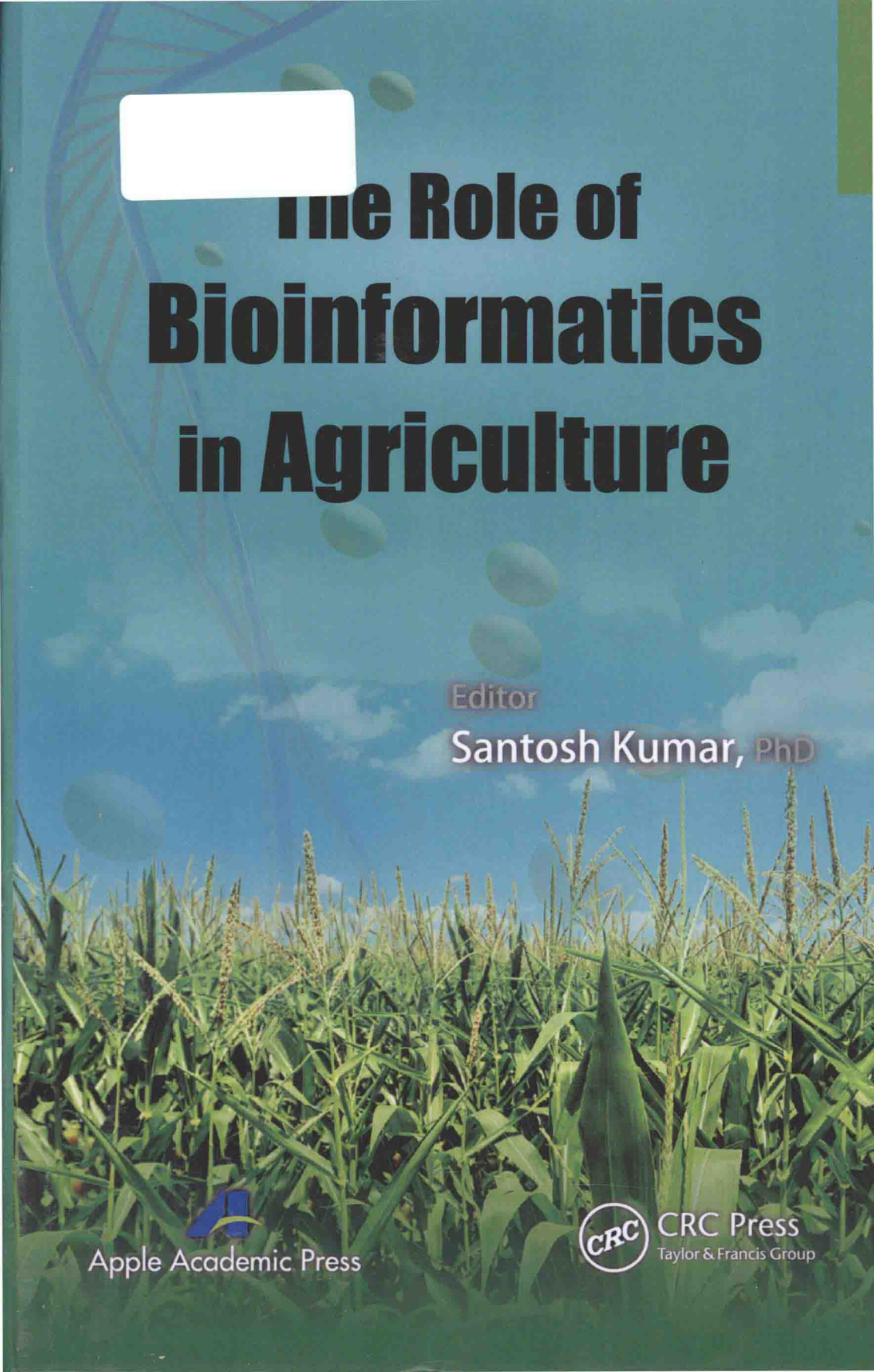
The Role of Bioinformatics in Agriculture

Editor
Santosh Kumar, PhD



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The Role of Bioinformatics in Agriculture

Advances in information technology and next generation sequencing have propelled the use of bioinformatics in agriculture, especially in the area of crop improvement. An extremely large amount of genomics data is available from plants and animals due to tremendous improvements in the field. The challenge is now to make sense and use of this wealth of data.

This book acquaints readers with state-of-the-art sequencing technologies, recent developments in computing algorithms, and certain biological perspectives that influence development of bioinformatics tools by giving specific examples from model plant species.

