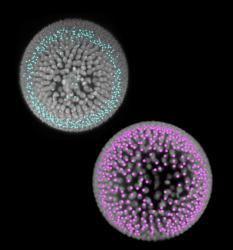
## **Developmental Biology Colloquium**

**Princeton University Spring 2021** 





**Shannon E. Keenan** Princeton University (FPO)

**Friday, April 30, 2021** 12:00 pm (EST)

> zoom: 963 6496 2954 password: celldev



## A multiscale characterization of ERK signaling in the early Drosophila embryo

The development of an organism requires a continuous assortment of inputs and outputs - an instruction manual for when cells should grow, divide, differentiate, change shape, etc... Spatial cellular signals act as inputs that initiate cascades of molecular interactions inside nearby cells. Accumulation of responses to cellular signals over time promotes the proper formation of the organism, the ultimate output. Decoding the steps from input to output requires characterizing various facets of signaling events at multiple levels. Here, we dissect dynamic responses to activation of the highly conserved Extracellular Signal-Regulated Kinase (ERK) pathway, which has been associated with cancer and disease. For this purpose, we utilize the Drosophila melanogaster embryo as a quantitative tool to easily manipulate inputs and observe outputs. First, we assess how ERK signaling regulates the function of a primary substrate, the transcriptional repressor Capicua. Regulation of repression and subsequent gene expression by ERK is a multi-step process. We determine the timescales and nature of the regulatory steps that govern how the embryo responds to dynamic signaling perturbations. We then describe a method to simultaneously observe the gene expression for a regulatory network downstream of active ERK that patterns tissue for one specific morphogenetic event known as posterior midgut formation. Our pipeline for acquiring and processing high-resolution 4D transcriptional data helps us understand how spatial dynamics of multiple interacting genes leads to cell specification downstream of a cellular signal. This work utilizes advanced molecular tools and techniques including optogenetics, light-sheet microscopy, CRISPR gene editing, and time-resolved ChIP-seq assays to elucidate questions of signaling dynamics and cell fate decisions. We believe this work brings us one step closer toward understanding how spatiotemporal cellular signals change developmental outcomes.