<<生物信息学中的数学方法引论>>

图书基本信息

书名:<<生物信息学中的数学方法引论>>

13位ISBN编号:9787030313812

10位ISBN编号:703031381X

出版时间:2011-6

出版时间:科学出版社

作者:伊茨耶夫

页数:294

版权说明:本站所提供下载的PDF图书仅提供预览和简介,请支持正版图书。

更多资源请访问:http://www.tushu007.com

<<生物信息学中的数学方法引论>>

内容概要

This book looks at the mathematical foundations of the models currently in use. This is crucial for the correct interpretation of the outputs of the models. A bioinformatician should be able not only to use software packages, but also to know the mathematics behind these packages. From this point of view, mathematics departments throughout the world have a major role to play in bioinformatics education by teaching courses on the mathematical foundations of the subject. Based on the courses taught by the author the book combines several topics in biological sequence analysis with mathematical and statistical material required for such analysis.

<<生物信息学中的数学方法引论>>

书籍目录

	part	i	sec	uence	anal	vsis
--	------	---	-----	-------	------	------

- 1 introduction: biological sequences
- 2 sequence alignment
- 2.1 sequence similarity
- 2.2 dynamic programming: global alignment
- 2.3 dynamic programming: local alignment
- 2.4 alignment with affine gap model
- 2.5 heuristic alignment algorithms
- 2.5.1 fasta
- 2.5.2 blast
- 2.6 significance of scores
- 2.7 multiple alignment
- 2.7.1 msa
- 2.7.2 progressive alignment

exercises

- 3 markov chains and hidden markov models
- 3.1 markov chains
- 3.2 hidden markov models
- 3.3 the viterbi algorithm
- 3.4 the forward algorithm
- 3.5 the backward algorithm and posterior decoding
- 3.6 parameter estimation for hmms
- 3.6.1 estimation when paths are known
- 3.6.2 estimation when paths are unknown
- 3.7 hmms with silent states
- 3.8 profile hmms
- 3.9 multiple sequence alignment by profile hmms

exercises

protein folding

- 4.1 levels of protein structure
- 4.2 prediction by profile hmms
- 4.3 threading
- 4.4 molecular modeling
- 4.5 lattice hp-model

exercises

- 5 phylogenetic reconstruction
- 5.1 phylogenetic trees
- 5.2 parsimony methods
- 5.3 distance methods
- 5.4 evolutionary models
- 5.4.1 the jukes-cantor model
- 5.4.2 the kimura model
- 5.4.3 the felsenstein model
- 5.4.4 the hasegawa-kishino-yano (hky) model
- 5.5 maximum likelihood method

<<生物信息学中的数学方法引论>>

h に	madal	com	narican
J.U	HIUUGEI	COIL	parison

exercises

part ii mathematical background for sequence analysis

- 6 elements of probability theory
- 6.1 sample spaces and events
- 6.2 probability measure
- 6.3 conditional probability
- 6.4 random variables
- 6.5 integration of random variables
- 6.6 monotone functions on the real line
- 6.7 distribution functions
- 6.8 common types of random variables
- 6.8.1 the discrete type
- 6.8.2 the continuous type
- 6.9 common discrete and continuous distributions
- 6.9.1 the discrete case
- 6.9.2 the continuous case
- 6.10 vector-valued random variables
- 6.11 sequences of random variables

exercises

7 significance of sequence alignment scores

- 7.1 the problem
- 7.2 random walks
- 7.3 significance of scores

exercises

elements of statistics

- 8.1 statistical modeling
- 8.2 parameter estimation
- 8.3 hypothesis testing
- 8.4 significance of scores for global alignments

exercises

- 9 substitution matrices
- 9.1 the general form of a substitution matrix.
- 9.2 pam substitution matrices
- 9.3 blosum substitution matrices

exercises

references

index

<<生物信息学中的数学方法引论>>

版权说明

本站所提供下载的PDF图书仅提供预览和简介,请支持正版图书。

更多资源请访问:http://www.tushu007.com