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Collana	Lecture Notes in Bioinformatics, , 2366-6331 ; ; 9043
Disciplina	572.80285
Soggetti	Bioinformatics Medical informatics Computer vision Biometric identification Pattern recognition systems Computational and Systems Biology Health Informatics Computer Vision Biometrics Automated Pattern Recognition
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	Includes index.
Nota di contenuto	Bioinformatics for healthcare and diseases -- A Segmentation-Free Model for Heart Sound Feature Extraction -- A Semantic Layer for Unifying and Exploring Biomedical Document Curation Results -- Blind and Visually Impaired students can perform computer-aided molecular design with an assistive molecular fabricator -- Characterization of pneumonia incidence supported by a business intelligence system -- Are wildfires and pneumonia spatially and temporally related? -- Health Technology Assessment Models Utilized in the Chronic Care Management -- Prediction of human gene phenotype associations by exploiting the hierarchical structure of the Human Phenotype Ontology -- Mortality Prediction with Lactate and Lactate Dehydrogenase -- Intellectual Property Protection for Bioinformatics and Computational

Biology -- Lupin allergy: uncovering structural features and epitopes of –conglutin proteins in Lupinus angustifolius L. with a focus on cross-allergenic reactivity to peanut and other legumes -- Biomedical Engineering -- Artificial Neural Networks in Acute Coronary Syndrome Screening -- A flexible denormalization technique for data analysis above a deeply-structured relational database: biomedical applications -- Multilayer clustering: Biomarker driven segmentation of Alzheimer's disease patient population -- Entropy analysis of atrial activity morphology to study atrial fibrillation recurrences after ablation procedure -- Wireless Technology -- Cost-effectiveness studies in cardiology: application of medical devices -- Biomedical image analysis -- Preliminary Research on Combination of Exponential Wavelet and FISTA for CS-MRI -- Accurate Microscopic Red Blood Cell Image Enhancement and Segmentation -- A Hyperanalytic Wavelet Based Denoising Technique for Ultrasound Images -- Detection of Pathological Brain in MRI scanning based on Wavelet-entropy and Naive Bayes Classifier -- PloidyQuantX: a quantitative microscopy imaging tool for ploidy quantification at cell and organ level in Arabidopsis root -- Study of the histogram of the hippocampus in MRI using the alpha-stable distribution -- A Novel Algorithm for Segmentation of Suspicious Microcalcification -- Regions on Mammograms -- A 3D Voxel Neighborhood Classification Approach within a Multiparametric MRI Classifier for Prostate Cancer Detection -- Towards precise segmentation of corneal endothelial cells -- Sliding box method for automated detection of the optic disc and macula in retinal images -- A simple hair removal algorithm from dermoscopic images -- Automatic segmentation system of emission tomography data based on classification system -- Biomedical signal analysis -- Alpha Rhythm Dominance in Human Emotional Attention States: An Experimentation with idling and binding Rhythms -- New insights in echocardiography based left-ventricle dynamics assessment -- Optimal Elbow Angle for MMG Signal Classification of Biceps Brachii -- during Dynamic Fatiguing Contraction -- From Single Fibre Action Potential to Surface Electromyographic Signal: A Simulation Study -- New algorithm for assessment of frequency duration of murmurs using Hilbert-Huang transform -- Heart rate regularity changes in older people with orthostatic intolerance -- Evolutionary Multiobjective Feature Selection in Multiresolution Analysis for BCI -- Dose calculation in a mouse lung tumor and in secondary organs during radiotherapy treatment: A Monte Carlo study -- Computational genomics -- Towards a More Efficient Discovery of Biologically Significant DNA Motifs -- Improved Core Genes Prediction for Constructing well-supported Phylogenetic Trees in large sets of Plant Species -- Comprehensive study of bivalent chromatin marks on promoters in mammalian embryonic stem cells -- Finding unknown nodes in phylogenetic graphs -- Supporting Bioinformatics Applications with Hybrid Multi-Cloud Services -- Relation between Insertion Sequences and Genome Rearrangements in Pseudomonas aeruginosa -- A genetic algorithm for motif finding based on statistical significance -- Identification and in silico analysis of NADPH oxidase homologues involved in allergy from an olive pollen transcriptome -- Identification of distinctive variants of the olive pollen allergen Ole e -- 5 (Cu,Zn Superoxide Dismutase) throughout the analysis of the olive pollen transcriptome -- A Computational Method for the Rate Estimation of Evolutionary Transpositions -- Genome Structure of Organelles Strongly Relates to Taxonomy of Bearers -- A unified integer programming model for genome rearrangement problems -- Statistical integration of p-values for enhancing discovery of radiotoxicity gene signatures -- Computational proteomics -- A

	pseudo de Bruijn graph representation for discretization orders for distance geometry -- Using Entropy Cluster-based Clustering for finding potential Protein Complexes -- A Weighted Cramer's V Index for the Assessment of Stability in the Fuzzy Clustering of Class C G Protein-Coupled Receptors -- P3D-SQL: Extending Oracle PL/SQL Capabilities Towards 3D Protein Structure Similarity Searching -- Evaluation of example-based measures for multi-label classification Performance -- Computational systems for modelling biological processes The MetaboX library: building metabolic networks from KEGG database -- Pseudoknots Prediction on RNA Secondary Structure Using Term Rewriting -- A model of the dynamics of a population of diabetics with and without complications with optimal control -- Logical Modeling and Analysis of Regulatory Genetic Networks in a Non Monotonic Framework -- The impact of obesity on type 2 Diabetes: Mathematical model -- Gene Expression vs Network Attractors -- A Computational Domain-based Feature Grouping Approach for Prediction of Stability of SCF Ligases -- A new approach to obtain EFMs using graph methods based on the shortest path between end nodes -- Identifiability of Nonlinear ODE Models in Systems Biology: Results from both Structural and Data-based methods -- Non-canonical imperfect base pair predictor: the RNA 3D structure modeling process improvement -- eHealth.
Sommario/riassunto	The two volume set LNCS 9043 and 9044 constitutes the refereed proceedings of the Third International Conference on Bioinformatics and Biomedical Engineering, IWBBIO 2015, held in Granada, Spain, in April 2015. The 135 papers presented were carefully reviewed and selected from 268 submissions. The scope of the conference spans the following areas: bioinformatics for healthcare and diseases, biomedical engineering, biomedical image analysis, biomedical signal analysis, computational genomics, computational proteomics, computational systems for modelling biological processes, eHealth, next generation sequencing and sequence analysis, quantitative and systems pharmacology, Hidden Markov Model (HMM) for biological sequence modeling, advances in computational intelligence for bioinformatics and biomedicine, tools for next generation sequencing data analysis, dynamics networks in system medicine, interdisciplinary puzzles of measurements in biological systems, biological networks, high performance computing in bioinformatics, computational biology and computational chemistry, advances in drug discovery, and ambient intelligence for bioemotional computing.