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| Note generali | Description based upon print version of record. |
| Nota di bibliografia | Includes bibliographical references at the end of each chapters. |
| Nota di contenuto | 1. Preface -- 2. Foreword -- 3.Association Mapping – A new Paradigm for Dissection of Complex traits in crops -- 4. The silent Assassins – Informatics of plant Viral Silencing Suppressors.5. Tackling the Heat Stress Tolerance in crop Plants: a Bioinformatics Approach -- 6. Comparative Genomics of Cereal Crops: Status and Future Prospects -- 7. A Comprehensive Overview on Application of Bioinformatics and Computational Statistics in Rice Genomics Towards an Amalgamated Approach for Improving Acquaintance Base -- 8. Contribution of Bioinformatics to Gene Discovery in Salt Stress Responses in Plants -- 9. Peanut Bioinformatics: Tools and Applications for Developing more Effective Immunotherapies for Peanut Allergy and Improving Food Safety -- 10. Plant MicroRNAs - An Overview -- 11. ESTs in plants: Where are we heading? -- 12. Bioinformatics Strategies Associated with Important Ethnic Medicinal Plants -- 13. Mining Knowledge from Omics Data -- 14. Cloud Computing in Agriculture -- 15. Bioinformatic Tools |

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| | in the Analysis of Determinants of Pathogenicity and Ecology of Entomopathogenic Fungi used as Microbial Insecticides in Crop Protection -- 16. Exploring the Genomes of Symbiotic Diazotrophs with Relevance to Biological Nitrogen Fixation -- 17. Plant-Microbial Interaction: A Dialogue between two Dynamic Bioentities -- 18. Machine Learning with Special Emphasis on Support Vector Machines (SVMs) in Systems Biology: A Plant Perspective -- 19. Xanthine Derivatives: A molecular Modeling perspective. . |
| Sommario/riassunto | A common approach to understanding the functional repertoire of a genome is through functional genomics. With systems biology burgeoning, bioinformatics has grown to a larger extent for plant genomes where several applications in the form of protein-protein interactions (PPI) are used to predict the function of proteins. With plant genes evolutionarily conserved, the science of bioinformatics in agriculture has caught interest with myriad of applications taken from bench side to in silico studies. A multitude of technologies in the form of gene analysis, biochemical pathways and molecular techniques have been exploited to an extent that they consume less time and have been cost-effective to use. As genomes are being sequenced, there is an increased amount of expression data being generated from time to time matching the need to link the expression profiles and phenotypic variation to the underlying genomic variation. This would allow us to identify candidate genes and understand the molecular basis/phenotypic variation of traits. While many bioinformatics methods like expression and whole genome sequence data of organisms in biological databases have been used in plants, we felt a common reference showcasing the reviews for such analysis is wanting. We envisage that this dearth would be facilitated in the form of this Springer book on Agricultural Bioinformatics. We thank all the authors and the publishers Springer, Germany for providing us an opportunity to review the bioinformatics works that the authors have carried in the recent past and hope the readers would find this book attention grabbing. . |