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Combinatorics of spaces of trees: an application of topology to phylogenetics

Various metrics are used in phylogenetics to study sets of evolutionary trees generated from gene sequences. We want to use some of these metrics to consider what persistent homology might be able to contribute to the study of these trees. Our "data points" are points in the space of all trees with n leaves, where n is the number of species considered. We will consider the family of edge complexes, indexed by a sequence of real numbers ϵ_i, obtained by adding an edge between two data points if their distance is less than or equal to ϵ_i. This gives us a filtration of the $((2n-3)!!-1)$-simplex with interesting homological properties, in particular for the quartet distance. Any given data set will give rise to a subsimplex of this $((2n-3)!!-1)$-simplex and a subfiltration. Understanding the properties of the surrounding simplicial complex and its filtration will be important in understanding which features are truly features of the data set we are considering. In this talk I will discuss the features of these simplicial complexes for low values of n and I will present some conjectures for what this means for higher values of n.