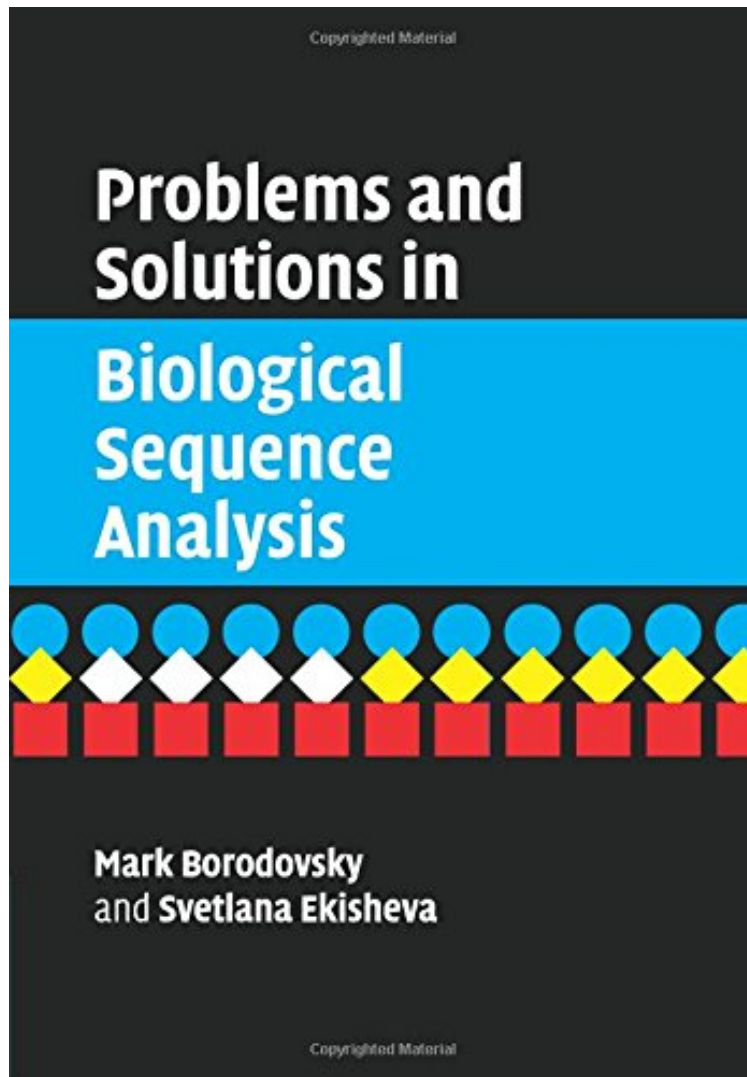


Problems and Solutions in Biological Sequence Analysis

Mark Borodovsky, Svetlana Ekisheva
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Mark Borodovsky, Svetlana Ekisheva : Problems and Solutions in Biological Sequence Analysis before purchasing it in order to gauge whether or not it would be worth my time, and all praised Problems and Solutions in Biological Sequence Analysis:

0 of 0 people found the following review helpful. A must have companion to Durbin's Biological Sequence Analysis By alex95037 To get the most out of Durbin's Biological Sequence Analysis this Problems and Solutions book is a must have. Problems and solutions fills in many of the gaps in Durbin's original book which is sorely lacking in practical examples. This book was pivotal in helping me understand some of the more esoteric concepts in Durbin's Biological Sequence Analysis. Buy both books together, you will not regret the purchase. 7 of 9 people found the

following review helpful. A Supplement to Biological Sequence Analysis By John Matlock Biological Sequence Analysis (BSA) by Durbin et al has become almost the defacto standard textbooy for teaching bioinformatics. And like most texts it presents a series of problems for the student to solve. Because of the rapid growth of bioinformatics, the schools have attracted a large number of students that have come from a wide variety of educational backgrounds. As a result, the presumptions made by the authors on the mathematical ability of the students studying BSA is at variance from the students now using the book. This book is intended to provide these students with a 'cram course' in the mathematics they will need to tackle the BSA problems. It starts by providing detailed solutions to the problems presented in BSA, it then extends the set of workable problems to further develop the problem solving skills of the students. This book might be viewed as a 360 page supplement to BSA. It's mathematics is not trivial, but is necessary for the student to succeed in the bioinformatics field. It is a book that the unprepared student will spend many hours studying.

This book is the first of its kind to provide a large collection of bioinformatics problems with accompanying solutions. Notably, the problem set includes all of the problems offered in Biological Sequence Analysis (BSA), by Durbin et al., widely adopted as a required text for bioinformatics courses at leading universities worldwide. Although many of the problems included in BSA as exercises for its readers have been repeatedly used for homework and tests, no detailed solutions for the problems were available. Bioinformatics instructors had therefore frequently expressed a need for fully worked solutions and a larger set of problems for use on courses. This book provides just that: following the same structure as BSA and significantly extending the set of workable problems it will facilitate a better understanding of the contents of the chapters in BSA and will help its readers develop problem solving skills that are vitally important for conducting successful research in the growing field of bioinformatics. All of the material has been class-tested by the authors at Georgia Tech, where the first ever M.Sc. degree program in Bioinformatics was held. MARK BORODOVSKY is the Regents' Professor of Biology and Biomedical Engineering and Director of the Center for Bioinformatics and Computational Biology at Georgia Institute of Technology in Atlanta. He is the founder of the Georgia Tech M.Sc. and Ph.D. degree programs in Bioinformatics. His research interests are in bioinformatics and systems biology. He has taught Bioinformatics courses since 1994. SVETLANA EKISHEVA is a Research Scientist at the School of Biology, Georgia Institute of Technology, Atlanta. Her research interests are in bioinformatics, applied statistics and stochastic processes. Her expertise includes teaching probability theory and statistics at universities in Russia and in the USA.

About the Author Mark Borodovsky is the Regents' Professor of Biology and Biomedical Engineering and Director of the Center for Bioinformatics and Computational Biology at Georgia Institute of Technology in Atlanta. He is the founder of the Georgia Tech M.Sc. and Ph.D. degree programs in Bioinformatics. His research interests are in bioinformatics and systems biology. He has taught Bioinformatics courses since 1994. Svetlana Ekisheva is a Research Scientist at the School of Biology, Georgia Institute of Technology, Atlanta. Her research interests are in bioinformatics, applied statistics and stochastic processes. Her expertise includes teaching probability theory and statistics at universities in Russia and in the USA.