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(57) Abstract :

In Systems Biology, identifying target genes within Gene Regulation Networks (GRNs) presents ongoing challenges. One promising approach involves exploring indirect gene regulatory hierarchical architectures, considering diverse topological structures and unknown regulatory factors. Such causal regulations can be investigated by incorporating perturbation experiments into the dataset. Current research often focuses on direct interaction networks, overlooking the potential influence of third-party entities in various forms of causal regulations. To address this gap, we present a hierarchical algorithm that leverages the Fused Least Absolute Shrinkage and Selection Operator (Fused-LASSO) technique with a Topological Overlap (TO) measure to reveal the underlying genetic wiring. We evaluate the efficacy of this model using data from the YEAST Cell Cycle and a human cancer cell line (HeLa). The algorithm identifies statistically significant hierarchical regulation patterns, shedding new light on gene regulation statistics while considering potential indirect interactions alongside direct interaction structures.

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