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Degree Project in Bioinformatics

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Title (English) Improved analysis of systemic molecular profiles using network bioinformatics		
Title (Swedish)		
Abstract Incorporating prior biological knowledge into methods for comparing systemic molecular profiles is believed to increase performance and interpretability. In this project, prior knowledge in the form of publicly available information about protein-protein interactions (PPIs) was used to develop (i) prediction (classification) models that utilized the modular structure of the PPIs and (ii) a method for pairwise mRNA gene expression profile comparisons guided by functional importance of individual genes suggested by the PPI information. The classification models were evaluated by predicting <i>in vitro</i> drug resistance based on DNA methylation data. The method for pairwise profile comparisons was evaluated using the Connectivity Map (CMAP) database. In conclusion, contrary to previous reports, we did not observe an increase in performance nor any gain in interpretability when incorporating PPI data into models for comparison of systemic molecular profiles.		
Keywords Network bioinformatics, Protein-protein interactions, Predictive modeling, Molecular medicine, Gene expression, CpG, DNA methylation, FMCA, Connectivity map, Zhang-Gant		
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