An Efficient Algorithm for the Zero-Recombinant Haplotype Configuration Problem

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We study the problem of reconstructing haplotype configurations from genotypes on pedigree data under the Mendelian law of inheritance and the zero-recombinant principle. We develop an efficient incremental algorithm that can solve the problem in O(knm+N) time, where k is the number of total nuclear families in a pedigree, n is the number of individuals, m is the number of markers, N is the total number of solutions with zero recombinant. The time complexity of the previous best known algorithm is O(n3m3+N). The algorithm starts from a single nuclear family and iteratively adds a new nuclear family to the processed ones through a common member shared by the nuclear family and a processed nuclear family. In each step, it explicitly collects all the constraints from all the processed nuclear families and represents them using segments of haplotype pairs in each member. At the end, the algorithm enumerates all the haplotype solutions with zero recombinant. Our work is of theoretical importance due to its efficiency, it is also practically useful for the construction of haplotypes from pedigrees on tightly linked markers and genetic linkage/association analysis in general.