Gestione e modellazione di dati bioinformatici (aa 2017-2018)
Articoli assegnati (ultimo aggiornamento 22-3-19)

Artificial Intelligence in Medicine, 66, 2016, 53-62	Analyzing depression tendency of web posts using an event-driven depression tendency warning model
Artificial Intelligence in Medicine 70 (2016) 12–30	Classification of auditory brainstem responses through symbolic pattern discovery
Briefings in Bioinformatics, 17(5), 2016, 831–840	Correct machine learning on protein sequences: a peer-reviewing perspective
Bioinformatics, 32(23), 2016, 3611–3618	Support vector machine model of developmental brain gene expression data for prioritization of Autism risk gene candidates
Artificial Intelligence in Medicine, 73, 2016, P. 1-13	Brain tumor segmentation from multimodal magnetic resonance images via sparse representation
BMC Bioinformatics 2016, 17(Suppl 18):464	SnoReport 2.0: new features and a refined Support Vector Machine to improve snoRNA identification
BMC Bioinformatics 2016, 17(Suppl 19):511	Automated identification of Monogeneans using digital image processing and K-nearest neighbour approaches
BMC Bioinformatics 2016 17(Suppl 13):357	Successful classification of cocaine dependence using brain imaging: a generalizable machine learning approach
BMC Bioinformatics 2016, 17(Suppl 17):537	Dynamic epigenetic mode analysis using spatial temporal clustering
BMC Bioinformatics 2016 17(Suppl 19):505	Classification of Suncus murinus species complex (Soricidae: Crocidurinae) in Peninsular Malaysia using image analysis and machine learning approaches
Scientific Reports 6, Article number: 34468 (2016)	Computer keyboard interaction as an indicator of early Parkinson's disease
Information Systems: Vol 59, 2016, Pages 79-93	The similarity-aware relational database set operators
BMC Bioinformatics 2016 17:459	Feature-based classification of human transcription factors into hypothetical subclasses related to regulatory function
Bioinformatics, vol 32, 17 2016, Pages i620–i628	XGSA: A statistical method for cross-species gene set analysis
Artif Intell Med. 2016 Sep;72:42-55	Prediction of lung cancer incidence on the low-dose computed tomography arm of the National Lung Screening Trial: A dynamic Bayesian network.
Artificial Intelligence in Medicine 73, 2016, 23-33	A comparative analysis of chaotic particle swarm optimizations for detecting single nucleotide polymorphism barcodes
BMC Bioinformatics 2016 17:545	Gene regulatory network inference using PLS-based methods
Briefings in Bioinformatics, bbw104	Predictive approaches for drug combination discovery in cancer
Artificial Intelligence in Medicine, 73, 2016, 14-22	Automated segmentation of white matter fiber bundles using diffusion tensor imaging data and a new density based clustering algorithm
Bioinformatics, 32,24, 2016, Pages 3717–3728	A new correlation clustering method for cancer mutation analysis
Bioinformatics, 32(22), 2016, 3444–3453	Drug drug interaction extraction from biomedical literature using syntax convolutional neural network

Bioinformatics, 32(3) 2016, Pages 388–397	CLUSTERnGO: a user-defined modelling platform for two-stage clustering of time-series data
Artificial Intelligence in Medicine, 73,2016, p 70-77	Prediction of anti-cancer drug response by kernelized multi-task learning
Bioinformatics, 32(9), 2016, 1366–1372	Utilizing the Jaccard index to reveal population stratification in sequencing data: a simulation study and an application to the 1000 Genomes Project

BMC Bioinformatics 2016 17(Suppl 8):278	Automated prediction of HIV drug resistance from genotype data
Bioinformatics. 2016 Feb 1;32(3):338-44	Rapid and enhanced remote homology detection by cascading hidden Markov model searches in sequence space.
IEEE/ACM Transactions on Computational Biology and Bioinformatics (Volume: 13, Issue: 5, September 1 2016), pag 947 – 953	Prediction the Substrate Specificities of Membrane Transport Proteins Based on Support Vector Machine and Hybrid Features
BMC Bioinformatics 2016, 17(Suppl 17):478	Prediction of HIV-1 protease cleavage site using a combination of sequence, structural, and physicochemical features
IEEE/ACM TRANSACTIONS ON COMPUTATIONAL BIOLOGY AND BIOINFORMATICS, VOL. 13, NO. 2, MARCH/APRIL 2016.	bLARS: An Algorithm to Infer Gene Regulatory Networks
BMC Bioinformatics 2016, 17(Suppl 17):466	A fast read alignment method based on seed-and-vote for next generation sequencing
BMC BioinformaticsBMC series – open, inclusive and trusted201617:323	Identification of DNA-binding proteins using multi-features fusion and binary firefly optimization algorithm
BMC Bioinformatics (2016) 17:140	pcaReduce: hierarchical clustering of single cell transcriptional profiles
BMC Bioinformatics 2016, 17(Suppl 8):285	PnpProbs: a better multiple sequence alignment tool by better handling of guide trees