Deep Learning Approaches to Bayesian Phylogenetic Inference

Speaker: Tianyu Xie (Peking University)

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Advisor: Cheng Zhang (Peking University)

Abstract: Reconstructing the evolutionary relationships among species, i.e., phylogenetic inference, has been one of the central problems in computational biology. With a phylogenetic prior and evolutionary substitution likelihood model, this problem is formulated as Bayesian phylogenetic inference of the posterior distribution over phylogenetic trees. Previous approaches often leverages Monte-Carlo type approaches, e.g., MCMC, which can suffer from slow convergence and local mode trapping in practice. In this talk, we discuss how to integrate variational inference with deep learning as a powerful solution to Bayesian phylogenetic inference. Specifically, we develop an autoregressive probabilisitc model called ARTree and its accelerated version to modeling the tree topologies, and a semi-implicit hierarchical construction for the branch lengths. We also introduce representation learning for phylogenetic trees to provide high-resolution representations that are ready-to-use for downstream tasks. These deep learning approaches to Bayesian phylogenetic inference achieve state-of-the-art inference accuracies and inspire broader follow-up innovations.