

# Identifying gene regulatory events using the coefficient of intrinsic dependence

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## Abstract

A variety of high-throughput techniques are now available for constructing comprehensive gene regulatory networks in systems biology. In this study, the coefficient of intrinsic dependence (CID) has adopted to infer gene regulatory network structure. The CID is model-free and can be applied to high dimensional datasets. We first apply CID to analyze the downstream genes co-regulated by one or multiple transcription factors based on microarray expression data. The CID is also applied to quantify the associations between two gene sets as well as to illustrate how gene sets, in signaling transduction pathways or subnetworks regulated by a set of transcription factors, can be discovered using microarray data. In conclusion, the CID provides a powerful tool for detecting general types of association, especially when the type of association is present in a form of non-linearity or variation. Hence, our approach has the potential to dissect and to construct a statistically relevant network from microarray data.