MIDDLE EAST TECHNICAL UNIVERSITY
DEPARTMENT OF STATISTICS

Inference of biochemical systems via MARS method and comparative analysis with GGM approach

Ezgi Ayyildiz, Melih Ağraz, Vilda Purutçuoğlu

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DEPARTMENT OF STATISTICS
MIDDLE EAST TECHNICAL UNIVERSITY
ANKARA 06531 – TURKEY

The gaussian graphical model (GGM) is one of the well-known modelling approaches to describe biological networks under steady-state conditions via the precision matrix of genomic data. Although there are different GGMs in literature, the L1-penalized lasso regression model is the most comprehensive method among alternatives as it can estimate the strength of interactions between genes while the structure of the actual network is unknown. But it has also certain drawbacks such that the estimated precision can be nonsymmetric and the computational demand is high for large systems. Here we consider to solve these problems via a non-parametric statistical approach, called the multivariate adaptive splines (MARS) whose parameter is inferred via the optimization approach. To compare the performance of both methods, we choose the specificity measure. The results indicate that though MARS gives close specificity for sparse networks, it is better, particularly, for dense systems and its structure is always symmetric. On the other hand from the time comparison we find that MARS is faster than GGM under all conditions. Thereby we believe that MARS can be considered as a strong and plausible alternative approach regarding GGM in the construction of complex biological systems.