BIOENGINEERING
Fall 2019 Seminar

Date: Thursday, September 5, 2019
Time: 12:00 pm - 1:00pm
Location: Exploratory Hall, Room L111
(Videoconferencing to SciTech, K. Johnson Hall Rm 254)

Eli Zunder, Ph.D.

Biography: Eli Zunder received his Ph.D. in Biophysics from UCSF in 2009, where he worked in Kevan Shokat's lab studying the role of PI3K signaling in insulin response, cancer, and drug resistance. Eli then pursued postdoctoral studies in Garry Nolan's lab at Stanford University, where he developed a cell barcoding method for mass cytometry that he used to study kinase inhibitor specificity across the human immune system, and developed a graph-based mapping algorithm to track iPSC reprogramming and intermediate cell state transitions. Since 2016, Eli has been an Assistant Professor in the Department of Biomedical Engineering at the University of Virginia. Research in the Zunder laboratory is focused on discovering the mechanisms that control the branch points and progression of cellular differentiation.

Title: Tracking embryonic and postnatal development of the mammalian nervous system at the single-cell level.

Abstract: The mammalian nervous system is estimated to contain 1000s of molecularly distinct cell types, and defining this catalog will provide a useful foundation for modern neuroscience. In addition to cellular identity, it is also important to consider how each cell type arose during embryonic/postnatal development or adult homeostasis, which can provide valuable insight into neurodevelopmental and neurodegenerative disorders. To investigate these questions of cell identity and origin, my research group has developed a neural mass cytometry platform that can be used for "rapid phenotyping" of neural tissues, at the rate of 1,000,000 cells per hour and 0.03¢ per cell. Using this high throughput approach, we performed time course analysis on microdissected brain regions (CNS) and dorsal root ganglia (PNS) of C57BL/6 mice, with daily time point replicates from embryonic day E11.5 to post natal day P4. Using a combination of published computational tools and newly developed methods that leverage temporal ordering, we identified the unique cell types present at each time point, and tracked how these cell types evolve over the course of development. In my presentation, I will go over the experimental and computational aspects of our neural mass cytometry platform, describe the fundamental insights we have gained into nervous system development, and expand on potential future directions for this approach. http://zunderlab.com/