

Multi-Omics Data Integration in Human Exposome Studies



Register Here →

FREE TO ATTEND

FORMAT

Online

Join from anywhere

DATES

September 30 –
December 16, 2026

SCHEDULE

Wednesdays

16:00 – 18:00h (CET)

PROGRAM

12 Sessions

3 modules

We are excited to announce the second edition of the online workshop series, **"Multi-Omics Data Integration in Human Exposome Studies."** While the first edition focused on foundational, introductory material, this second edition goes a step further.

This workshop series introduces participants to state-of-the-art analytical frameworks and statistical workflows recently developed in the exposomics field. Designed as a highly practical, hands-on experience, these seminars will provide participants not only with theoretical concepts of exposomic analyses but with code and resources for their implementation — empowering participants to apply the presented techniques in their own research.

About the Workshop Series

The integration of multiple omics layers with environmental data represents a cornerstone for advancing precision environmental health and epidemiology. However, combining these complex datasets introduces significant computational and methodological challenges.

We begin with the foundations of multi-block dimensionality reduction, the workhorse for distilling high-dimensional, collinear exposomics layers into low-dimensional, biologically meaningful signatures. From there, our speakers will present methodological solutions for some of the field's most pressing challenges: relating exposures to biology through mediation and causal frameworks; disentangling the "mixture problem" of simultaneous environmental stressors; reconstructing the connectivity between molecular and exposure layers through network-based approaches; and incorporating emerging omic layers that bridge the environment and the host.

Participants will also explore specialised strategies to overcome recurrent data limitations, including missing and incomplete data, imbalanced outcomes, and longitudinal analyses that capture dynamic exposome-omic stability and time lags. Finally, the workshop turns to the AI frontier: the emerging role of Large Language Models (LLMs) and generative AI tools in multi-omics workflows, and the concept of XAI (eXplainable Artificial Intelligence) — a growing trend that promotes trustworthy, interpretable algorithms and post-hoc tools for understanding the relationships between features and their contribution to a prediction.

Code & Materials

We will grant direct and free access to all session code and materials, during and after the workshop, on our GitHub and YouTube channel.

Who Should Attend

Master's/PhD students, researchers, clinicians, and other professionals in exposomics, epidemiology, or toxicology interested in how omics data — including the exposome — can be integrated in epidemiological research.

Research Topics

Full program and speaker list coming soon.

Module 1 · Foundations of Exposomics Data Integration & Multi-Block Dimensionality Reduction

- 1 Introduction to exposomics data integration: an overview of approaches
- 2 Foundations of dimensionality reduction and multi-block data integration

Module 2 · From Exposures to Biology: a Tour of Exposomics Data Integration Frameworks in Practice

- 3 Multivariate mediation frameworks in environmental epidemiology
- 4 Statistical frameworks for evaluating complex co-exposures and mixtures
- 5 RGCCA for exposomic data integration in youth health
- 6 Network-based approaches for multi-omics and environmental data integration and interpretation
- 7 Integrating the microbiome as emergent omic layer in environmental health
- 8 Longitudinal methods and frameworks for multi-omics and environmental data integration
- 9 Outcome-wide analysis for exposomics

Module 3 · Machine Learning & AI Frontiers

- 10 eXplainable Artificial Intelligence (XAI) for making predictions in exposomics
- 11 eXplainable machine learning for unbalanced regression; dealing with missingness and data integration in exposomics
- 12 Frontiers in exposomics: using Large Language Models (LLMs) to integrate external knowledge in exposomics frameworks

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More information & updates: www.isglobal.org/en/exposome-hub

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