Biophysically Motivated Phylogenies

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Abstract : Current methods for building phylogenetic trees from gene expression data consider mean expression levels. With single-cell technologies, we can leverage more information about cell dynamics by considering the entire distribution of gene expression across cells. Using biophysical modeling, we propose a method for constructing phylogenetic trees from scRNA-seq data, building on Felsenstein's method of continuous characters. This method can highlight genes whose level of expression may be unchanged between species, but whose rates of transcription/decay may have evolved over time.

Keywords : phylogenetics, single-cell, biophysical modeling, transcription
Conference Title : ICP 2025 : International Conference on Phylogenetics
Conference Location : Tokyo, Japan
Conference Dates : January 07-08, 2025