Innovative title providing a systematic account of new alignment-free methods in genomics and bioinformatics, emphasizing their potential to add predictive capabilities to address major and current questions in the science of biology

Predictive Methods for Genomics and Evolution provides a cohesive overview of major alignment-based and alignment-free methods in genomics and bioinformatics, primarily based on DNA/RNA. Throughout the book, contrasts between current conventional methods and novel alignment-free methods are presented and evaluated across a wide range of topics.

Written by a team of experienced academics with significant research experience in the field, *Predictive Methods for Genomics and Evolution* discusses major topics including:

- Major unresolved problems in biology including the most fundamental concept of species, the nature of evolution and speciation, phylogenetic inference, pathogenicity, and the origin of life
- Novel interpretations of current hypotheses from a biological perspective with wide-ranging applications in bioinformatics and medicine
- Insights on the shift in the research status quo towards a wider application of more efficient alignment-free methodologies, fueled by the increased availability of data, deeper knowledge of DNA/RNA structure and powerful methods from the fields of machine learning and data science.

Predictive Methods for Genomics and Evolution is an essential guide on the subject for professionals, academics, researchers, and students within the fields of genomics, evolutionary biology, phylogenetics and taxonomy, and computational biology and bioinformatics, as well as medical practitioners in related fields.

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