



Leibniz-Institut für Analytische
Wissenschaften – ISAS – e.V.

Dortmund & online

COLLOQUIUM

MAPtoGO: extending gene ontology analysis to lipidomics-centered multiomics data

Speaker:

Dr Dominik Kopczynski, is an Assistant Professor of “Data Science in Mass Spectrometry-Based Omics” at the University of Vienna. He heads a research group at the Institute of Analytical Chemistry there, which specializes in the development of efficient algorithms for computer-assisted lipidomics and proteomics.

Time:

Thursday, July 16, 2026 – 1 pm

Venue:

ISAS Campus, Lecture Hall
Otto-Hahn-Straße 6b
44227 Dortmund

&

WebEx: <https://t1p.de/k43bw>

Meeting-ID: 2785 703 0438

Password: 4kdPh2Djvk2

Abstract

Over-representation analysis (ORA) is beginning to be applied in lipidomics to interpret datasets, for example by identifying statistically significant enrichments such as excess of unsaturated fatty acids or overrepresented lipid classes (e.g., more phosphatidylcholine species). While these approaches reveal global compositional trends, they often lack a direct connection to biological processes, metabolic pathways, or disease-relevant functions. Consequently, important patterns in lipid remodeling, signaling, and membrane organization may be overlooked. Bridging the gap between enriched lipid features and functional biological annotations is therefore essential for more mechanistic and interpretable lipidomics analyses.

To address this challenge, we developed MAPtoGO, the Multiomics Analysis Platform towards Gene Ontology for simultaneous GO-based enrichment across proteomics, lipidomics, metabolomics, and transcriptomics. The platform enables unified interpretation of biomolecules, identifying enriched GO terms, metabolic pathways, physicochemical categories, and disease associations in a single analysis. Users provide two lists per molecule type: a background list of all detected biomolecules and a subset of significantly regulated ones. MAPtoGO supports proteins (UniProt), lipids (LIPID MAPS or shorthand nomenclature), transcripts (Ensembl), and metabolites (trivial names or ChEBI), linking them to GO terms and pathways via public databases. Enrichment is calculated using Fisher's exact test with Benjamini-Hochberg FDR correction. The web interface includes example datasets, downloadable results, and statistical plots for deep visualization and easy interpretation.

In conclusion, this novel multiomics enrichment analysis adds a valuable dimension to comprehensive computational multiomics pipelines. It enables direct connections between study-specific conditions and terms across multiple domains that includes biological processes, molecular functions, metabolic pathways, and disease associations, offering critical insights into the underlying biology of multiomics studies. With this novel approach, researchers are able now to investigate considerably faster their studies and gain a better understanding of the underlying processes that cause the changes in molecular composition. We implemented MAPtoGO in a lightweight web application that is openly available [<https://lifs-tools.org/map-to-go>] and free of charge. The application is fully integrated with Goslin enabling the smooth interpretation of lipid name dialects from various software outputs.