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Sequence-based network models provide researchers with valuable information regarding biological networks and structural components of microorganisms. Although these models can be used to identify cellular structure and potential gene functions, they do not provide a general systems overview of the interactions among these networks. To help predict network interactions and microbial response to environmental factors, a number of systems-based models have recently been developed. In this study, we will evaluate the use of two different systems-based models in predicting transcriptional gene responses. Transcriptional regulatory networks will be constructed using annotated genome sequences, available microarray data, and information on transcription factors and binding sites for the bacterium, *Shewanella*. In addition, we will use the Shewanella Knowledgebase, an integrative database, to extract experimental data and integrate current *Shewanella* datasets with results from our models to further understand transcriptional gene and microbial responses by *Shewanella*. Results from this study will not only evaluate the value of systems-based models in predicting regulatory responses, but will also be used to generate specific hypothesis regarding growth rates of *Shewanella* in natural sediments.

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