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Collana	Lecture Notes in Bioinformatics ; ; 9044
Disciplina	570.285
Soggetti	Bioinformatics Health informatics Optical data processing Biometrics (Biology) Pattern recognition Computational Biology/Bioinformatics Health Informatics Image Processing and Computer Vision Biometrics Pattern Recognition
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
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Note generali	Bibliographic Level Mode of Issuance: Monograph
Nota di contenuto	e-Health Informed Foreign Patient and Physician Communication: The Perspective of Informed Consent -- Empirical Analysis of the Effect of eHealth on Medical Expenditures of Patients with Chronic Diseases -- Impact of health apps in health and computer science publications. A systematic review from 2010 to the present day -- Automated extraction of food intake indicators from continuous meal weight measurements -- System Development Ontology to Discover Lifestyle Patterns Associated with NCD -- USSD technology a low cost asset in complementing Public Health Workers work processes -- Energy Efficiency Study of representative Microcontrollers for Wearable Electronics -- Analysis of Inter-Rater Reliability of the Evaluation of

Radiologists Assessment After Image Processing -- A LOD-based service for extracting Linked Open Emergency Health are Data -- Development of an Auditory Cueing System to Assist Gait in Patients with Parkinson's Disease -- Linear accelerator bunkers: Shielding Verification -- New IT tools and methods improving lifestyle of young people -- XTENS - a JSON-based digital repository for Biomedical Data Management -- An Innovative Framework for Personalized Health and Wellness Support -- An Ontology for Dynamic Sensor Selection in Wearable Activity Recognition -- Proposal for interoperability standards applications in the health sector -- An event-driven architecture for biomedical data integration and Interoperability -- Next generation sequencing and sequence analysis Local Search for Multiobjective Multiple Sequence Alignment -- Alignment Free Frequency Based Distance Measures for Promoter Sequence Comparison -- Energy-Efficient Architecture For DP Local Sequence Alignment: Exploiting ILP and DLP -- Hierarchical Assembly of Pools -- SimpliSMS: A Simple, Lightweight and Fast Approach for Structured Motifs Searching -- Quantitative and Systems Pharmacology -- Successes and Pitfalls in Scoring Molecular Interactions -- The use of Random Forest to predict binding affinity in docking -- Hidden Markov Model (HMM) for Biological Sequence Modeling Strong Inhomogeneity in Triplet Distribution Alongside a Genome -- Predicting sub-cellular location of proteins based on hierarchical clustering and hidden Markov models -- Advances in Computational Intelligence for Bioinformatics and Biomedicine -- Multi genetic risk quantification for SNP array based direct-to-consumer genomic services -- Computational inference in systems biology -- A Price we Pay for Inexact Dimensionality Reduction -- An Ensemble of Cooperative Parallel Metaheuristics for Gene Selection in Cancer Classification -- Tools for Next Generation Sequencing data analysis DEgenes Hunter - A self-customised gene expression analysis workflow for non-model organisms -- Bioinformatics Analyses to Separate Highly Divergent mRNAs from Unknown Sequences in de novo Assembled Transcriptomes -- Evaluation of combined genome assemblies: a case study with fungal Genomes -- Using multivariate analysis and bioinformatic tools to elucidate the functions of a cyanobacterial global regulator from RNA-Seq data obtained in different genetic and environmental backgrounds -- HvDBase: a web resource on Hydra Vulgaris transcriptome -- Nucleotide Sequence Alignment and Compression via Shortest Unique Substring -- Dynamics networks in system medicine Modeling of the Urothelium with an Agent Based Approach -- Systematic comparison of machine learning methods for identification of miRNA species as disease biomarkers -- Numerical Investigation of Graph Spectra and Information Interpretability of Eigenvalues -- Interdisciplinary puzzles of measurements in biological systems Mixture model based efficient method for magnetic resonance spectra quantification -- Noise and baseline ltration in mass spectrometry -- BioWes from design of experiment, through protocol to repository: control, standardization, and back-tracking -- Measurement in biological systems from the self - organisation point of View -- FRAP & FLIP: Two sides of the same coin? -- Biological Networks: Insight from interactions MicroRNA Target Prediction Based upon Metastable RNA Secondary Structures -- Inference of Circadian Regulatory Pathways based on Delay Differential Equations -- Towards an effective telemedicine: an interdisciplinary approach -- Simplifying tele-rehabilitation devices for their practical use in non-clinical environments -- Non-intrusive patient monitoring for supporting general practitioners in following diseases evolution -- Interactive business models for Telerehabilitation after Total Knee

Replacement: Preliminary results from Tuscany -- Ontological Personal Healthcare using Medical Standards -- High Performance Computing in Bioinformatics, Computational Biology and Computational Chemistry -- Applications of High Performance Computing in Bioinformatics, Computational Biology and Computational Chemistry -- Computing Biological Model Parameters by Parallel Statistical Model Checking -- Mobile access to on-line analytic bioinformatics tools -- isDNA: A tool for real-time visualization of plasmid DNA Monte-Carlo simulations in 3D -- Transport Properties of RNA Nanotubes using Molecular Dynamics Simulation -- Molecular Dynamics Simulations of Ligand Recognition upon Binding Antithrombin: A MM/GBSA Approach -- Predicting atherosclerotic plaque location in an iliac bifurcation using a hybrid CFD/biomechanical approach -- Identification of Biologically Significant Elements using Correlation Networks in High Performance Computing Environments -- Enhancing the parallelization of Non-Bonded Interactions Kernel for Virtual Screening on GPUs -- Advances in Drug Discovery -- Prediction of Functional Types of Ligands for G Protein-Coupled Receptors with Dynamically Discriminable States Embedded in Low Dimension -- Improving activity prediction of Adenosine A2B receptor antagonists by machine learning methods -- Support Vector Machines Prediction of drug solubility on GPUs -- DIA-DB: a web-accessible database for the prediction of diabetes drugs -- Molecular docking and Biological evaluation of functionalized benzo[h]quinolines as Colon cancer agents -- Predicting cross-reactivity from computational studies for pre-evaluation of specific hepatic glycogen phosphorylase inhibitors -- Ambient Intelligence for Bioemotional Computing Externalising Moods and Psychological States to Smooth Pet-robot/Child Interaction through Bluetooth Communication -- Patient Lifecycle Management: An Approach for Clinical Processes -- Advertising liking recognition technique applied to neuromarketing by using low-cost eeg headset -- Heart Rate Variability indicating Stress visualized by Correlations Plots -- Emotions and Diabetes.

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### 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.

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