



Mathematical Biology Seminar

Monday, January 22, 2024

3 pm MDT - 457 CAB (in person)

Join Zoom Meeting

<https://ualberta-ca.zoom.us/j/98497695684?pwd=SG5pcUVR50xucW5xd0xBTm1VVcUUtEUT09>

Meeting ID: 984 9769 5684

Passcode: 32123



Christopher Miles

Department of Mathematics

University of California, Irvine

Decoding spatial stochastic RNA dynamics from static imaging data with point process inference

Advances in microscopy can now provide snapshot images of individual RNA molecules within a nucleus. Decoding the underlying spatiotemporal dynamics is important for understanding gene expression, but challenging due to the static, heterogeneous, and stochastic nature of the data. I will write down a stochastic reaction-diffusion model and show that observations of this process follow a spatial point (Cox) process constrained by a reaction-diffusion PDE. Inference on this data resembles a classical inverse problem but differs in the observations of individual particles rather than concentrations. We perform inference using variational Bayesian Monte Carlo with promising results. However, many open computational and modeling challenges remain in the development of scalable and extendable techniques for this inverse problem.

This work is in collaboration with the Fangyuan Ding lab of Biomedical Engineering at UCI.

COLLABORATIVE MATHEMATICAL BIOLOGY GROUP
MATHEMATICAL & STATISTICAL SCIENCES
UNIVERSITY OF ALBERTA