

Abstract Submitted  
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**Detecting Functional Structures in E. coli Gene Networks from Expression Data**<sup>1</sup> TIANLONG CHEN, Department of Physics, Univ of Houston, MADELEINE OPITZ, Center for NanoScience, Faculty of Physics, Ludwig-Maximilians-Universität München, KEVIN E. BASSLER, Department of Physics, Univ of Houston — The rapidly growing amount of available gene expression data for many organisms makes the development of robust systematic methods for determining the structure and function of regulatory networks from that data an important goal. Recently, methods that use the context likelihood of relatedness to infer a network and then use modularity maximizing community detection algorithms on the inferred network to find the functional structure were shown to be effective [PLoS Comput. Biol. 8, e1002391 (2012)]. Improvements of these methods will be presented and applied to systematically study Escherichia coli expression data. First robust functionally related communities of genes are identified and then the structure of the more closely related genes within those communities are determined. Results will be compared with gene ontology terms and the RegulonDB database. Predictions of a number of significant new regulatory relations are found.

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