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Application of Bayesian networks for prognosis of breast cancer patient's outcomes

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Background & Purpose: Nowadays due to the technological progress in medicine it is possible to yield a lot of unique information about each patient. This allows one to think about the personalized approach that considers not only patient's individual clinical features but also tumor's bio-molecular features and provides a treatment for each patient. One of the possible ways are probabilistic models on the base of Bayesian networks (BNs), since they are capable of self-learning and self-improvement as the accumulation of experimental information and are insensitive to possible erroneous or incomplete data. BNs with naive topology has been used for a prediction of progression or death in breast cancer patients on the base of different prognostic parameters including expression and tumor's cell localization of multifunctional protein YB-1.

Materials & Method: 323 breast cancer patients were enrolled in this trial. 32 clinical and bio-molecular parameters including YB-1 expression and tumor's cell localization were assessed for prognosis. Two end points (EP) have been chosen for prognosis: Tumor's progression (EP-P) and patient's death (EP-D) and they have been represented by root nodes of the two-respective naive BNs. For estimation of prognosis quality, the area under the ROC-curve, AUC, has been used. Construction BNs, their learning, prognosis, AUC calculations and BNs optimization are performed by author's original programs. The simple algorithm of BN optimization with respect to the number of nodes is used. This algorithm allows to increase the quality of BN prognosis and to find the most important variables of the network. The parallel program implementing the algorithm of optimization has demonstrated good scalability with an increase in the computational cores number.

Result: The optimal BNs contain 7 of the most important nodes and have high-quality prognosis (AUC=0.83 for EP-P and 0.91 for EP-D), in contrast to primary BNs (AUC=0.63 for EP-P and 0.62 for EP-D). The expression of YB-1 mRNA is among of 7 prognostic parameters determining the risk of the patient's death. The optimal BN's data were used to plot of the histograms to stratify patients by groups of the unfavorable outcomes and to compute the probability of these outcomes.

Conclusion: The use of a BN with naive topology is shown to be effective for determination the most important prognostic parameters in breast cancer patients. The optimal BNs with high-quality prognosis' power are found. Histograms of the unfavorable outcomes that might be used in the expert system of personified medicine are created. BNs can be applied to large patient's databases containing thousands of patients and thousands of their variables.

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