Computational analysis of biological structures and networks

Results for Thematic Workshop on Advanced Learning paradigms in Medical bioinformatics

Monday 21-1-19: 8.30-11-30 (room G)	**Result**
A random forest model based classification scheme for neonatal amplitude-integrated EEG	14/15
Active learning for human protein-protein interaction prediction	14/15
Active machine learning for transmembrane helix prediction	15/15
Fuzzy cognitive map ensemble learning paradigm to solve classification problems: Application to autism identification	14/15
Semi-supervised machine learning for automated species identification by collagen peptide mass fingerprinting	13/15
A novel method for predicting kidney stone type using ensemble learning	15/15
Bioimaging-based detection of mislocalized proteins in human cancers by semi-supervised learning	**
Random ensemble learning for EEG classification	14.5/15
Prediction of protein-protein interactions from amino acid sequences with ensemble extreme learning machines and principal component analysis	15/15
Learning protein binding affinity using privileged information	**
iRSpot-EL: identify recombination spots with an ensemble learning approach	14/15
Genome-wide sequence-based prediction of peripheral proteinsusing a novel semi-supervised learning technique	**

Wednesday 23-1-19: 8.30-11-30 (room G)	
Drug-target interaction prediction via class imbalance-aware ensemble learning	15/15
Combining active learning and semi-supervised learning techniques to extract protein interaction sentences	15/15
Improving protein fold recognition by randomforest	14/15
Building multiclass classifiers for remote homology detection and fold recognition	**
Positive-Unlabeled Learning for inferringdrug interactions based on heterogeneousattributes	15/15
A novel semi-supervised algorithm for the taxonomic assignment of metagenomic reads	14/15
Unsupervised multiple kernel learning for heterogeneous data integration	15/15
Positive-unlabeled learning for the prediction of conformational B-cell epitopes	13/15
Facilitating prediction of adverse drug reactions by using knowledge graphs and multi-label learning models.	15/15
Deciding when to stop: efficient experimentation to learn to predict drug-target interactions	14/15
Predicting drug side effects by multi-label learning and ensemble learning	13.5/15

Note for students who received “**”:
please come to my office on Friday 25th January, h 10.00