Statistical machine learning for learning representations of embryonic development



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During embryonic development, single cells read in local information from their environments and use this information to move, divide and specialize. As a result, the environments themselves change. However, it remains unclear how gene expression programs interact with cell morphology and mechanical forces to orchestrate organogenesis in early embryos. Recent advances in single cell techniques and in toto imaging enable unique venues in exploring this link between genomics and biophysics, which dynamically maps cells to organisms.

In this talk, Dr. Dumitrascu will describe statistical machine learning frameworks aimed at understanding how tissue level mechanical and morphometric information impact gene expression patterns in spatio-temporal contexts. These tools are used to understand boundary formation in the early development of mouse embryos and to align data from light sheet recordings of pre-gastrulation development.

Thursday, August 31, 2023, 3:30-4:30PM Eastern

133 Rosenau Hall

Zoom Link: https://unc.zoom.us/j/95131277245

Meeting ID: 951 3127 7245

Passcode: 203117

