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Autore	Fernandenz, Gonzalez Jiulian
Titolo	Bronces jurîdicos romanos de Andalucîa / Julián González Fernández
Pubbl/distr/stampa	[s.l.] : Consejerîa de Cultura, 1990
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Livello bibliografico	Monografia

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Pubbl/distr/stampa	Dedham, MA : Research Communications Ltd., c1994
ISBN	0964042304
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Altri autori (Persone)	Crane, Valerieauthor
Altri autori (Enti)	National Science Foundation (U.S.)
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	Titolo	Research in Computational Molecular Biology : 28th Annual International Conference, RECOMB 2024, Cambridge, MA, USA, April 29-May 2, 2024, Proceedings
	Pubbl/distr/stampa	Cham : , : Springer, , 2024 ©2024
	ISBN	1-0716-3989-7
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	Descrizione fisica	1 online resource (508 pages)
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	Lingua di pubblicazione	Inglese
	Formato	Materiale a stampa
	Livello bibliografico	Monografia
	Nota di contenuto	Intro -- Preface -- Organization -- Contents -- Fast Approximate IsoRank for Scalable Global Alignment of Biological Networks -- 1 Introduction -- 2 Algorithm -- 2.1 IsoRank -- 2.2 Approximate IsoRank -- 2.3 Computational Complexity -- 3 Experiments -- 3.1 Synthetic Networks -- 3.2 Biological Networks -- 3.3 Competing Methods -- 4 Discussion -- 4.1 Synthetic Networks -- 4.2 Biological Networks -- References -- Sequential Optimal Experimental Design of Perturbation Screens Guided by Multi-modal Priors -- 1 Introduction -- 2 Background -- 3 Method -- 3.1 Sequential Design of Perturb-Seq Experiment -- 3.2 Data-Driven Motivation for Incorporating Prior Knowledge -- 3.3 IterPert: A Multi-modal Prior-Guided Active Learning Strategy -- 4 Experiment -- 5 Related Works -- 6 Discussion -- A Data Processing on Multi-modal Priors -- B Fusion Operator -- C Error Bars for Baselines -- D Baseline Performance for Genome-Scale Perturbation Screen -- References -- Efficient Analysis of Annotation Colocalization Accounting for Genomic Contexts -- 1 Introduction -- 2 Methods -- 2.1 A Generative Model -- 2.2 The Context-Aware Markov Chain Null Model -- 2.3 Computing the Mean and Variance of the Overlap and Shared Bases Test Statistics -- 2.4 Mean and Variance of Any Separable Statistic -- 2.5 Multiple Chromosomes -- 3 Experiments -- 4 Discussion -- References -- Secure Federated Boolean Count Queries Using Fully-Homomorphic Cryptography -- 1 Introduction -- 2

