

Realizing phylogenies with local information

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Results that say local information is enough to guarantee global information provide the theoretical underpinnings of many reconstruction algorithms in evolutionary biology. Such results include Buneman's Splits-Equivalence Theorem and the Tree-Metric Theorem. The first result says that, for a collection \mathcal{C} of binary characters, pairwise compatibility is enough to guarantee compatibility for \mathcal{C} , that is, there is a phylogenetic (evolutionary) tree that realizes \mathcal{C} . The second result says that, for a distance matrix D , if every 4×4 distance submatrix of D is realizable by an edge-weighted phylogenetic tree, then D itself is realizable by such a tree. In this talk, we investigate these and other results of this type. Furthermore, we explore the closely-related task of determining how much information is enough to reconstruct the correct phylogenetic tree.