1172-68-239   **Yufeng Wu***, 371 Fairfield Way, Unit 2155, University of Connecticut, Storrs, CT 06269.
Computational Approaches for the Inference of Phylogenetic Network.

Phylogenetic network is a model for complex evolution in species and populations where reticulate evolution plays a central role. Inference of phylogenetic network has been studied extensively in computational biology recently. Both theoretical results and practical software tools have been obtained over the years. Still, compared to the traditional phylogenetic tree model, phylogenetic network is still not as widely used. This is in part due to the computational challenges and also biological complexity of reticulate evolution. In this talk, I will provide a brief introduction to two results of my research on phylogenetic network inference. The first part is about providing a lower bound on the number of reticulate events in a phylogenetic network that is required to "contain" a set of given phylogenetic trees. The second part is about a more recent and more practical work on the inference of population admixture network from population genetic data. This approach is based on multispecies coalescent and outperforms a popular existing approach. Research partly supported by US National Science Foundation under grants IIS-0803440, CCF-1116175, and CCF-1718093. (Received August 30, 2021)