

1. Record Nr.	UNINA9910789002303321
Titolo	The role of bioinformatics in agriculture // edited by Santosh Kumar, 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
Note generali	Description based upon print version of record.
Nota di bibliografia	Includes bibliographical references at the end of each chapters.
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 IMPROVEMENT PART 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 OF DIFFERENTIAL EXPRESSION USING RNA-SEQUENCING; CHAPTER 10: ANALYZING THE MicroRNA TRANSCRIPTOME IN PLANTS USING DEEP

SEQUENCING DATA; CHAPTER 11: MAIZE (Zea Mays L.) GENOME DIVERSITY AS REVEALED BY RNA SEQUENCING; CHAPTER 12: MOLECULAR MECHANISMS OF EPIGENETIC VARIATION IN PLANTS CHAPTER 13: METAGENOMICS: A GUIDE FROM SAMPLING TO DATA ANALYSISPART III: SINGLE NUCLEOTIDE POLYMORPHISM IS THE IDEAL MARKER; CHAPTER 14: SNP MARKERS AND THEIR IMPACT ON PLANT BREEDING; CHAPTER 15: GENOTYPING-BY-SEQUENCING IN PLANTS; AUTHOR NOTES; Back Cover

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
