



Algorithms for Computational Biology [Second International Conference, AICoB 2015, Mexico City, Mexico, August 4-5, 2015, Proceedings /

Dediu, Adrian-Horia
 Hernández-Quiroz, Francisco
 Martín Vide, Carlos
 Rosenblueth, David A

Computer science Bioinformatics Computer Science Computational
 Biology/Bioinformatics

Monografía

This book constitutes the proceedings of the Second International Conference on Algorithms for Computational Biology, AICoB 2015, held in Mexico City, Mexico, in August 2015. The 11 papers presented in this volume were carefully reviewed and selected from 23 submissions. They were organized in topical sections named: genetic processing; molecular recognition/prediction; and phylogenetics

<https://rebiunoda.pro.baratznet.cloud:38443/OpacDiscovery/public/catalog/detail/b2FpOmNlbGVicmF0aW9uOmVzLmJhcmFOei5yZW4vMTc5Mjk2NzA>

Título: Algorithms for Computational Biology [Recurso electrónico] :] Second International Conference, AICoB 2015, Mexico City, Mexico, August 4-5, 2015, Proceedings edited by Adrian-Horia Dediu, Francisco Hernández-Quiroz, Carlos Martín-Vide, David A. Rosenblueth

Mención de serie: Lecture Notes in Computer Science 9199

Contenido: Genetic Processing -- Generalized Hultman Numbers and the Distribution of Multi-break Distances -- Implicit Transpositions in Shortest DCJ Scenarios -- Constraint-Based Genetic -- Compilation -- Molecular Recognition/Prediction P2RANK: Knowledge-Based Ligand Binding Site Prediction Using Aggregated Local Features -- StreaM - A Stream-Based Algorithm for Counting Motifs in Dynamic Graphs -- Convolutional LSTM Networks for Subcellular Localization of Proteins -- Phylogenetics -- Hybrid Genetic Algorithm and Lasso Test Approach for Inferring Well Supported Phylogenetic Trees Based on Subsets of Chloroplastic Core Genes -- Constructing and Employing Tree Alignment Graphs for Phylogenetic Synthesis -- A More Practical Algorithm for the Rooted Triplet Distance -- Likelihood-Based Inference of Phylogenetic Networks from Sequence Data by PhyloDAG -- Constructing Parsimonious Hybridization Networks from Multiple Phylogenetic Trees Using a SAT-Solver

Restricciones de acceso: Acceso restringido a miembros del Consorcio de Bibliotecas Universitarias de Andalucía

Detalles del sistema: Modo de acceso: world wide web

Fuente de adquisición directa: Springer (e-Books)

ISBN: 9783319212333 978-3-319-21233-3 9783319212326

Autores: Dediu, Adrian-Horia Hernández-Quiroz, Francisco Martín Vide, Carlos Rosenblueth, David A

Baratz Innovación Documental

- Gran Vía, 59 28013 Madrid
- (+34) 91 456 03 60
- informa@baratz.es