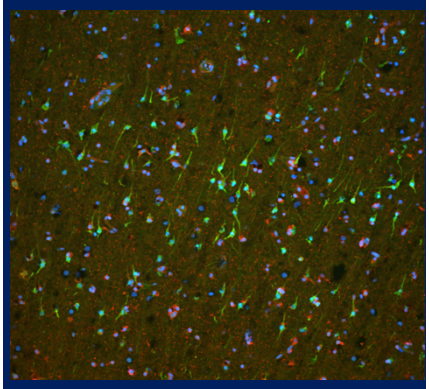
QUANTITATIVE & SYSTEMS BIOLOGY COLLOQUIUM: Cognitive genomics: cell type-specific brain evolution and neuronal function

Genevieve Konopka
University of California, Los Angeles

Date:
September 10, 2026

Time:
10:30 AM – 11:45 AM

Location:
SSB 130



About The Speaker:

Dr. Genevieve Konopka, Ph.D., is a Professor and Chair of Neurobiology at UCLA David Geffen School of Medicine. She received BS degrees in Brain & Cognitive Sciences and Biology from MIT and her PhD in Neurobiology from Harvard University. Dr. Konopka is a leading figure in the field of neurogenomics, known for her work on the transcriptional and genetic mechanisms underlying human brain evolution and neuropsychiatric disorders. Dr. Konopka's research has centered on the use of transcriptomic and epigenomic approaches to investigate the molecular basis of cognition, language, and disease, with a strong emphasis on autism spectrum disorder and schizophrenia. Her research using comparative genomics has also revealed conserved and species-specific gene expression programs, shedding light on what makes the human brain unique.

Abstract:

How do genes drive the development of cell types that build the human brain and give rise to cognition? More specifically, how does human cognitive behavior emerge from a set of evolutionarily adapted genomic programs? Although most human behaviors represent gradations of adaptations shared with other mammals, the human condition remains distinctive. Our unique combination of language, abstract reasoning, creativity, and technological innovation, along with our susceptibility to both neurodevelopmental and neurodegenerative disorders affecting cognition, sets us apart. In my seminar, I will present our work to explore cell-type-specific gene regulation using single-cell transcriptomics and multi-omics approaches. I will discuss our findings that uncovered alterations in oligodendrocyte lineage proportions in human cortical evolution. I will also detail our work that has uncovered dynamic shifts in neuronal gene networks during human memory encoding, showing evidence for how we have furthered this approach to understand gene expression activity in the living human brain.

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