Record Nr. UNINA9910822816203321 The role of bioinformatics in agriculture / / edited by Santosh Kumar, **Titolo** PhD Pubbl/distr/stampa Waretown, NJ:,: Apple Academic Press, Inc. Boca Raton, FL:,: CRC Press,, [2014] ©2014 **ISBN** 0-429-17320-2 1-4822-3907-8 Edizione [First edition.] Descrizione fisica 1 online resource (483 p.) Disciplina 630.285 Soggetti Agricultural informatics Agriculture - Data processing **Bioinformatics** Lingua di pubblicazione Inglese **Formato** Materiale a stampa Livello bibliografico Monografia Description based upon print version of record. Note generali Includes bibliographical references at the end of each chapters. Nota di bibliografia Nota di contenuto Front Cover; ABOUT THE EDITOR; CONTENTS; ACKNOWLEDGMENT AND HOW TO CITE; LIST OF CONTRIBUTORS; INTRODUCTION; PART I: GENOME DATA MINING THROUGH MODERN SEQUENCING TECHNOLOGIES: CHAPTER 1: COMPARISON OF NEXT-GENERATION SEQUENCING SYSTEMS; CHAPTER 2: WHY ASSEMBLING PLANT GENOME SEQUENCES IS SO CHALLENGING; CHAPTER 3: GENOME WALKING BY **NEXT GENERATION SEQUENCING APPROACHES; CHAPTER 4:** MOLECULAR TOOLS FOR EXPLORING POLYPLOID GENOMES IN PLANTS; CHAPTER 5: WHEAT GENOMICS: PRESENT STATUS AND FUTURE PROSPECTS; CHAPTER 6: DEVELOPMENT IN RICE GENOME RESEARCH BASED ON ACCURATE GENOME SEQUENCE CHAPTER 7: GENOMIC DATABASES FOR CROP IMPROVEMENTPART II: GOING BEYOND DNA VARIATIONS TO UNDERSTAND ENVIRONMENTAL APPLICATIONS: CHAPTER 8: UNCOVERING THE COMPLEXITY OF TRANSCRIPTOMES WITH RNA-SEQ; CHAPTER 9: EFFICIENT EXPERIMENTAL DESIGN AND ANALYSIS STRATEGIES FOR THE DETECTION

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## Sommario/riassunto

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. 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 challenge is now to make sense and use o