RUTGERS
School of Arts and Sciences

# Department of Statistics

**Andrew Nobel**
**Department of Statistics and Operations Research**
**University of North Carolina - Chapel Hill**

## *Stationary Optimal Transport with Applications to Graph Alignment*

**Wednesday, April 6, 2022**
**11:45 AM**

**Zoom Meeting: Meeting ID: 963 9005 8784**
**Password: 606979**

https://rutgers.zoom.us/j/96390058784?pwd=c3VGOFIvYUxRanV5Tk5kS2R0dTVsQT09

**Light refreshments will be served**

**Abstract**: Optimal transport seeks to find couplings of two given distributions with minimum expected cost. This talk considers the setting in which the distributions of interest are stationary stochastic processes, and the cost function depends only on a finite number of coordinates. In this setting, I will argue that it is appropriate, and desirable, to restrict attention to stationary couplings, also known as joinings.

The first part of the talk will address estimation of optimal joinings from observations of two ergodic processes. I will then consider optimal transport for Markov chains via transition couplings, beginning with fast computation based on techniques from reinforcement learning. As an illustration, I will show how optimal joinings of Markov chains can be used to effectively compare two weighted graphs with potentially different node sets. This approach yields interpretable alignments of nodes and edges, has a desirable edge-preserving property, and implicitly account for graph factors when these exist.

**Bio**: Andrew Nobel is the Robert Paul Ziff Distinguished Professor of Statistics and Operations Research at UNC Chapel Hill. His research interests include optimal transport, dynamical systems, and statistical genomics. His research encompasses mathematical foundations and methodological development, as well as real-world applications. His work has addressed an array of problems, including uniform ergodic theorems for VC-classes, matrix reconstruction in Gaussian noise, analysis and implementation of biclustering procedures for large average submatrices, community detection in weighted networks, and analysis of joint and individual variation in multi-view genomic data. Nobel is a fellow of the IMS, and is currently an Associate Editor at JRSS-B.

DEPARTMENT OF STATISTICS
esharkey@stat.rutgers.edu • 848-445-2690 • stat.rutgers.edu