Haplotype Inference with Recombinations

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Abstract
A major goal of the human genome project is to build a haplotype map. Building on the work of Gusfield and Eskin, we propose a new model for inferring haplotypes from genotypes which captures recombinations. Attempt to solve this model leads us to four variants of regular 3-colorings on graphs. The easiest reduces to 2-SAT and hence is in P but the others are NP-complete. We also study these other coloring problems on random graphs and present algorithms that properly color almost all such graphs which have high enough probability of edges.