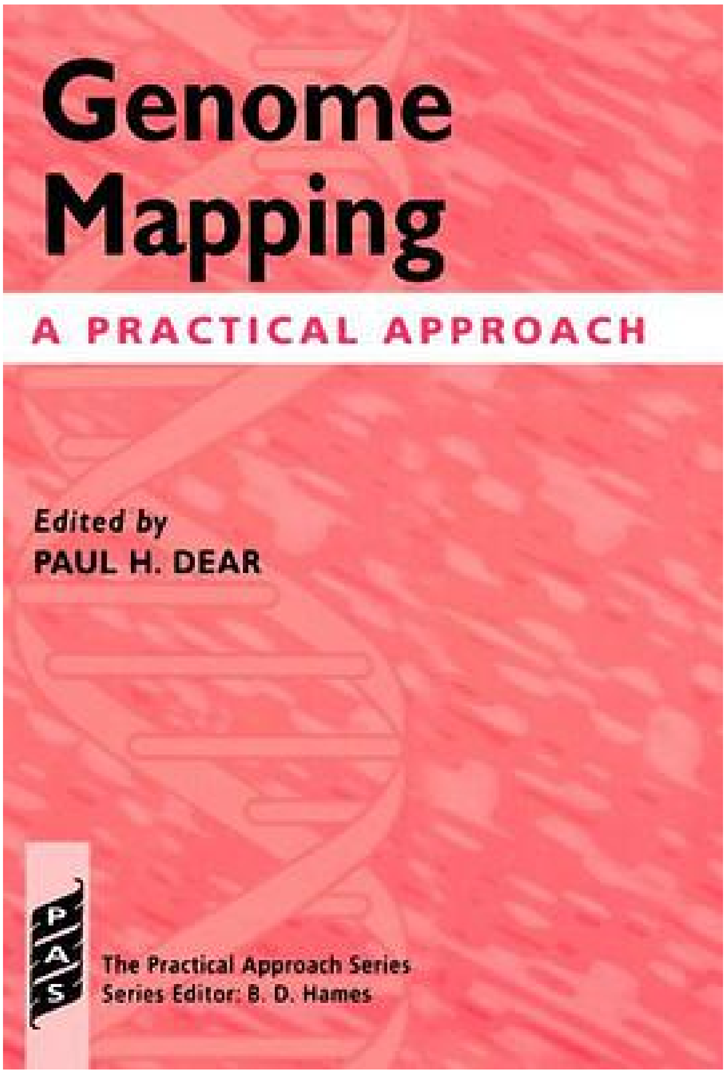
Genome Mapping



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Genome analysis has undergone a period of explosive growth in recent years. This book describes up-to-date methods for genome mapping, arranged in order of increasing resolution, from linkage analysis to restriction mapping. Topics covered include linkage mapping of human, animal, and plant genomes; mapping of quantitative trait loci; radiation hybrid mapping; HAPPY mapping; somatic cell hybrids; flow-sorted and microdissected chromosomes; fluorescence in situ hybridization; contig assembly; chromosome walking; and long-range restriction mapping. Two appendices describe sources of freely available biological and computational resources relevant to genome analysis.

作者介绍:

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评论

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