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Mapping ancestral genomes with massive gene loss: a matrix sandwich problem

Reconstructing ancestral genomes generally requires markers that are present in all extant descendants. Motivated by the reconstruction of plant and vertebrate genomes, we introduce a new method that handles non-universal markers, by combining the consecutive-ones property with the classical notion of sandwich graph. This leads to a notion of sandwich consecutive-ones matrix. We initiate a study of this problem and apply our results on real datasets. Collaboration with Eric Tannier, Jerome Salse and Haris Gavranovic.