

Riconoscimento e Recupero dell'informazione per Bioinformatica (aa 2016-2017)

Update 12/3/2018 – Titoli già assegnati

Bioinformatics (2015) 31 (15): 2505-2513.	Identification of a small set of plasma signalling proteins using neural network for prediction of Alzheimer's disease
BMC Bioinformatics. 2015; 16(Suppl 17): S1.	Identifying representative drug resistant mutants of HIV
Bioinformatics, 31(13), 2015, 2115–2122.	Pattern recognition methods to relate time profiles of gene expression with phenotypic data: a comparative study
Bioinformatics (2015) 31 (23): 3725-3732	TIPR: transcription initiation pattern recognition on a genome scale
BMC Bioinformatics (2015) 16:158	In-vitro diagnosis of single and poly microbial species targeted for diabetic foot infection using e-nose technology"
BMC Bioinformatics 2015, 16(Suppl 1):S9	viralmiR: a support vector machine based method for predicting viral microRNA precursors
Artificial Intelligence in Medicine 64 (2015) 105–115:	Learning from healthy and stable eyes: a new approach for detection of glaucomatous progression
Artificial Intelligence in Medicine. 20(2), 469–481;	A Gaussian mixture model based cost function for parameter estimation of chaotic biological systems
Bioinformatics (2015)	Gene selection for the reconstruction of stem cell differentiation trees: a linear programming approach
BMC Bioinformatics201516(Suppl 9):S3	Differential diagnosis of pleural mesothelioma using Logic Learning Machine
BMC Bioinformatics201516(Suppl 17):S5	A computational method for drug repositioning using publicly available gene expression data
BMC Bioinformatics (2015) 16:351	HMMvar-func: a new method for predicting the functional outcome of genetic variants
BMC Bioinformatics201516(Suppl 18):S4	Automated identification of copepods using digital image processing and artificial neural network
Science Advances Vol. 1, no. 8, e1500325	An auditory feature detection circuit for sound pattern recognition
BMC Bioinformatics201516:74	Inferring dynamic gene regulatory networks in cardiac differentiation through the integration of multi-dimensional data
Artificial intelligence in medicine 64(3) 195–204	Robust feature selection to predict tumor treatment outcome
BMC Bioinformatics (2015) 16:35	Data-intensive analysis of HIV mutations
Bioinformatics (2015) 31 (24):3946-3952.	Hierarchical boosting: a machine-learning framework to detect and classify hard selective sweeps in human populations
Bioinformatics (2015) 31 (21):3413-3420.	DINGO: Differential Network Analysis in Genomics
Bioinformatics (2015) 31 (8): 1226-1234.	Identifying cancer-related microRNAs based on gene expression data
Bioinformatics 2015 15;31(8):1183-90	Faster sequence homology searches by clustering subsequences.
BMC Bioinformatics 2015 16(Suppl 18):S1	An adaptive genetic algorithm for selection of blood-based biomarkers for prediction of Alzheimer's disease progression
BMC Bioinformatics2015 16(Suppl 18):S14	Characterizing informative sequence descriptors and predicting binding affinities of heterodimeric protein complexes
BMC Bioinformatics2015 16(Suppl 7):S9	A probabilistic approach for pediatric epilepsy diagnosis using brain functional connectivity networks
BMC Bioinformatics201516(Suppl 4):S7	Analysis of miRNA expression profiles in breast cancer using biclustering

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Artificial Intelligence in Medicine 64(3), 2015, pp 205–215	Cardiac magnetic resonance image-based classification of the risk of arrhythmias in post-myocardial infarction patients
BMC Bioinformatics 2015 16:147	Deep convolutional neural networks for annotating gene expression patterns in the mouse brain
BMC Bioinformatics 2015 16(Suppl 17):S8	Automated parameter estimation for biological models using Bayesian statistical model checking
Nature Reviews Genetics 16, 133–145 (2015)	Computational and analytical challenges in single-cell transcriptomics
BMC Bioinformatics 2015 16:68	Classification of bioinformatics workflows using weighted versions of partitioning and hierarchical clustering algorithms
BMC Bioinformatics (2015) 16:413	MixChIP: a probabilistic method for cell type specific protein-DNA binding analysis
BMC Bioinformatics 2015 16:417	Multi-label multi-instance transfer learning for simultaneous reconstruction and cross-talk modeling of multiple human signaling pathways
BMC Bioinformatics 2015 16:417	The relative vertex clustering value - a new criterion for the fast discovery of functional modules in protein interaction networks
BMC Bioinformatics 2015 16(Suppl 4):S3	Alignment of time course gene expression data and the classification of developmentally driven genes with hidden Markov models
BMC Bioinformatics 2015 16:196	A bio-inspired computing model for ovarian carcinoma classification and oncogene detection
Bioinformatics. 2015 Apr 1;31(7):1102-10	The genomic and functional characteristics of disease genes
Briefings in Bioinformatics, 16 1 2015, P. 16–23	Discovering hospital admission patterns using models learnt from electronic hospital records
Bioinformatics, 31 – 24 2015pp 3970–3976	Fast and accurate approximate inference of transcript expression from RNA-seq data
Bioinformatics, 31(24), 2015, 3881–3889	