

CAGE: a tool for identifying genes with correlated spatiotemporal expression

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Unraveling complex genetic networks is important for understanding the mechanisms underlying organismal biology and disease. The emergence of high-throughput genomics provides the opportunity to utilize “big-data” in biology to gain insight into the structure of these networks. However, relative to the amount of biological data available, there is a lack of bioinformatics tools that leverage these data sets to formulate testable hypotheses. This presentation describes CAGE, a web-accessible application that conducts integrative analysis of *Drosophila melanogaster* mRNA expression data to discover genes with correlated spatiotemporal expression. We would predict that genes showing this correlation may be co-regulated or share similar biological functions. CAGE therefore allows us to identify candidate genes involved in a given process, to discover regulatory interactions in genetic networks, and to verify the quality of gene clustering techniques.