new patients, supporting personalized treatment recommendations, thus enabling true precision medicine.

Our talk presents a framework for leveraging ML-based causal inference with explainable Artificial Intelligence methods (xAI) in late-phase clinical trials. Using simulated trials, we demonstrate how xAI can be employed across various causal inference methods (e.g., meta-learners with ML base learners) to generate actionable and robust results. The xAI framework utilizes model-agnostic (post-hoc) techniques to enhance interpretability.

We employ global interpretability techniques, such as permutation variable importance, SHapley Additive exPlanations (SHAP), and Partial Dependency Plots, to reveal key covariates influencing model predictions and treatment effects as well as assessing the relationship between model predictions and covariate values. Local interpretability methods, like counterfactual explanations, simulate “what if” scenarios, aiding trial interpretation and future planning.

Integrating xAI fosters trust among stakeholders, including regulatory bodies, by providing clear explanations for model predictions and detecting biases and confounders. Combining causal inference with xAI offers a robust framework for generating hypotheses on treatment effect heterogeneity and visualizing model decision processes, leading to accurate, transparent, and interpretable models for better decision-making.

(also submitted as individual presentation)

Predicting the probability of clinical trials success from AI-based approaches using multimodal data:

Clinical trials are essential for the drug development lifecycle but often face uncertain outcomes due to safety, efficacy, or patient enrolment problems. It is widely known that the overall probability of clinical trial success is very limited (around 10%) and leading to unnecessary development cost and time, and most importantly unnecessary patient exposition. Predicting the probability of success of a clinical trial before it starts is therefore key for informed decision making and efficient drug development plan. Nowadays, with the spectacular breakthrough of AI/ML, there is active research in using these innovative approaches to support this goal and could be extended to drug positioning, indication prioritization or population optimization. Some recent works consider deep-learning approaches such as graphical or recurrent neural networks, or fine-tuned large language models. Benchmarks with large and multi-modal data sources are essential to achieve better prediction accuracy, such as with clinical trial information, drug chemical structure, target disease, pharmacokinetics and toxicology information, or even electronic health records. This presentation will provide an overview of current research in this hot topic, together with critical thinking, as well as some internal development. In such a project, the development of fit-for-purpose benchmarks is even more critical than the AI-based model development itself. Even if several efforts have been initiated to create large clinical trial benchmarks, important improvements are still needed, and practical considerations will be shared. Bringing together expertise in AI/ML as well as in drug development and clinical research is key for project success.

(also submitted as individual presentation)