

Mathematical Biology Seminar

Monday, October 24, 2022

3 pm MDT (In person)

3-25 SAB

Join Zoom Meeting

https://ualberta-ca.zoom.us/j/98497695684?pwd=SG5pcUVRS0xucW5xd0xBTm1VVCtEUT09 Meeting ID: 984 9769 5684 Passcode: 32123

Kevin Leder

Associate Professor, Industrial and Systems Engineering University of Minnesota

Computational techniques for understanding heterogeneous tumors

The development of precision medicine for cancer requires accurately quantifying the dynamics of tumor evolution. Two reasons this can be difficult are the limited number of times we can observe the tumor and intra-tumor heterogeneity that is difficult to completely characterize. In this presentation, I will first discuss an approach that uses high throughput drug screens to quantify the heterogeneity present in patient tumor samples. This information can then be used to guide future treatment decisions. I will next discuss the use of the site frequency spectrum (SFS) to learn vital information about a tumor sample based on observations at a single time point.

COLLABORATIVE MATHEMATICAL BIOLOGY GROUP

MATHEMATICAL & STATISTICAL SCIENCES UNIVERSITY OF ALBERTA

