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Reverse-Engineering the Evolutionary and Developmental Dynamics of the Gap Gene Network

Evolutionary developmental biology tries to close the gap between molecular evolution and phenotypic change. This requires a quantitative systems-level understanding of the gene networks underlying development across multiple levels from the molecular to the organismic. Obtaining such an understanding is challenging due to the large number of factors involved. We depend on computational models for this task. I present a reverse-engineering approach, where gene regulatory interactions are inferred from quantitative expression data, using data-driven mathematical models (called gene circuits). Gene circuit models of the gap gene network of Drosophila reproduce observed gene expression with high precision and temporal resolution and reveal a dynamic mechanism for the control of positional information through shifts of gap gene expression domains. We are extending this approach to a comparative study of the gap gene network between different species of dipterans (flies, midges and mosquitoes). I present preliminary results on data quantification and modeling for gap genes in the scuttle fly Megaselia abdita, and the moth midge Clogmia albipunctata. Our approach yields predictions of how changes of gene regulatory feedback affect the timing and positioning of expression domains. These predictions will be tested experimentally using RNA interference in all three species. No such quantitative systems-level analysis of an evolving gene regulatory network has been achieved to date.