

The Inferring Method of the large scale regulatory network for omics studies

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Recent advances in measurement techniques have provided a large number of time series data simultaneously. These data are important for understanding complex systems such as gene regulatory networks and metabolic pathways required to infer networks. We have proposed an efficient inferred method, the hybrid method, for such problems using S-system, the real-coded genetic algorithm (RCGA) along with adaptive real-coded ensemble crossover (AREX) combined with the just generation gap (JGG) and the modified Powell method. At this present, we have succeeded in optimizing more than 270 real-valued parameters using this method. Although the hybrid method is powerful compared with conventional numerical optimization methods, it is still insufficient for inferring large networks with more than 10 components. In this study, we attempted to infer the 30 components network, which requires optimizing more than 900 parameters, by applying our improved inferring method.

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