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SIXTEEN Restriction Mapping; CHAPTER SEVENTEEN Rearranging Genomes: Gates and Hurdles; APPENDIX A Drawing RNA Cloverleaves; APPENDIX B Space-Saving Strategies for Alignment; APPENDIX C A Data Structure for Disjoint Sets; APPENDIX D Suggestions for Further Reading; Bibliography; Index

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Sommario/riassunto

This introduction to computational molecular biology will help programmers and biologists learn the skills needed to start work in this important, expanding field. The author explains many of the basic computational problems and gives concise, working programs to solve them in the Perl programming language. With minimal prerequisites, the author explains the biological background for each problem, develops a model for the solution, then introduces the Perl concepts needed to implement the solution. The book covers pairwise and multiple sequence alignment, fast database searches for homologous sequences, protein motif identification, genome rearrangement, physical mapping, phylogeny reconstruction, satellite identification, sequence assembly, gene finding, and RNA secondary structure. The concrete examples and step-by-step approach make it easy to grasp the computational and statistical methods, including dynamic programming, branch-and-bound optimization, greedy methods, maximum likelihood methods, substitution matrices, BLAST searching, and Karlin-Altschul statistics. Perl code is provided on the accompanying CD.

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