

Modulon Identification for Stress and Housekeeping Regulons Using Bacterial Gene Expression Array Data

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Abstract: We performed a complex analysis of *E. coli* transcriptome, developing the software, based on improved supervised approach for modulon identification and compared the consistency of prediction for different regulons.

We developed an easy-to-handle software for calculating the cliques of potentially co-expressed genes using a structured reference set. The technique has been tested on several stress-related (heat shock, LexA, oxydative stress) and housekeeping (substance and energy metabolism) *E. coli* regulons, verifying questionable regulon members and predicting the new ones. We succeeded in prediction of additional modulon participants and compared the results to those obtained from several independent datasets. The results obtained by implementation of our software are consistent with the available experimental data. Among the chosen set stress and some substance metabolism regulons proved to be more self-consistent.

The use of structured set of known genes allow to get clusters of potentially coexpressed genes which are more compact and reasonable from the biological point of view. Coordinated expressions of genes belonging to different regulons renders it possible to reveal global structure of bacterial regulatory network.

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