Integrative inference of gene-regulatory networks in Escherichia coli using information theoretic concepts and sequence analysis.

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Details

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Abstract

Although Escherichia coli is one of the best studied model organisms, a comprehensive understanding of its gene regulation is not yet achieved. There exist many approaches to reconstruct regulatory interaction networks from gene expression experiments. Mutual information based approaches are most useful for large-scale network inference.

Involved units

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Topics

Networks of host- fungal pathogen interaction

Identifier

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