MQ-DATAMIND Workshop

Proteomics and mental health: using large-scale population-based plasma proteomic data to examine causal mechanisms and blood-based biomarkers for mental health conditions

Optional readings for session 1:

1. Sun BB, Suhre K, Gibson BW. Promises and Challenges of populational Proteomics in Health and Disease. Mol Cell Proteomics. 2024 Jul;23(7):100786. <https://doi.org/10.1016/j.mcpro.2024.100786>

*Broader perspective: This paper explains how new proteomic technologies allow researchers to measure thousands of proteins in large populations, helping to find biomarkers and improve disease prediction. It highlights both the opportunities and challenges of using proteomics in large-scale studies.*

1. Schuermans, A., Pournamdari, A.B., Lee, J. *et al.* Integrative proteomic analyses across common cardiac diseases yield mechanistic insights and enhanced prediction. *Nat Cardiovasc Res* **3**, 1516–1530 (2024). <https://doi.org/10.1038/s44161-024-00567-0>

*Example of method integration (cardiac diseases): This study integrates large-scale proteomics with epidemiological analyses, Mendelian randomization, and prediction modelling to identify proteins linked to major cardiac diseases and highlight potential therapeutic targets using UK Biobank data.*

1. Kang J, Yang L, Jia T, Zhang W et al. Plasma proteomics identifies proteins and pathways associated with incident depression in 46,165 adults. Sci Bull (Beijing). 2025 Feb 26;70(4):573-586. <https://doi.org/10.1016/j.scib.2024.09.041>

*Example of method integration (depression): This study integrates observational analyses of proteomic, brain imaging, and stress-related data with genetic methods such as Mendelian randomisation to identify proteins linked to the onset of depression using UK Biobank data.*

1. Korthauer, K., Kimes, P.K., Duvallet, C. *et al.* A practical guide to methods controlling false discoveries in computational biology. *Genome Biol* **20**, 118 (2019). <https://doi.org/10.1186/s13059-019-1716-1>

*Statistical methods: This paper systematically compares classic and modern false discovery rate (FDR) methods, showing that incorporating informative covariates can increase power without sacrificing error control. It is useful for researchers because it provides practical guidance on choosing FDR-controlling approaches best suited to their data and study design.*