

Numerical Methods in Bioinformatics : An Introduction

This book presents the numerical methods for Bioinformatics study as following: several numerical substitutions represent the DNA and protein sequences as the numerical or graphical sequences; Fourier and wavelet transforms are used in gene identification and protein comparison; based on the data set of microarray or lipidomics with huge amount experiment data, suitable statistical and algebraic methods are used in studying biological features of two sets; under the representations of feature vectors, the classifications of two biological molecules are completed by clustering analysis; the models of differential and difference equations have been constructed which represent the biological dynamic process; and the techniques of missing data inputting have helped to estimate the missing entries coming from biological observations and experiments, and so on. In addition, some biological concepts involved by these methods are introduced also.

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