NILARS: an efficient algorithm based on linear regression for inferring gene networks

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Motivation

The existing algorithms based on multiple linear regression for inferring gene networks from expression data (including our previously described NIR and NIRest) can obtain satisfactory solutions, but their use is limited to small data sets because of computational complexity limits. A technique that produces a sub-optimal solution within a reasonable time is necessary for inferring gene networks from large data sets (such as those obtained from current generation Affymetrix chips).

Methods

In this work we describe an efficient algorithm, called NILARS (Network inference Least Angle Regression), to infer gene networks based on multiple linear regression. The algorithm uses gene expression data from DNA microarray and a greedy method, LARS (Least Angle Regression), to compute the coefficient of regression. An additional benefit of LARS is the availability of an effective model selection method based on the Mallows Cp statistics, which was adapted to the study of gene expression data.

Results

Compared to other methods for inferring gene networks, the proposed algorithm obtains good performance in a relatively short time (~ 24h) when processing a large number of genes (> 10.000) and expression experiments (~ 100). The algorithm has a computational complexity which is polynomial (in time and space) in the number of genes and in the number of expression experiments. Additional key features of our tool are techniques to
i) estimate also those genes that are perturbed, and
ii) detect and act on the outliers in the expression data to reduce their negative effect on the regression algorithm.
We present a performance evaluation using both synthetic and real data, to compare our methodology with other leading tools.

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