

Estimating the activity of transcription factors by the effect on their target genes.

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Abstract

Understanding regulation of transcription is central for elucidating cellular regulation. Several statistical and mechanistic models have come up the last couple of years explaining gene transcription levels using information of potential transcriptional regulators as transcription factors (TFs) and information from epigenetic modifications. The activity of TFs is often inferred by their transcription levels, promoter binding and epigenetic effects. However, in principle, these methods do not take hard-to-measure influences such as post-transcriptional modifications into account.

Beteiligte Forschungseinheiten

Netzwerkmodellierung

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