Integrating proteomics in medical decision support systems using Bayesian networks

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"Omics"-technologies such as microarrays and proteomics have changed cancer research. Integration of these sources of information with clinical data offers considerable opportunities for improving the results of mathematical analyses. In cancer research clinical data is often available when a microarray study or proteomics study is carried out. This data offers an independently gathered and possibly complementary source of information. However, clinical data are usually not taken into account and the high dimensional data are the focus of attention.

Recently we developed a method for integrating clincical and microarray data using Bayesian networks by treating both data sources on an equal footing. This method doesn't make any assumptions about which data is integrated. Therefore proteomics data will be integrated in the current models. Mass spectrometry is being used increasingly to detect proteomic patterns in mixtures of proteins derived from biological samples (e.g. biomarker identification). This technology yields complex data for which the features of interest are peaks. Baseline correction, intensity normalization and filtering are important steps before subsequent analyses. Significant peaks are selected by p-values, assuming that each m/z value is independent.This will allow to build a classifier based on clinical, microarray and proteomics data to predict e.g. prognosis.

06-121

   Gevaert O., Ojeda F., Timmerman D., De Moor B., ``Integrating proteomics in medical decision support systems using Bayesian networks", in *Proc. of the conference on In-Silico Analysis of Proteins - Swiss-Prot (Swiss-Prot)*, Fortaleza, Brazil, Aug. 2006, pp. 1-2., Lirias number: 180825.