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(57) Abstract :

Analyzing the intricate dynamics within a Gene Regulatory Network (GRN) derived from transcriptome data obtained from microarray or RNA-seq experiments is instrumental in unraveling key drivers in cancer research. Transcription Factor (TF) genes orchestrate protein complexes that modulate the transcription of diverse target genes. However, the temporal regulation of these transcriptional activities occurs selectively at specific activation time points, raising questions about the uniformity of regulatory capabilities across different stages, especially concerning periodicity. In addressing these challenges, we introduce RIFT, an algorithm designed to track the temporal differential regulatory patterns of Differentially Expressed (DE) target genes influenced by either individual TF genes or clusters of TF genes in extensive time series (TS) data. Validated on HeLa cell cycle data and benchmarked against leading state-of-the-art approaches, RIFT identifies stringent and target-specific significant TF genes for DE genes. This capability promises novel insights into genetic interactions.

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