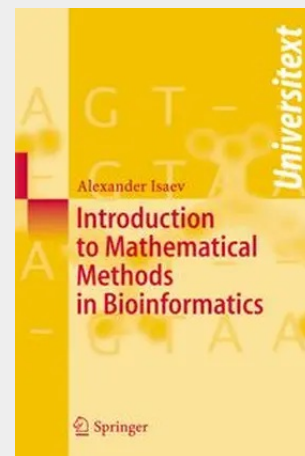


Introduction to Mathematical Methods in Bioinformatics

This book looks at the mathematical foundations of the models currently in use. All existing books on bioinformatics are software-orientated and they concentrate on computer implementations of mathematical models of biology. This book is unique in the sense that it looks at the mathematical foundations of the models, which are crucial for correct interpretation of the outputs of the models.

toMathematical Methodsin Bioinformatics With 76 Figures and 3 Tables Alexander Isaev
Australian National University Department of Mathematics Canberra, ACT 0200 Australia
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The use of general descriptive names, registered names, trademarks, etc. in this publication does not imply, even in the absence of a specific statement, that such names are exempt from the relevant protective laws and regulations and therefore free for general use. Cover design: Erich Kirchner, Heidelberg A Typesetting by the author and SPi using a Springer LT X macro package E Printed on acid-free paper: SPIN:11809142 41 /2141 /SPi-543210 To Esya and Masha Preface Broadly speaking, Bioinformatics can be defined as a collection of mathematical, statistical and computational methods for analyzing biological sequences, that is, DNA, RNA and amino acid (protein) sequences.



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