

# **From DNA sequence to network behavior: functional properties of genetic regulatory networks**

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## **Abstract**

Systems Biology is predicated on the integration of large volumes of data from multiple experimental technologies (sequence, microarray, proteomics, chip, etc.), with data mined from the literature and data bases. Current model-building methods emphasize static

network maps of protein-protein, and protein-DNA interactions. I will give an overview of our tools and techniques for model building and model analysis, focusing on the need to go beyond static interaction maps and towards understanding the dynamic behavior of biochemical networks using examples from sea urchin embryonic development and yeast metabolism.