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Collana	Lecture Notes in Bioinformatics ; ; 9044
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Soggetti	Bioinformatics Health informatics Optical data processing Biometrics (Biology) Pattern recognition Computational Biology/Bioinformatics Health Informatics Image Processing and Computer Vision Biometrics Pattern Recognition
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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.

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.
