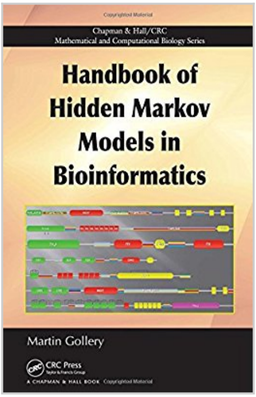

Handbook of Hidden Markov Models in Bioinformatics (Chapman & Hall/CRC Mathematical and Computational Biology)

By Martin Gollery

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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 develop and use an automated bioinformatics workflow, the author describes how to make custom HMM databases using HMMER, SAM, and PSI-BLAST. He also helps you select the right program to speed up searches. The final chapter explores several applications of HMM methods, including predictions of subcellular localization, posttranslational modification, and binding site.

By learning how to effectively use the databases and methods presented in this handbook, you will be able to efficiently identify features of biological interest in your data.

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- Sales Rank: #4883130 in Books
- Brand: Brand: Artech House
- Published on: 2008-06-12
- Original language: English
- Number of items: 1
- Dimensions: 9.75" h x 6.25" w x .50" l, .90 pounds
- Binding: Hardcover
- 176 pages

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