MMPU Seminar

From Genes to Programmes to Traits: Building Causal Models for Human Genetics with GWAS and Perturb-Seq

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Abstract: Genome-wide association studies (GWAS) provide a unique and powerful tool for identifying causal links from variants to genes to human traits and diseases. Although modern GWAS gives an information-rich readout of the relevant variants and genes, it remains very challenging to turn this into mechanistic models of disease and clinical applications. In this talk I will describe how new genome-wide CRISPR-based perturbations provide a critical interpretive key for human genetics data, including our recent proof-of-concept study inferring causal graphs for red blood cell-related traits such as haemoglobin levels, and our new genome-wide perturb-seq of primary T cells in multiple stimulation contexts. I will close with a broader discussion of opportunities and open challenges in this field.

Place: BioQuant, Im Neuenheimer Feld 267, Room 041
Date: Friday, 13 February 2026
Time: 11:00 – 12:00
Host: Molecular Medicine Partnership Unit, Oliver Stegle and Wolfgang Huber

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