

California State University, Fresno  
Department of Biology Colloquium Seminar Series  
presents...

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## The continuum of *Drosophila* embryonic development at single cell resolution



Friday, April 8, 2022  
3:00 – 4:00 pm

Single cell technologies are a powerful new means to study metazoan development, enabling comprehensive surveys of cellular diversity at profiled timepoints, and shedding light on the dynamics of regulatory element activity and gene expression changes during the *in vivo* emergence of each cell type. However, nearly all such atlases of embryogenesis remain limited by sampling density, i.e. the number of discrete time points at which individual embryos are harvested. Given the rapidity with which molecular and cellular programs unfold, this limits the resolution at which regulatory transitions can be characterized.

To construct a continuous representation of embryogenesis *in vivo*, one would ideally sample embryos continuously. Although not possible with most model organisms, it is potentially possible in *D. melanogaster*, where collections of timed and yet somewhat asynchronous embryos are easy to obtain. *Drosophila* could therefore serve as a test case to develop a framework for the inference of continuous regulatory and cellular trajectories during embryogenesis. Of course, as *Drosophila* is a preeminent model organism that has yielded many advances in the biological and biomedical sciences, obtaining a single cell atlas of *Drosophila* embryogenesis is also an important goal in itself.

In this study, we report a continuous, single cell atlas of chromatin accessibility and gene expression that spans *Drosophila* embryogenesis. We profiled chromatin accessibility in almost one million, and gene expression in half a million, nuclei from eleven tightly staged, overlapping windows of embryogenesis. Leveraging the asynchronicity of embryos within each collection, we developed a statistical model to estimate the age of each nucleus more precisely, resulting in continuous views of molecular and cellular transitions throughout embryonic development. From these data, we identify cell types, infer their developmental relationships, and link cell type-specific changes in transcription factor expression to changes in the accessibility of their cognate motifs. Looking forward, this strategy may facilitate future investigations of *in vivo* gene regulation throughout *Drosophila* embryogenesis at arbitrarily high temporal resolution.

Zoom virtual meeting:

<https://fresnostate.zoom.us/j/84543877621?pwd=VmduNjFub1BEV09aSU1SRmRiZFlBdz09>

If you need a disability-related accommodation or wheelchair access, please contact Lindasue Garner at the Department of Biology at (559) 278-2001 or e-mail [lgarner@csufresno.edu](mailto:lgarner@csufresno.edu) at least one week prior to the event.