
Graphing cellular regulatory networks

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Abstract

Since the second half of the 20th Century, biologists increasingly represents interactions between molecular components (genes, proteins, etc.) in terms of graphs. As long as these graphs remain relatively modest in size or in complexity, they were directly use as device to integrate data, reason about the underlying process and convey information for didactical purpose or scientific exchanges. With the advent of genome-wide methods to identify gene/protein interactions (e.g. double-hybrid, mass spectrometry, ChIP-seq, etc.), graph-based representations are still used to represent interaction data, but our intuition is not sufficient to comprehend the content of the gigantic graphs produced (encompassing thousands of nodes and even more connections). This led to the development of novel standards and algorithms to extract biological relevant information from these graphs. In parallel, different mathematical methods applied to these graph currently enable formal, dynamical analyses of cell behavior, for normal or perturbed conditions. These graph-based representation lie at the core of the trendy fields called "systems biology". Focusing on examples related to cell differentiation and embryonic development, I will attempt to decipher different aspects of these representations to emphasize the interplays between visual, cognitive and computational dimensions.

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