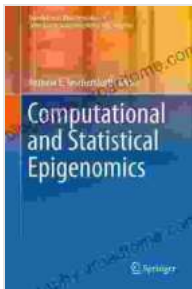# Computational and Statistical Epigenomics Translational Bioinformatics: A Comprehensive Guide to Advanced Epigenetic Analysis

Epigenetics, the study of heritable changes in gene expression that do not involve changes in the DNA sequence, is a rapidly growing field with the potential to revolutionize our understanding of biology and medicine. Computational and statistical epigenomics, which combines computational and statistical methods with epigenetic data, is a powerful tool for researchers seeking to understand the complex relationships between epigenetic modifications and gene expression.

Computational and Statistical Epigenomics (Translational Bioinformatics Book 7)

★★★★★ 5 out of 5

Language	: English
File size	: 5722 KB
Text-to-Speech	: Enabled
Enhanced typesetting	: Enabled
Print length	: 226 pages

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This book provides a comprehensive overview of computational and statistical epigenomics, from basic concepts to advanced methods and applications. It is written by leading experts in the field and is designed to be accessible to researchers with a wide range of backgrounds, from those

new to the field to those with experience in computational biology or statistics.

Key Features

- Covers all aspects of computational and statistical epigenomics, from basic concepts to advanced methods and applications

- Written by leading experts in the field

- Accessible to researchers with a wide range of backgrounds

- Includes practice problems and exercises to help readers apply the methods they learn

Table of Contents

1. to Epigenetics

2. Computational Methods for Epigenomics

3. Statistical Methods for Epigenomics

4. Applications of Computational and Statistical Epigenomics

5. Future Directions in Computational and Statistical Epigenomics

Audience

This book is intended for researchers in computational biology, statistics, and epigenetics. It is also a valuable resource for students in these fields who are interested in learning about the latest advances in computational and statistical epigenomics.
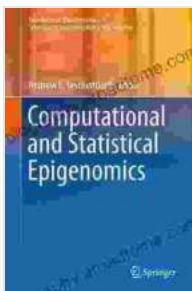
Reviews

"This book provides a comprehensive and up-to-date overview of computational and statistical epigenomics. It is a valuable resource for researchers in the field and for students who are interested in learning about the latest advances in this rapidly growing area of research." - Professor Michael Zhang, University of California, San Diego

"This book is a must-read for anyone interested in the field of computational and statistical epigenomics. It provides a clear and concise to the basic concepts and methods, and also covers the latest advances in the field. The authors have done an excellent job of making this complex topic accessible to researchers with a wide range of backgrounds." - Professor Mark Gerstein, Yale University

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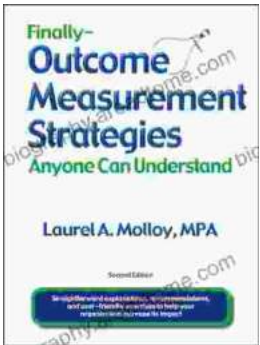
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