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Nota di contenuto	-- Enhancing gene set analysis in embedding spaces a novel best match approach. -- Prompt based Learning on Large Protein Language Models Improves Signal Peptide Prediction. -- Decoil Reconstructing extrachromosomal DNA structural heterogeneity from longread sequencing data. -- Privacy Preserving Epigenetic PaceMaker Stronger Privacy and Improved Efficiency. -- Mapping Cell Fate Transition in Space and Time. -- Approximate IsoRank for Scalable Global Alignment of Biological Networks. -- Sequential Optimal Experimental Design of Perturbation Screens Guided by Multimodal Priors. -- Efficient Analysis of Annotation Colocalization Accounting for Genomic Contexts. -- Secure federated Boolean count queries using fully homomorphic cryptography. -- FragXsiteDTI Revealing Responsible Segments in Drug Target Interaction with Transformer Driven Interpretation. -- An integer programming framework for identifying stable components in asynchronous Boolean networks. -- ImputeCC enhances integrative Hi C based metagenomic binning through constrained random walk based imputation. -- Graph based genome inference from Hi C data. -- Meta colored de Bruijn graphs. -- Color Coding for the Fragment Based Docking Design and Equilibrium Statistics of Protein Binding ssRNAs. -- Automated design of efficient search schemes for lossless approximate pattern matching. -- CELL E

A Text To Image Transformer for Protein Localization Prediction. -- A Scalable Optimization Algorithm for Solving the Beltway and Turnpike Problems with Uncertain Measurements. -- Overcoming Observation Bias for Cancer Progression Modeling. -- Inferring Metabolic States from Single Cell Transcriptomic Data via Geometric Deep Learning. -- Computing robust optimal factories in metabolic reaction networks. -- Undesignable RNA Structure Identification via Rival Structure Generation and Structure Decomposition. -- Structure and Function Aware Substitution Matrices via Learnable Graph Matching. -- Secure Discovery of Genetic Relatives across Large Scale and Distributed Genomic Datasets. -- GFETM Genome Foundation based Embedded Topic Model for scATAC seq Modeling. -- SEM sized based expectation maximization for characterizing nucleosome positions and subtypes. -- Centrifuger lossless compression of microbial genomes for efficient and accurate metagenomic sequence classification. -- BONOBO Bayesian Optimized sample specific Networks Obtained By Omics data. -- regLM Designing realistic regulatory DNA with autoregressive language models. -- DexDesign A new OSPREY based algorithm for designing de novo D peptide inhibitors. -- Memory bound and taxonomy aware kmer selection for ultra large reference libraries. -- SpaCeNet Spatial Cellular Networks from omics data. -- Discovering and overcoming the bias in neoantigen identification by unified machine learning models. -- MaSk LMM A Matrix Sketching Framework for Linear Mixed Models in Association Studies. -- Community structure and temporal dynamics of viral epistatic networks allow for early detection of emerging variants with altered phenotypes. -- Maximum Likelihood Inference of Time scaled Cell Lineage Trees with Mixed type Missing Data. -- TRIBAL Tree Inference of B cell Clonal Lineages. -- Mapping the topography of spatial gene expression with interpretable deep learning. -- GraSSRep Graph Based Self Supervised Learning for Repeat Detection in Metagenomic Assembly. -- PRS Net Interpretable polygenic risk scores via geometric learning. -- Haplotype aware sequence alignment to pangenome graphs. -- Disease Risk Predictions with Differentiable Mendelian Randomization. -- DIISCO A Bayesian framework for inferring dynamic intercellular interactions from time series single cell data. -- Protein domain embeddings for fast and accurate similarity search. -- Processing bias correction with DEBIAS M improves cross study generalization of microbiome based prediction models. -- VICTree a Variational Inference method for Clonal Tree reconstruction. -- DeST OT Alignment of Spatiotemporal Transcriptomics Data. -- Determining Optimal Placement of Copy Number Aberration Impacted Single Nucleotide Variants in a Tumor Progression History. -- Accurate Assembly of Circular RNAs with TERRACE. -- Semi Supervised Learning While Controlling the FDR With an Application to Tandem Mass Spectrometry Analysis. -- CoRAL accurately resolves extrachromosomal DNA genome structures with long read sequencing. -- A Scalable Adaptive Quadratic Kernel Method for Interpretable Epistasis Analysis in Complex Traits. -- Optimal Tree Metric Matching Enables Phylogenomic Branch Length Estimation. -- Inferring allele specific copy number aberrations and tumor phylogeography from spatially resolved transcriptomics. -- Contrastive Fitness Learning Reprogramming Protein Language Models for Low N Learning of Protein Fitness Landscape. -- Scalable summary statistics based heritability estimation method with individual genotype level accuracy. -- scMulan a multitask generative pre trained language model for single cell analysis.

Sommario/riassunto

This book constitutes the proceedings of the 28th Annual International

Conference on Research in Computational Molecular Biology, RECOMB 2024, held in Cambridge, MA, USA, during April 29–May 2, 2024. The 57 full papers included in this book were carefully reviewed and selected from 352 submissions. They were organized in topical sections as follows: theoretical and foundational algorithm contributions and more applied directions that engage with new technologies and intriguing biological questions.