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While most textbooks on bioinformatics focus on genetic algorithms and treat protein structure prediction only superficially, this course book assumes a novel and unique focus. Adopting a didactic approach, the author explains all the current methods in terms of their reliability, limitations and user-friendliness. She provides practical examples to help first-time users become familiar with the possibilities and pitfalls of computer-based structure prediction, making this a must-have for students and researchers.