TOWARDS THE AUTOMATED GENERATION OF INFLAMMATION PATHWAY HYPOTHESES FROM EXPERIMENTAL DATA AND PRIOR KNOWLEDGE

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ABSTRACT

Drug discovery and development are expensive and time consuming. Decisions affecting the advancement of potential therapeutics prior to clinical trials are in part based upon focused validation studies involving surrogate markers. Clinical trial failure rates of potential therapeutics are high, and therefore the development of more predictive validation studies from more comprehensive data sets is needed. These studies could be applied to the early identification of potential therapeutics destined to failure.

Increased pathway knowledge can be used to identify more predictive markers and understand complex marker relationships. Initial efforts towards the automated generation of inflammation pathway hypotheses are presented. Efforts include 1) database knowledge capture and visualization, 2) algorithmic interpretation of prior knowledge within a rule set, 3) a comparison of Bayesian, maximum likelihood, and mutual information techniques on an inflammation pathway example - combining microarray data with prior knowledge, and 4) modeling gene expression with difference equations. Initial implementation tools include Oracle, Java, and Matlab.

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