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3.2 Feature Extraction -- 3.3 Classifier Module -- 4 Experiments -- 4.1 Datasets -- 4.2 Implementation and Evaluation -- 4.3 Comparison on Target Datasets -- 4.4 DrugBank -- 4.5 Interpretation -- 5 Conclusion -- References -- An Integer Programming Framework for Identifying Stable Components in Asynchronous Boolean Networks -- 1 Introduction -- 2 Preliminaries -- 2.1 Boolean Networks -- 2.2 Linear Threshold Functions -- 2.3 Network Dynamics -- 3 ILP Framework for Finding Quasi-Attractors -- 3.1 Lg Representation -- 3.2 Quasi-attractor Detection -- 3.3 External Nodes -- 3.4 Implementation Details -- 4 Results -- 4.1 Synthetic Networks -- 4.2 Real Biological Networks -- 5 Conclusions -- References -- ImputeCC Enhances Integrative Hi-C-Based Metagenomic Binning Through Constrained Random-Walk-Based Imputation -- 1 Introduction -- 2 Results -- 2.1 Overview of ImputeCC -- 2.2 ImputeCC Achieved Accurate Preclustering for Contigs Containing Single-Copy Marker Genes -- 2.3 ImputeCC Retrieved the Most High-Quality Genomes from the Mock metaHi-C Datasets -- 2.4 ImputeCC Markedly Outperformed Existing Binners on Real metaHi-C Datasets -- 2.5 Running Time Analysis of the ImputeCC -- 3 Materials and Methods -- 3.1 Datasets -- 3.2 Data Preprocessing -- 3.3 The Framework of ImputeCC Binning -- 3.4 Evaluating the Quality of Recovered MAGs from the Mock and Real metaHi-C Datasets -- 3.5 MAG Analyses on Real metaHi-C Datasets -- 3.6 Other Binners Used in Benchmarking -- 4 Discussions -- References -- Graph-Based Genome Inference from Hi-C Data -- 1 Introduction -- 2 Inferring the Sample Genome from Hi-C Data with Genome Graphs -- 2.1 Problem Definition of Genome Inference -- 2.2 The Hardness of the Problem -- 2.3 Computation of the Function -- 2.4 Graph-Based Dynamic Programming Algorithm -- 2.5 Heuristics for Computing q -- 2.6 Accuracy of the Heuristic Algorithm.
2.7 Practical Improvements to Efficiency and Accuracy -- 3 Experimental Results -- 3.1 Construction of a Genome Graph with Hi-C Reads Mapped -- 3.2 Graph Hi-C Workflow Improves TAD Identification -- 4 Discussion -- References -- Meta-colored Compacted de Bruijn Graphs -- 1 Introduction -- 2 Preliminaries: Modular Indexing of Colored Compacted de Bruijn Graphs -- 3 Meta-colored Compacted de Bruijn Graphs -- 3.1 Definition -- 3.2 Data Structures Used and Two-Level Intersection Algorithm -- 3.3 The Optimization Problem -- 3.4 The SCPO framework -- 4 Experiments -- 5 Conclusions -- References -- Color Coding for the Fragment-Based Docking, Design and Equilibrium Statistics of Protein-Binding ssRNAs -- 1 Introduction -- 2 Method and Algorithms -- 2.1 Ensuring Self-avoidance Through Color Coding -- 2.2 Reducing Clashes Through Monochromatic Clique Covers -- 2.3 Rational ssRNA Design as a Relaxation of Docking -- 2.4 Equilibrium Statistics -- 3 Results -- 3.1 Stability Analysis -- 3.2 Impact of Monochromatic Clique Covers -- 3.3 Docking Through Energy-Minimization Under Different Fragment Definitions -- 3.4 Design -- 4 Conclusions and Perspectives -- References -- Automated Design of Efficient Search Schemes for Lossless Approximate Pattern Matching -- 1 Introduction -- 2 Preliminaries -- 3 A Greedy Heuristic for Improving Search Schemes -- 4 Integer Linear Program Formulation -- 5 Dynamic Selection -- 6 Experiments and Results -- 6.1 Dataset

and Computational Environment -- 6.2 Better Search Schemes -- 6.3 Application to Lossless Read Mapping -- 7 Conclusion -- References -- CELL-E: A Text-to-Image Transformer for Protein Image Prediction -- 1 Introduction -- 2 Results -- 2.1 The CELL-E Model -- 2.2 Performance Evaluation -- 2.3 Analysis of NLS Using CELL-E -- 3 Discussion -- 4 Methods -- 4.1 Model Specifics -- 4.2 Nucleus Image Encoder.
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1 Introduction -- 2 Methods -- 2.1 The ETM Component -- 2.2 The GFM Component -- 2.3 Leveraging the Peak Embedding from GFM in ETM -- 2.4 Transfer Learning of GFETM -- 3 Results -- References --
SEM: Size-Based Expectation Maximization for Characterizing Nucleosome Positions and Subtypes -- 1 Introduction -- 2 Methods -- 3 Results -- 4 Conclusion -- References.
Centrifuger: Lossless Compression of Microbial Genomes for Efficient and Accurate Metagenomic Sequence Classification.