

Identifying pathogenic signaling and regulatory networks by integrating microarray data with prior knowledge

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Abstract: Recent years have seen much focus on identifying signaling and regulatory networks importantly involved in disease progression. Although there has been an extensive use of various high-throughput methods for this task, the major pathogenic pathways are still not completely understood. Quite often the set of genes or proteins identified as altered in genome-wide screens show a poor overlap with the expected disease pathways. These findings are difficult to interpret, yet, crucial in order to improve the understanding of the molecular processes underlying the disease progression. We present a novel Bayesian method where microarray gene expression data is used in concert with protein-protein interactions, transcription factor binding data and protein homology data to identify important signaling and regulatory networks. Applied to microarray heart failure and melanoma data, the method shows ability to reconstruct established disease pathways, as well as shedding new light on signaling and regulatory events involved in disease development.