

Network topology-based detection of differential gene regulation and regulatory switches in cell metabolism and signaling.

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[Details](#)



Abstract

Common approaches to pathway analysis treat pathways merely as lists of genes disregarding their topological structures, that is, ignoring the genes' interactions on which a pathway's cellular function depends. In contrast, PathWave has been developed for the analysis of high-throughput gene expression data that explicitly takes the topology of networks into account to identify both global dysregulation of and localized (switch-like) regulatory shifts within metabolic and signaling pathways. For this purpose, it applies adjusted wavelet transforms on optimized 2D grid representations of curated pathway maps.

Beteiligte Forschungseinheiten

Netzwerkmodellierung

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