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## Unveiling Complex Patterns: An Information-Theoretic Approach to High-Order Behaviors in Microarray Data

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The information-theoretic framework provides valuable insights into the dynamics of correlated groups within networks. Although established methodologies exist for measuring new information, storage, and transmission, accurately quantifying changes in information remains challenging. Information change in networks pertains to redundancy and synergy among systems that collectively contain information about a specific target. Redundancy refers to the overlapping information accessible through individual source systems independently, while synergy describes information accessible only when multiple systems are jointly considered. Partial Information Decomposition (PID) is an advanced method designed to differentiate unique, redundant, and synergistic components of shared information. These distinctions, however, cannot be directly captured through traditional information-theoretic measures alone. In this research, we utilize the PID approach on publicly accessible microarray gene expression datasets from two separate studies involving patients diagnosed with Hepatocellular Carcinoma (HCC) and Autism Spectrum Disorder (ASD).

Through comparative analysis of gene and sample synergy clusters with conventional correlation clusters, our approach reveals higher-order patterns, including differentially expressed genes and significantly enriched biological functions directly associated with disease phenotypes. These insights demonstrate how the PID approach applied to gene expression data can enhance our understanding of genetic underpinnings related to the physiological manifestations of complex diseases.

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