Topic: Genomic, Human disease, Neuroscience

Abstract:

The thousands of disease risk genes and loci identified through human genetic studies far outstrip our current capacity to systematically study their functions. I will discuss our attempt to develop a scalable genetic screen approach, in vivo Perturb-seq, and apply this method to the functional evaluation of a panel of autism spectrum disorder (ASD) risk genes. We identified recurrent and cell type-specific gene signatures from both neuronal and glial cell classes that are affected by genetic perturbations and pointed at elements of both convergent and divergent cellular effects across many ASD risk genes. In addition, I will also briefly discuss the research directions in my lab, established in July 2021, in applying spatial transcriptomic approaches to study cell intrinsic and extrinsic effects of these disease risk genes. Our lab will use these systematic approaches, connecting genomic technology development with rigorous dissection of molecular mechanisms, to learn new insight about how complex inputs are integrated into the developing brain.