Inference of dynamical gene-regulatory networks based on time-resolved multi-stimuli multi-experiment data applying NetGenerator V2.0.

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Abstract

Inference of gene-regulatory networks (GRNs) is important for understanding behaviour and potential treatment of biological systems. Knowledge about GRNs gained from transcriptome analysis can be increased by multiple experiments and/or multiple stimuli. Since GRNs are complex and dynamical, appropriate methods and algorithms are needed for constructing models describing these dynamics. Algorithms based on heuristic approaches reduce the effort in parameter identification and computation time.

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