Thursday, November 16th, 2023 4:00 PM, Room 204, Caldwell Building

Dr. Mendev Gill

Assistant Professor in the Department of Statistics at the University of Georgia

Mixture models for improved inference of evolutionary dynamics

Scientific studies in many areas of the biology routinely employ evolutionary analyses based on the probabilistic inference of phylogenetic trees from molecular sequence data. Evolutionary processes that act at the molecular level are highly variable, and properly accounting for heterogeneity in evolutionary processes is crucial for more accurate phylogenetic inference. Nucleotide substitution rates and patterns are known to vary among sites in multiple sequence alignments, and progress has been made by partitioning alignments into categories corresponding to different substitution models. Determining appropriate partitions can be difficult, however, and better model fit can be achieved through flexible Bayesian mixture modeling approaches that simultaneously infer the number of partitions, the partition that each site belongs to, and the evolutionary parameters corresponding to each partition. We consider several different mixture models and observe improved performance through approaches that account for spatial patterns in alignments. To enable these models to scale efficiently to large data sets, we adapt efficient Markov chain Monte Carlo algorithms and exploit opportunities for parallel computing.

About the Speaker

Mandev Gill is an Assistant Professor in the Department of Statistics at the University of Georgia. Before arriving at UGA, he completed his Ph.D. at the University of California, Los Angeles and then worked as a postdoctoral researcher at KU Leuven in Belgium. His research focuses on Bayesian statistical and computational methods for studying infectious disease dynamics.

