



Methods for Computational Gene Prediction

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Inferring the precise locations and splicing patterns of genes in DNA is a difficult but important task, with broad applications to biomedicine. The mathematical and statistical techniques that have been applied to this problem are surveyed and organized into a logical framework based on the theory of parsing. Both established approaches and methods at the forefront of current research are discussed. Numerous case studies of existing software systems are provided, in addition to detailed examples that work through the actual implementation of effective gene-predictors using hidden Markov models and other machine-learning techniques. Background material on probability theory, discrete mathematics, computer science, and molecular biology is provided, making the book accessible to students and researchers from across the life and computational sciences. This book is ideal for use in a first course in bioinformatics at graduate or advanced undergraduate level, and for anyone wanting to keep pace with this rapidly-advancing field.

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