

| | |
|-------------------------|---|
| 1. Record Nr. | UNINA9910627277503321 |
| Titolo | Practical applications of computational biology and bioinformatics, 16th international conference (PACBB 2022) // Florentino Fdez-Riverola [and four others] editors |
| Pubbl/distr/stampa | Cham, Switzerland : , : Springer, , [2023] ©2023 |
| ISBN | 3-031-17024-5 |
| Descrizione fisica | 1 online resource (122 pages) |
| Collana | Lecture notes in networks and systems ; ; 553 |
| Disciplina | 570.285 |
| Soggetti | Bioinformatics Computational biology |
| Lingua di pubblicazione | Inglese |
| Formato | Materiale a stampa |
| Livello bibliografico | Monografia |
| Nota di bibliografia | Includes bibliographical references and index. |
| Nota di contenuto | Intro -- Preface -- Acknowledgements -- Organization -- Contents -- TooT-BERT-T: A BERT Approach on Discriminating Transport Proteins from Non-transport Proteins -- 1 Introduction -- 2 Related Work -- 3 Materials and Methods -- 3.1 Dataset -- 3.2 Protein Sequence Representation -- 3.3 Fine-Tuning a BERT Model -- 3.4 Logistic Regression -- 3.5 Evaluation -- 3.6 Evaluation Metrics -- 4 Results and Discussion -- 4.1 Fine-Tuning ProtBERT-BFD and MembraneBERT -- 4.2 Logistic Regression with Fine-Tuned ProtBERT-BFD -- 4.3 Comparison of TooT-BERT-T with State-of-the-Art Models -- 5 Conclusion -- References -- Machine Learning and Deep Learning Techniques for Epileptic Seizures Prediction: A Brief Review -- 1 Introduction -- 2 Signal Processing and Feature Extraction -- 2.1 Feature Extraction -- 2.2 Feature Selection -- 3 Seizure Detection and Classification -- 4 Seizure Prediction -- 4.1 Animal Models -- 4.2 Human Subjects -- 5 Conclusion -- References -- The Covid-19 Decision Support System (C19DSS) - A Mobile App -- 1 Introduction -- 2 Background -- 3 C19DSS -- 3.1 Architecture -- 3.2 Usability Evaluation -- 3.3 Preliminary Use -- 4 Discussion -- 5 Conclusions -- References -- Towards a Flexible and Portable Workflow for Analyzing miRNA-Seq Neuropsychiatric Data: An Initial Replicability Assessment -- 1 Introduction -- 2 Materials and Methods -- 2.1 Data Acquisition |

-- 2.2 myBrain-Seq Implementation -- 2.3 Experimental Setup -- 3 Results and Discussion -- 3.1 Quality Control -- 3.2 Application of the Same Statistical Thresholds as the Original Articles -- 3.3 Comparison Between the Original Results, MiARma-Seq Results and MyBrain-Seq Results -- 4 Conclusion -- References -- The NAD Interactome, Identification of Putative New NAD-Binding Proteins -- 1 Introduction -- 2 Methods -- 2.1 Data Collection and Definition of Protein Datasets. 2.2 Datasets Analysis -- 2.3 Identification of Putative New NAD-Binding Proteins -- 3 Results -- 3.1 NAD-Binding Proteins (NADBDPs) Dataset -- 3.2 NAD-Protein-Protein Interactions (NAD-PPIs) Dataset -- 3.3 Pathway Enrichment Analysis -- 3.4 Characterization of Protein Domains of the NADBDPs Dataset -- 3.5 Identification of Putative NAD-Binding Proteins -- 4 Discussion -- 5 Conclusion -- References -- Multiple Instance Learning Based on Mol2vec Molecular Substructure Embeddings for Discovery of NDM-1 Inhibitors -- 1 Introduction -- 2 Materials and Methods -- 2.1 Dataset Collection -- 2.2 Labeling the Database -- 2.3 Calculating Mol2vec Embeddings -- 2.4 Classification and Ranking Frame Work -- 3 Results and Discussion -- 3.1 Results -- 4 Conclusion -- References -- Towards Improving Bio-Image Segmentation Quality Through Ensemble Post-processing of Deep Learning and Classical 3D Segmentation Pipelines -- 1 Introduction -- 2 Previous Research on Ensemble Methods for Segmentation -- 3 Methodology -- 3.1 3D Segmentation Pipelines -- 3.2 Dataset -- 3.3 Fusion Algorithm 1: Label Set Intersection -- 3.4 Fusion Algorithm 2: Region Adjacency Graphs -- 3.5 Fusion Algorithm 3: Boundary Fusion with 3D Watershed -- 3.6 Segmentation Evaluation Metric -- 4 Results -- 4.1 Results from Original Pipelines -- 4.2 Results from Fusion Algorithm 1 -- 4.3 Results from Fusion Algorithm 2 -- 4.4 Results from Fusion Algorithm 3 -- 5 Discussions -- 6 Data and Code Availability -- References -- Exploring Xylella fastidiosa's Metabolic Traits Using a GSM Model of the Phytopathogenic Bacterium -- 1 Introduction -- 2 Materials and Methods -- 2.1 Software -- 2.2 Metabolic Model Reconstruction -- 2.3 Identification of Potential Drug Targets -- 3 Results and Discussion -- 3.1 Model Validation -- 3.2 Drug Targeting -- 4 Conclusion -- 5 Supplementary Materials -- References. Genomic Regions with Atypical Concentration of Inverted Repeats -- 1 Introduction -- 2 Methods -- 2.1 Distance Between Inverted Repeats -- 2.2 Measuring the Concentration of Inverted Repeats -- 2.3 Windows Selection -- 3 Results -- 4 Discussion and Conclusion -- References -- EvoPPI 2: A Web and Local Platform for the Comparison of Protein-Protein Interaction Data from Multiple Sources from the Same and Distinct Species -- 1 Introduction -- 2 Methods -- 2.1 Data -- 2.2 Web Interface Updates -- 2.3 Using EvoPPI Locally -- 3 Results and Discussion -- 4 Conclusion -- References -- Author Index.
