

Dynamic Correlation Analysis for Omics Data

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Abstract: In high-throughput data, dynamic correlation between genes, i.e. changing correlation patterns under different biological conditions, can reveal important regulatory mechanisms. Given the complex nature of dynamic correlation, and the underlying conditions for dynamic correlation may not manifest into clinical observations, it is difficult to recover such signal from the data. Current methods seek underlying conditions for dynamic correlation by using certain observed genes as surrogates, which may not faithfully represent true latent conditions. In this study we develop a new method that directly identifies strong latent signals that regulate the dynamic correlation of many pairs of genes, named DCA: Dynamic Correlation Analysis. At the center of the method is a new metric for the identification of gene pairs that are highly likely to be dynamically correlated, without knowing the underlying conditions of the dynamic correlation. We validate the performance of the method with extensive simulations. In real data analysis, the method reveals novel latent factors with clear biological meaning, bringing new insights into the data.