Mar. 21  **Aaron Kleinman**, UC Berkeley

*Neighbor-joining and balanced minimum evolution*

Neighbor-joining (NJ) is perhaps the most famous and widely-used distance-based phylogenetic reconstruction method. Although discovered in 1987, it wasn’t until the 21st century that the algorithm was fully understood. In this talk I will relate the history of NJ and give a uniqueness result for balanced minimum evolution, the theoretical underpinning of the algorithm.