Ackert Hall, Room 120
Wednesday, April 17, 2024
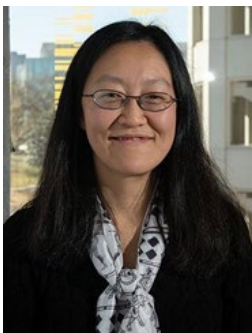**4:00 P.M.**

K-State
Biochemistry

Molecular **Biophysics**
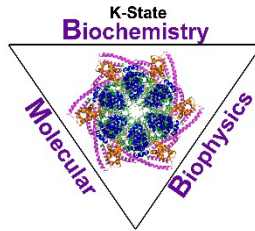
Coffee and Cookies
Chalmers Hall, Room 168
3:45 P.M.

Biochemistry & Molecular Biophysics Seminar

Microtechnology and Deep Learning for Neurogenetics

Hang Lu

Chemical and Biological Engineering
Georgia Institute of Technology

My lab is interested in engineering machine learning tools and micro systems to address questions in systems neuroscience, developmental biology, and cell biology that are difficult to answer with conventional techniques. Microfluidics provide the appropriate length scale for investigating molecules, cells, and small organisms; moreover, one can also take advantage of unique phenomena associated with small-scale flow and field effects, as well as unprecedented parallelization and automation to gather quantitative and large-scale data about complex biological systems. In parallel, ML technologies have now vastly expanded the capabilities for scientific inquiry, both in data processing and data interpretation.

We are particularly interested in the questions of how the brain is assembled during development (and changes during aging) and information is processed by brain circuits. We work with a powerful genetic system - the free-living soil nematode *C. elegans*. In this talk, I will introduce powerful mathematical and physics-based tools to accelerate the biological understanding. I will talk about two recent developments in discrete microfluidic systems exploiting multiphase and dynamical behavior of the fluids and microswimmers (i.e. *C. elegans*) (Aubry, *Small*, 2022; Sun, *Adv Healthcare Mat'l*, 2021). I will also talk about a powerful graph-theory-based framework to build probabilistic models of brain atlases (Chaudhary, *eLife*, 2021), as well as a deep-learning tool to denoise calcium activities in the brain (Chaudhary, *NComm*, 2022). These machine-learning approaches greatly reduce bias, enable automated and robust cell identification and signal extraction, and will enable a variety of applications including gene-expression analysis, whole-brain imaging, and connectomics.