

533a Generalization of Network Component Analysis

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Network Component Analysis (NCA) is the method to determine transcription factor activities (TFA) and control strengths (CS) from DNA microarray data and partial connectivity information between transcription factors and promoters. In contrast to classical approaches such as principal component analysis (PCA) or independent component analysis (ICA), NCA uses the available information about connectivity structure from transcriptional regulatory networks to restrict the decomposition to a unique solution. Although it requires the network topology as priori, i.e. whether connections between TFs and promoters exist, it does not make any further assumption, so the control strengths still remain unknown. Therefore, NCA also differs from Least Squares method, which often assumes that either TFA or CS are known, and try to determine the another. We have successfully used NCA as a framework for deducing regulatory signal such as determine interactions among various signaling pathways in *Saccharomyces cerevisiae*, define the network response to reactive nitrogen oxide species in *Escherichia coli* K-12. However, the existing version of NCA has some limitation in application and numerical implementation. Several improvements have been accomplished. 1) The NCA criteria are relaxed so that much fewer data points are required. 2) When the NCA criteria are not satisfied, a generalized method is used to obtain the data decomposition. 3) A numerical method is introduced to improve the stability of numerical solution. 4) A user friendly program has been developed that implement these modifications.