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(G*) Applying constraints on biomolecular network interactions through variability in perturbation response data

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Perturbation experiments—where the response of a system of interest is observed after exposure to drugs or disruptions—are commonly used to identify interactions in biochemical reaction networks. However, it is often the case that the data is only analysed for its deterministic averages, and analysis techniques also rely on specific knowledge of each perturbation's targets. We use constraints on interaction topology between the correlation and variation of molecular responses in two-component systems to analyse large-scale drug perturbation studies, in the absence of specific knowledge of the perturbations. We further show how analysis of variability in deterministic molecular responses is affected by non-linearity, stochasticity, and finite-sampling of perturbations.

Keyword-1

perturbation experiment

Keyword-2

biochemical reaction networks

Keyword-3

variability

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