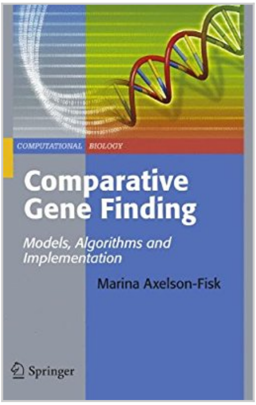

Comparative Gene Finding: Models, Algorithms and Implementation (Computational Biology)

By Marina Axelson-Fisk

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Comparative genomics is a new and emerging field, and with the explosion of ava- able 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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Comparative Gene Finding: Models, Algorithms and Implementation (Computational Biology) By Marina Axelson-Fisk Bibliography

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Editorial Review

Review

From the reviews:

“I found it to be a sufficiently comprehensive documentation of gene finding approaches and techniques. … Therefore, this book’s publication was extremely welcome news. Readers should really have a good background … in order to fully benefit from this book. … synopsis will hopefully give potential readers a fairly good idea of the nature of the book. In summary, this book is as good as it could be for the purposes it states.” (M. M. Tanik, ACM Computing Reviews, September, 2010)

From the Back Cover

Comparative genomics is an emerging field, which is being fed by an explosion in the number of possible biological sequences. This has led to an immense demand for faster, more efficient and more robust computer algorithms to analyze this large amount of data.

This unique text/reference describes the state of the art in computational gene finding, with a particular focus on comparative approaches. Providing both an overview of the various methods that are applied in the field, and a concise guide on how computational gene finders are built, the book covers a broad range of topics from probability theory, statistics, information theory, optimization theory and numerical analysis. The text assumes the reader has some background in bioinformatics, especially in mathematics and mathematical statistics. A basic knowledge of analysis, probability theory and random processes would also aid the reader.

Topics and features:

- Describes how algorithms and sequence alignments can be combined to improve the accuracy of gene finding
- Introduces the basic biological terms and concepts in genetics, and provides an historical overview of algorithm development
- Explores the gene features most commonly captured by a computational gene model, and describes the most important sub-models used
- Discusses the algorithms most commonly used for single-species gene finding
- Investigates approaches to pairwise and multiple sequence alignments
- Explains the basics of parameter training, covering a number of the different parameter estimation and optimization techniques commonly used in gene finding
- Illustrates how to implement a comparative gene finder, explaining the different steps and various accuracy assessment measures used to debug and benchmark the software

A useful text for postgraduate students, this book provides valuable insights and examples for researchers wishing to enter the field quickly. In addition to the specific focus on the algorithmic details surrounding computational gene finding, readers obtain an introduction to the fundamentals of computational biology and biological sequence analysis, as well as an overview of the important mathematical and statistical applications in bioinformatics.

Dr. Marina Axelson-Fisk is an Associate Professor at the Department of Mathematical Sciences of Chalmers University of Technology, Gothenburg, Sweden.

Users Review

From reader reviews:

Frank Huynh:

What do you concentrate on book? It is just for students because they're still students or this for all people in the world, exactly what the best subject for that? Only you can be answered for that question above. Every person has different personality and hobby for each and every other. Don't to be obligated someone or something that they don't wish do that. You must know how great along with important the book Comparative Gene Finding: Models, Algorithms and Implementation (Computational Biology). All type of book could you see on many methods. You can look for the internet methods or other social media.

Craig Nazario:

Reading can called brain hangout, why? Because if you are reading a book especially book entitled Comparative Gene Finding: Models, Algorithms and Implementation (Computational Biology) your brain will drift away trough every dimension, wandering in each aspect that maybe unfamiliar for but surely can become your mind friends. Imaging every word written in a book then become one application form conclusion and explanation that maybe you never get previous to. The Comparative Gene Finding: Models, Algorithms and Implementation (Computational Biology) giving you another experience more than blown away your thoughts but also giving you useful details for your better life in this particular era. So now let us demonstrate the relaxing pattern is your body and mind will likely be pleased when you are finished examining it, like winning a sport. Do you want to try this extraordinary spending spare time activity?

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