

Thematic Workshop

Computational analysis of biological structures and networks

Assigned papers aa 18-19 (last update 15-6-2020)

BMC Bioinformatics 2010 11 (Suppl 1) :S57	Active learning for human protein-protein interaction prediction
BMC Bioinformatics 2010,11(Suppl 1):S58	Active machine learning for transmembrane helix prediction
BMC Bioinformatics 2018 19:241	Semi-supervised machine learning for automated species identification by collagen peptide mass fingerprinting
BMC Bioinformatics 2013, 14(Suppl 8):S10	Prediction of protein-protein interactions from amino acid sequences with ensemble extreme learning machines and principal component analysis
Bioinformatics, 34(6),2018, Pp1009–1015	Unsupervised multiple kernel learning for heterogeneous data integration
BMC Bioinformatics2010,11(Suppl 1) S6	Genome-wide sequence-based prediction of peripheral proteins using a novel semi-supervised learning technique
BMC Bioinformatics2014,15(Suppl 11):S14	Improving protein fold recognition by random forest
Artificial Intelligence in Medicine, vol 84, 2018, Pp 117-126	A novel method for predicting kidney stone type using ensemble learning
BMC Bioinformatics 2016 17 (Suppl 19) :509	Drug-target interaction prediction via class imbalance-aware ensemble learning
Briefings in Bioinformatics, 2017 Aug 18	Facilitating prediction of adverse drug reactions by using knowledge graphs and multi-label learning models.
Bioinformatics,31(7), 2015, Pp 1111–1119,	Bioimaging-based detection of mislocalized proteins in human cancers by semi-supervised learning
BMC Bioinformatics201516:213	Deciding when to stop: efficient experimentation to learn to predict drug-target interactions
BMC Bioinformatics 2006, 7:455	Building multiclass classifiers for remote homology detection and fold recognition
BMC Bioinformatics201617:22	A novel semi-supervised algorithm for the taxonomic assignment of metagenomic reads
Bioinformatics, 33-1, 2017, Pp 35–41	iRSpot-EL: identify recombination spots with an ensemble learning approach
BioMedical Engineering 2014 - 13 (Suppl 2) :S4	A random forest model based classification scheme for neonatal amplitude-integrated EEG
Artificial Intelligence in Medicine 84 (2018) 146–158	Random ensemble learning for EEG classification
Applied Soft Computing 12 (12), 2012, pp. 3798-3809	Fuzzy cognitive map ensemble learning paradigm to solve classification problems: Application to autism identification
BMC Bioinformatics201112 (Suppl 12) :S4	Combining active learning and semi-supervised learning techniques to extract protein interaction sentences
Nature Scientific Reports volume 7, Article number: 45269 (2017)	A Hierarchical Feature and Sample Selection Framework and Its Application for Alzheimer's Disease Diagnosis

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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 (Suppl 18):S12	Positive-unlabeled learning for the prediction of conformational B-cell epitopes
BMC Bioinformatics (2015) 16:365	Predicting drug side effects by multi-label learning and ensemble learning
BMC Bioinformatics (2017) 18:140	Positive-Unlabeled Learning for inferring drug interactions based on heterogeneous attributes
BMC Bioinformatics 2018 19:425	Learning protein binding affinity using privileged information
BMC Bioinformatics 2018 19 (Suppl 20) :502	Biomedical semantic indexing by deep neural network with multi-task learning
Ecotoxicol Environ Saf. 2019 Apr 23;179:71-78	QSAR modelling study of the bioconcentration factor and toxicity of organic compounds to aquatic organisms using machine Learning and ensemble methods
Bioinformatics, 28(20), 2012, 2640–2647	Positive-unlabeled learning for disease gene identification
BMC Bioinformatics 2018 19 (Suppl 20) :502	Biomedical semantic indexing by deep neural network with multi-task learning
Ecotoxicol Environ Saf. 2019 Apr 23;179:71-78	QSAR modelling study of the bioconcentration factor and toxicity of organic compounds to aquatic organisms using machine Learning and ensemble methods
BMC Bioinformatics 2012 13 (Suppl 15) :S3	Implementation of multiple-instance learning in drug activity prediction
Proteome Sci. 2013 Nov 7;11(Suppl 1):S17	Semi-supervised method for biomedical event extraction.
Bioinformatics, bty910	Semi-supervised learning of Hidden Markov Models for biological sequence analysis
Scientific Reports 7, Article number: 10044 (2017)	Finding disagreement pathway signatures and constructing an ensemble model for cancer classification Scientific Reports
Bioinformatics, bty995	Protein–protein interaction sites prediction by ensemble random forests with synthetic minority oversampling technique
BMC Bioinformatics volume 15: 143 (2014)	Efficient discovery of responses of proteins to compounds using active learning
BMC Bioinformatics 18: 266 (2017)	Predicting anatomic therapeutic chemical classification codes using tiered learning
BMC Bioinformatics volume 20, Article number: 273 (2019)	Robust identification of molecular phenotypes using semi-supervised learning