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Material and Methods -- 3 Results -- 3.1 Auto-phylo Modules -- 3.2 Setting up an Auto-phylo Pipeline -- 3.3 Bacterial AOs May Have a Function Similar to Animal GULOs -- 3.4 Identification of Bacterial Species Groups that Have AOs Closely Related to Animal GULOs -- 4 Conclusion -- References -- Feature Selection Methods Comparison: Logistic Regression-Based Algorithm and Neural Network Tools -- 1 Introduction -- 1.1 Classification Problem -- 1.2 Feature Selection Methods -- 2 Methods and Materials -- 2.1 Logistic Regression-Based Algorithm -- 2.2 Neural Networks Approach -- 2.3 Materials -- 3 Results -- 3.1 Logistic Regression-Based Algorithm -- 3.2 Neural Networks Approach -- 3.3 Results Comparison -- 4 Conclusions -- References -- A New GIMME-Based Heuristic for Compartmentalised Transcriptomics Data Integration -- 1 Introduction -- 2 Methods -- 2.1 Flux Balance Analysis -- 2.2 Gene Inactivity Moderated by Metabolism and Expression.
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Sommario/riassunto

This book aims to promote the interaction among the scientific community to discuss applications of CS/AI with an interdisciplinary character, exploring the interactions between sub-areas of CS/AI, bioinformatics, chemoinformatics, and systems biology. The success of bioinformatics in recent years has been prompted by research in molecular biology and molecular medicine in several initiatives. This year’s technical program presents both high quality and diversity, with contributions in well-established and evolving areas of research. The PACBB’23 technical program has selected 9 full papers in the main track and, as in past editions, it will be special issues in ranked journals. This symposium is organized by the LASI and Centro Algoritmi of the University of Minho (Portugal). The authors would like to thank all the contributing authors, the members of the program committee, national associations (AEPIA, APPIA), and the sponsors (AIR Institute).