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Variational Inference with Node Embeddings (VINE) for scalable Bayesian phylogenetics

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Li Ka Shing Center, Room:130

Abstract:

Bayesian phylogenetic inference is now widely used but remains heavily reliant on Markov chain Monte Carlo (MCMC) sampling, which is computationally intensive and requires careful convergence monitoring. Variational inference (VI) is an appealing alternative that approximates posterior distributions without sampling, but existing variational approaches for phylogenetics have seen limited adoption owing to constraints in accuracy, speed, and scalability. In this talk, I will introduce Variational Inference with Node Embeddings (VINE), a variational phylogenetic inference method with striking improvements over prior work. VINE supports both standard DNA substitution models and CRISPR barcode-mutation models for cell-lineage phylogenies. Its key innovations are: embedding taxa in a high-dimensional Euclidean space; backpropagating gradients through fast distance-based phylogeny inference algorithms; introducing a sampling-free approximate estimator for the VI evidence lower bound; and enhancing posterior flexibility using normalizing flows. Across simulated and empirical datasets, VINE yields accurate posterior approximations for datasets with as many as 1000 taxa in a fraction of the time required for state-of-the-art MCMC-based methods.

Two recommended papers to read:

-https://www.biorxiv.org/content/10.64898/2025.12.24.696405v2<https://www.biorxiv.org/content/10.64898/2025.12.24.696405v2>

-https://www.cell.com/cell-genomics/fulltext/S2666-979X(26)00055-8<https://www.cell.com/cell-genomics/fulltext/S2666-979X(26)00055-8>

In addition, here is an introduction to variational inference that students might find useful:

https://link.springer.com/article/10.1023/A:1007665907178<https://link.springer.com/article/10.1023/A:1007665907178>