The book covers a wide range of topics in this field, including

- functioning, accuracy, and cost of sequencing from second generation sequencers
- development of several protocols for the application of next generation sequencing technologies
- advances in wheat, maize, and rice genomics
- a concise list of plant genome databases and other resources for individual crop improvement
- computational tools that are required to understand the large amount of complex small RNA data generated through high throughput sequencing
- the heritability of epigenetic changes and the potential to drive natural variation
- more

About The Editor

Dr. Santosh Kumar obtained his BSc agriculture degree in plant breeding from Punjab Agricultural University, Ludhiana, India. He obtained his MSc working on wheat phytosiderophores from the Indian Agricultural Research Institute, New Delhi, India, and PhD working on control of flowering and germination in barley from the University of Manitoba, Canada. At present, Dr. Kumar is stationed at the Cereal Research Centre, Manitoba, Canada, working for the University of Manitoba. Dr. Kumar has studied various disciplines in plant sciences and received many awards throughout his academic career. His current interests include crop genomics and bioinformatics. Dr. Kumar is member of various plant science societies in Canada and the US. Dr. Kumar has publications that include research articles, a review paper, and a book chapter in areas of plant physiology, genetics, and bioinformatics.

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The chapters in this book were previously published in various places and in various formats. By bringing them together here in one place, we offer the reader a comprehensive perspective on recent investigations into the role of bioinformatics in agriculture. Each chapter is added to and enriched by being placed within the context of the larger investigative landscape. Specifically:

- Chapter 1 provides a description of hands-on experience with functioning, accuracy, and cost of sequencing from second generation sequencers. The authors also discuss the applications of data generated through high throughput second generation sequencers.
- Chapter 2 focuses on the typical challenges of plant genomes that explains why plant genomics is less developed than animal genomics. It provides a discussion on factors hindering accurate plant genome assembly.
- Chapter 3 sheds light on the development of several protocols for the application of next generation sequencing technologies to genome walking.
- Chapter 4 focuses on technologies and strategies that may allow an in-depth analysis of polyploid genomes. Origin and genetics of polyploids as well as the main tools available for genome and gene expression analysis are discussed. The implications of next generation sequencing in study of polyploids is also discussed.
- Chapter 5 discusses the advances in wheat genomics and also describes the available resources which can be used for future genomics research; this review is important because wheat has a large genome and is a relatively difficult for genomics research.
- Chapter 6 focuses on producing accurate genome sequences of rice and studying its functional and evolutionary implications for comparative genomics
- Chapter 7 is a concise list of plant genome databases, resources for individual crop improvement and potential course of action for future improvement of genome databases.
- Chapter 8 surveys the RNA-Seq methods and the bioinformatics challenges that follow in analyzing the sequence data.
- Chapter 9 provides insights into power and accuracy of differential gene estimation based on different experimental designs.

- Chapter 10 sheds light on the computational tools that are required to understand the large amount of complex small RNA data generated through high throughput sequencing.
- Chapter 11 focuses on evaluation of genome diversity in maize by analyzing expression profile of genes. Maize is one of the most important cereals used as human and animal feed throughout the world. For this reason, maize has evolved to be genetically and phenotypically diverse. Not only genes but gene expression products also contribute to genetic and phenotypic plasticity.
- Chapter 12 discusses the heritability of epigenetic changes and its potential to drive natural variation. The epigenetic modifications alter gene expression without any change in the nucleotide sequence but by changing structural conformation of chromatin. They are key to adaptations occurring in short time spans.
- Chapter 13 summarizes the current protocols in metagenomics, experimental designs, guidance on sample processing, sequencing technology and sequence assembly, annotation, statistical analysis, data management and dissemination.
- Chapter 14 discusses the historical perspective of SNP development and the current experimental designs for SNP discovery and validation using specific examples. Molecular markers are regarded as foundation of genetic analysis and are indispensable for efficient breeding. The single nucleotide polymorphic sites are the ideal markers as they can be identified on the genome wide scale by a single experiment. The next generation sequencing has simplified SNP identification and validation.
- Chapter 15 summarizes an approach where sequencing data is used simultaneously to discover and validate SNPs thereby bypassing the entire marker development stages. With more and more genomes being sequenced through next generation sequencing, this is a timely review that summarizes the current state of genotyping-by-sequencing on genome wide scale.

We wish to thank the authors who made their research available for this book, whether by granting permission individually or by releasing their research as open source articles. When citing information contained within this book, please do the authors the courtesy of attributing them by name, referring back to their original articles, using the credits provided at the beginning of each chapter.

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