

# Hang Lu

## Abstract

### *Engineering Microsystems and Computational Pipelines to Understand the Brain*

My lab is interested in engineering micro systems and computational tools to address questions in systems neuroscience, developmental biology, and cell biology that are difficult to answer with conventional techniques. 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 two sets of powerful mathematical and physics-based tools accessible by engineers 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*). By designing the microfluidic system cleverly using appropriately chosen dimensionless numbers, we can have exquisite control of the samples and experimental conditions. I will also talk about a powerful graph-theory-based framework to build probabilistic models of brain atlases. This machine-learning approach greatly reduces bias, enables automated and robust cell identification, and will enable a variety of applications including gene-expression analysis, whole-brain imaging, and connectomics.