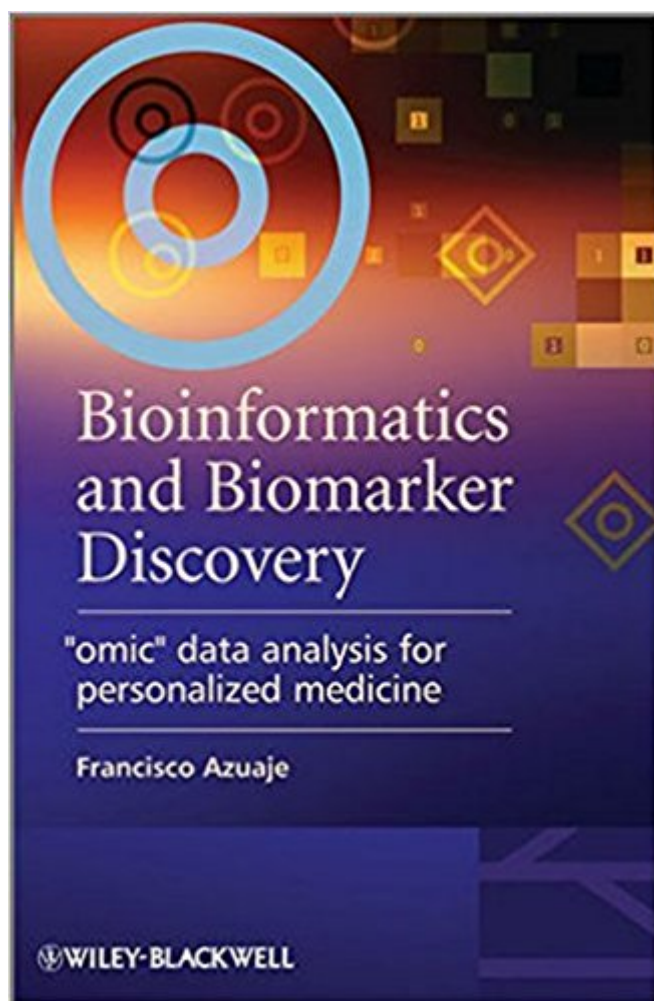The book was found

Bioinformatics And Biomarker Discovery: "Omic" Data Analysis For Personalized Medicine

Synopsis

This book is designed to introduce biologists, clinicians and computational researchers to fundamental data analysis principles, techniques and tools for supporting the discovery of biomarkers and the implementation of diagnostic/prognostic systems. The focus of the book is on how fundamental statistical and data mining approaches can support biomarker discovery and evaluation, emphasising applications based on different types of "omic" data. The book also discusses design factors, requirements and techniques for disease screening, diagnostic and prognostic applications. Readers are provided with the knowledge needed to assess the requirements, computational approaches and outputs in disease biomarker research. Commentaries from guest experts are also included, containing detailed discussions of methodologies and applications based on specific types of "omic" data, as well as their integration. Covers the main range of data sources currently used for biomarker discovery Covers the main range of data sources currently used for biomarker discovery Puts emphasis on concepts, design principles and methodologies that can be extended or tailored to more specific applications Offers principles and methods for assessing the bioinformatic/biostatistic limitations, strengths and challenges in biomarker discovery studies Discusses systems biology approaches and applications Includes expert chapter commentaries to further discuss relevance of techniques, summarize biological/clinical implications and provide alternative interpretations

Book Information

Hardcover: 248 pages

Publisher: Wiley; 1 edition (March 8, 2010)

Language: English

ISBN-10: 047074460X

ISBN-13: 978-0470744604

Product Dimensions: 7 x 0.8 x 10 inches

Shipping Weight: 1.4 pounds (View shipping rates and policies)

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Best Sellers Rank: #646,235 in Books (See Top 100 in Books)   #104 inÃ Â Books > Medical Books > Medical Informatics   #116 inÃ Â Books > Textbooks > Medicine & Health Sciences > Medicine > Clinical > Endocrinology   #174 inÃ Â Books > Computers & Technology > Computer Science > Bioinformatics

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Bioinformatics and Biomarker Discovery: Ã¢â ¬Å"OmicÃ¢â ¬Â• Data Analysis for Personalized Medicine is designed to introduce biologists, clinicians and computational researchers to fundamental data analysis principles, techniques and tools for supporting the discovery of biomarkers and the implementation of diagnostic/prognostic systems. The focus of the book is on how fundamental statistical and data mining approaches can support biomarker discovery and evaluation, emphasizing applications based on different types of Ã¢â ¬Å"omicÃ¢â ¬Â• data. The book also discusses design factors, requirements and techniques for disease screening, diagnostic and prognostic applications. Readers are provided with the knowledge needed to assess the requirements, computational approaches and outputs in disease biomarker research. Commentaries from guest experts are also included, containing detailed discussions of methodologies and applications based on specific types of Ã¢â ¬Å"omicÃ¢â ¬Â• data, as well as their integration. Covers the main range of data sources currently used for biomarker discoveryÃ Â Puts emphasis on concepts, design principles and methodologies that can be extended or tailored to more specific applicationsÃ Â Offers principles and methods for assessing the bioinformatic/biostatistic limitations, strengths and challenges in biomarker discovery studies Discusses systems biology approaches and applications Includes expert chapter commentaries to further discuss relevance of techniques, summarize biological/clinical implications and provide alternative interpretations

Francisco Azuaje has more than fifteen years of research experience in the areas of computer science, medical informatics. His contributions have been reflected in several national and international research projects and an extensive publication record in journals, conference proceedings and books. Dr Azuaje is a Senior Member of the IEEE. He held a lectureship and readership in computer science and biomedical informatics at Trinity College Dublin, Ireland, and at the University of Ulster, UK, from January 2000 to February 2008. He is currently leading research in translational bioinformatics and systems biology approaches to prognostic biomarker development at the Laboratory of Cardiovascular Research, CRP-SantÃƒÂ©, Luxembourg. He has been a member of the editorial boards of several journals and scientific committees of international conferences disseminating research at the intersection of the physical and computer sciences, engineering and biomedical sciences. He is an Associate Editor of the IEEE Transactions on Nanobioscience and BioData Mining. Dr Azuaje co-edited the books: Data Analysis and Visualization in Genomics and Proteomics, Artificial Intelligence Methods and Tools for Systems Biology, and Advanced Methods and Tools for ECG Data Analysis. He is currently a Section Editor

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