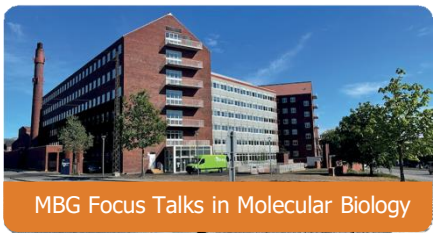
MBG FOCUS TALK

Monday 27 May 2024 at 09:15
1870-816 (Faculty Club)



Professor Bjarni Jóhann Vilhjálmsson

The National Centre for Register-based Research, Aarhus University

Integrating Omics Data to Understand Phenotypic Heterogeneity and Develop Robust and Inclusive Prediction Models

Large population-scale human omics data currently being generated holds the promise of revolutionizing our understanding of functional genomic mechanisms underlying health outcomes and other phenotypes. My research is driven by the motivation to integrate and analyze these diverse data sources to unravel the genomic basis of complex diseases. By developing and applying advanced statistical methodologies, I aim to make use of multimodal datasets to address several challenges in genetics. In this talk, I will highlight four of these challenges. First, I will focus on understanding the genetic architecture of phenotypes and heterogeneity of phenotypes. I will demonstrate how we can use state-of-the-art and highly-scalable Bayesian methods to infer genetic architecture. Second, I will present how integrating demographic and family history can boost statistical power in genetic and epidemiological analyses. Third, I will present recently proposed methods to improve genetic risk prediction and examine how we can integrate multimodal data to further improve clinical risk models. Fourth, I will discuss health inequality in risk prediction, and propose research directions aimed at making clinical prediction models more inclusive, robust and better calibrated.

AARHUS UNIVERSITY