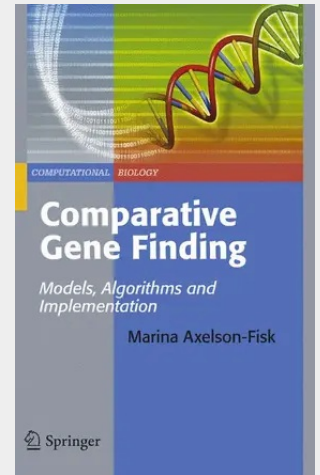


Comparative Gene Finding

Comparative genomics is a new and emerging field, and with the explosion of available biological sequences the requests for faster, more efficient and more robust algorithms to analyze all this data are immense. This book is meant to serve as a self-contained instruction of the state-of-the-art of computational gene finding in general and of comparative approaches in particular. It is meant as an overview of the various methods that have been applied in the field, and a quick introduction into how computational gene finders are built in general. A beginner to the field could use this book as a guide through to the main points to think about when constructing a gene finder, and the main algorithms that are in use. On the other hand, the more experienced gene finder should be able to use this book as a reference to different methods and to the main components incorporated in these methods. I have focused on the main uses of the covered methods and avoided much of the technical details and general extensions of the models. In exchange I have tried to supply references to more detailed accounts of the different research areas touched upon. The book, however, makes no claim on being comprehensive.

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