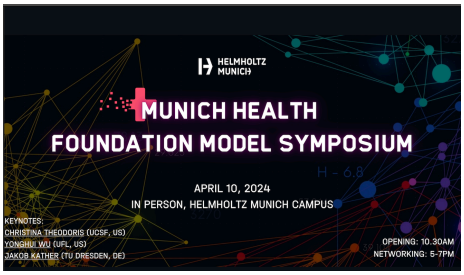

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Uncovering early single-cell marker of Eczema with scMR

Eczema is the most common inflammatory skin disease, with a prevalence of 25% in school-aged children and 10% in adults (Brown, 2016). Despite its high incidence, molecular drivers are still unknown. Revealing these causal risk factors provides essential disease onset prediction and prevention opportunities, e.g., targeting them with new and repurposed drugs.

Mendelian Randomization (MR) provides a robust framework for testing the causality of molecular drivers on disease onset using genetic data. Traditionally applied to bulk expression data, MR methods for biomarkers derived from single-cell analyses are missing.

To bridge this gap, we introduce our new method scMR. The novel integration of single-cell data allows us to identify cell-type and state-specific eQTLs (sc-eQTLs) with unparalleled granularity. By applying summary-based Mendelian Randomization to these sc-eQTLs, we can assess how genetically influenced changes in gene expression within cell states or types may causally impact disease risk.

We apply scMR to single-cell RNA sequencing data from peripheral blood mononuclear cells (Yazar et al., 2022), alongside their donors' genetic information and GWAS summary data on eczema (Budu-Aggrey et al., 2023) to identify new single cell markers for eczema.

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