Autism is a highly heritable neurodevelopmental condition characterized by social/communication difficulties, repetitive behaviors, and restricted interests. In this talk, I will describe how we have used whole-genome sequencing data from large cohorts of families with autism to better understand how different types of rare genetic variation affect autism susceptibility, including single nucleotide variants, indels, structural variants, mitochondrial variants, and tandem repeat expansions. I will also discuss the substantial gap between the estimated heritability of autism (~75%) and the proportion of autism cases that can currently be genetically explained (~15%), along with potential strategies for addressing this “missing heritability”.

**Brett Trost, PhD**
SickKids Research Institute

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**Date:** Wednesday, February 28, 2024  
**Time:** 3:00 p.m.  
**via Zoom:**  
[https://zoom.us/j/91629298094?pwd=TklFamQrcW04c0daRnhxSGRpUUsQQT09](https://zoom.us/j/91629298094?pwd=TklFamQrcW04c0daRnhxSGRpUUsQQT09)  

**Host:** Timothy R. Hughes, PhD