A General Bayesian Framework for Inclusion of Prior Information in Regulatory Network Inference

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Regulatory network inference (RNI) is an attempt to characterize the regulatory network of prokaryotes through the integration of multiple genomic data sources. Traditional RNI approaches such as relevance networks (Butte & Kohane 2000) and context likelihood of relatedness (CLR) (Faith et al. 2007) are described as agnostic in that they ignore the wealth of *a priori* knowledge about regulatory mechanisms and use only gene expression measurements. Here we outline a natural Bayesian extension of the relevance network and CLR procedures that can incorporate prior biological knowledge. We demonstrate power gains with the incorporation of operon information when inferring the E. Coli co-regulation network. Further work is underway to incorporate more complex forms of biological information.