**An Integrated Approach to Reconstructing Genome-Scale Transcriptional Regulatory Networks**

One of the goals of systems biology is the mapping of gene interactions and regulatory networks from complex data sets. In many biological systems, a large part of the response to environmental signaling occurs at the level of transcription. A detailed understanding of the factors that control the genome-level transcriptomic response and modeling of such regulatory networks will greatly enable synthetic design of microbes tailored for biofuel production. Researchers at GLBRC have developed a new way to construct transcriptional regulatory networks (TRNs) that utilizes comparative genomic analyses of closely related microbes, global gene expression patterns, and the intrinsic properties of transcription factors. Using this workflow, a reconstructed TRN of the well-studied bacterium *Escherichia coli* was shown to capture a significantly larger fraction of the sub-networks and associated lifestyles than those generated by traditional approaches. Additional validation was demonstrated with the photosynthetic bacterium *Rhodobacter sphaeroides*, whereby known regulatory systems were accurately depicted within the TRN. Importantly, the TRN revealed new regulators, gene targets, and links between sub-networks that, when examined further, should yield a deeper understanding of the metabolic diversity of this bacterium. The researchers also show that this integrated workflow generates high information content, large scale TRNs for other organisms that were used to assemble the genome-scale TRN. Thus, this powerful bioinformatics tool can be used to uncover novel regulatory mechanisms from a variety of biological systems that may be useful for the control of biofuel production. The new approach to TRN reconstruction will soon be available to the scientific community through Kbase.

**References:** Imam S, Noguera DR, Donohue TJ (2015) An integrated approach to reconstructing genome-scale transcriptional regulatory networks. PLoS Computational Biology 11: e1004103.

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