Handbook of hidden Markov models in bioinformatics

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Abstrak

Demonstrating that many useful resources, such as databases, can benefit most bioinformatics projects, the Handbook of Hidden Markov Models in Bioinformatics focuses on how to choose and use various methods and programs available for hidden Markov models (HMMs). The book begins with discussions on key HMM and related profile methods, including the HMMER package, the sequence analysis method (SAM), and the PSI-BLAST algorithm. It then provides detailed information about various types of publicly available HMM databases, such as Pfam, PANTHER, COG, and metaSHARK. After outlining ways to deve.