

Study of Coordinative Gene Expression at The Biological Process Level

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Cellular processes are not isolated groups of events. Nevertheless, in most microarray analyses, they tend to be treated as standalone units. To shed light on how various parts of the interlocked biological processes are coordinated at the transcription level, there is a need to study the between-unit expressional relationship directly. RESULTS: We approach this issue by constructing an index of correlation function to convey the global pattern of coexpression between genes from one process and genes from the entire genome. Processes with similar signatures are then identified and projected to a process-to-process association graph. This top-down method allows for detailed gene-level analysis between linked processes to follow up. Using the cell-cycle gene-expression profiles for *Saccharomyces cerevisiae*, we report well-organized networks of biological processes that would be difficult to find otherwise. Using another dataset, we report a sharply different network structure featuring cellular responses under environmental stress.

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