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Reconstructing and comparing the evolution of genomic mutations from discrete data.

The reconstruction of trees from discrete data and the comparison of trees built from different methods are two closely related fundamental topics in Computational Biology. With the advent of next generation sequencing (NGS) technologies, these research topics have gained a renewed attention from mathematicians and computer scientists since NGS data are cheaply and widely available, hence making the construction of large phylogenies a necessity, even in fields that were not explored before. Two important examples of problems in this direction are (1) inferring an evolutionary history in cancer genomics, and (2) reconstructing an evolutionary history of species from the evolution of several independently-evolved genes. We discuss some recent results on a general combinatorial framework for modeling the reconstruction of evolutionary trees under a generalization of the Perfect Phylogeny model. We first explore the algorithmic solutions based on a graph modeling of the problem of reconstructing trees from binary data. Then we show a related approach based on the idea of completing matrices obeying certain constraints: this approach leads to a solution based on Integer Linear Programming. We show the applications of these concepts to evolutionary cancer genomics. (Received July 24, 2017)