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Degree Project in Bioinformatics

Masters Programme in Molecular Biotechnology Engineering,
Uppsala University School of Engineering

UPTEC X 14 032	Date of issue 2014-08	
Author	Matilda Åslin	
Title (English)	Improved analysis of multivariate mutation and drug target data using network bioinformatics	
Title (Swedish)		
Abstract	<p>This thesis is focused on the concept that protein-protein interaction (PPI) data can be used to improve the analysis of multivariate data. It included further development of the already published algorithm QuantMap and development of a new linear prediction model. QuantMap is a clustering algorithm able to group chemicals/drugs according to their bioactivity profiles. This is done by comparing the PPI network expanded from their target proteins. In the new version of QuantMap a random walk algorithm is used to expand the network, rather than expansion to the nearest neighbours. The new linear prediction model, adapted for biological data, is based on ridge regression with a modified penalty term. The penalty term was designed so that proteins with similar interaction profiles get similar weights, while proteins with different interaction profiles get different weights. The new version of QuantMap resulted in a more robust method, while more testing is needed to elucidate the potential of the new linear model.</p>	
Keywords	Multivariate data analysis, Protein-protein interaction, Machine learning, Molecular medicine, Predictive modeling, Network bioinformatics, Linear regression	
Supervisors	Prof. Mats Gustafsson & Doc. Ulf Hammerling Department of Medical Sciences, Uppsala University	
Scientific reviewer	Dr. Eva Freyhult Department of Medical Sciences, Uppsala University	
Project name	Sponsors	
Language	Security	
English	Secret until 2015-08	
ISSN 1401-2138	Classification	
Supplementary bibliographical information	Pages	
	33	
Biology Education Centre Box 592, S-751 24 Uppsala	Biomedical Center Tel +46 (0)18 4710000	Husargatan 3, Uppsala Fax +46 (0)18 471 4687