BIOMEDICAL DATA SCIENCE PRESENTS:
BIODS 260C
5/25/23 1:30PM-2:50PM
MSOB X303 (ZOOM LINK BELOW)

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Title:

Inference from single cell lineage tracing data generated via genome editing and a novel test for phylogenetic association.

Abstract:

Single cell lineage tracing data obtained via genome editing with Crispr/Cas9 technology enables us to better understand important developmental processes at an unprecedented resolution. In the first part of the seminar, I will present a model that allows us to infer cell lineage phylogenies and lineage population size trajectories in a maximum likelihood or Bayesian framework. We assume an efficient coalescent model on cell phylogenies and propose a mutation model that describes how synthetic CRISPR target arrays generate observed variation after many cell divisions. We apply our method to two different CRISPR technologies. In the second part of the seminar, I will present a model for trait evolution inspired by the Chinese Restaurant process. We use this model to derive a test for phylogenetic binary trait association and apply it to test several hypotheses in phylogenetics, infectious diseases and cancer.

References:

1. Zhang J, Preising GA, Schumer M, Palacios JA. CRP-Tree: A phylogenetic association test for binary traits.
2. Yang et al., Lineage tracing reveals the phylodynamics, plasticity, and paths of tumor evolution, Cell 2022

Bio:

In her research, Professor Palacios seeks to provide statistically rigorous answers to concrete, data-driven questions in population genetics, epidemiology, and comparative genomics, often involving probabilistic modeling of evolutionary forces and the development of computationally tractable methods that are applicable to big data problems. Past and current research relies heavily on the theory of stochastic processes and recent developments in machine learning and statistical theory for big data; future research plans are aimed at incorporating the effects of selection and population structure in Bayesian inference of evolutionary parameters such as effective population size and recombination rates, and development of more realistic and computationally efficient methods for phylodynamic methods of infectious diseases.

Zoom link:
https://stanford.zoom.us/j/92124459914pwd=cFpJYXVLOExUVjMzZkNsYXA0b0RxUT09&from=addon
Meeting ID: 943 2440 5118
Password: 366430