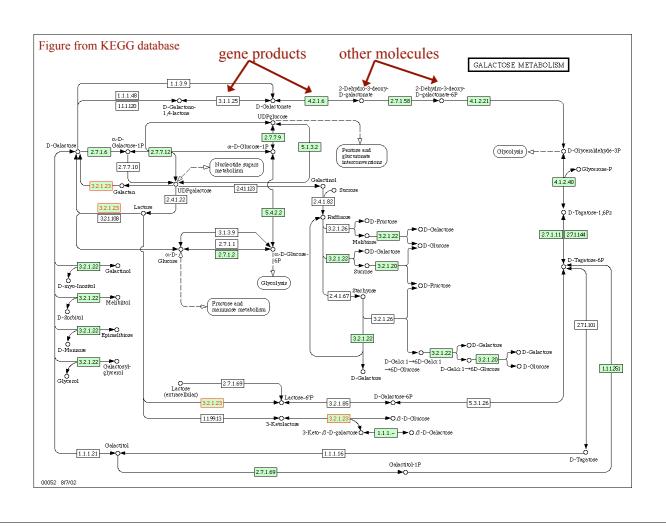
Representation, Learning and Inference in Models of Cellular Networks

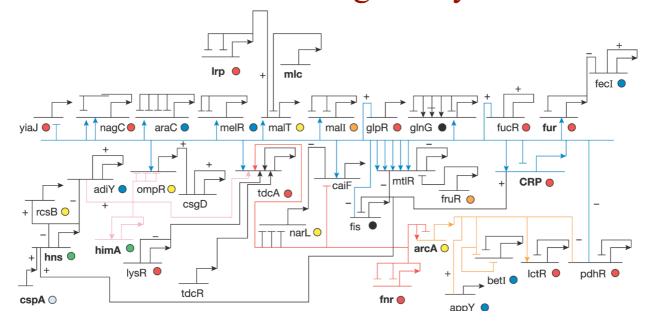
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Spring 2009

Various Subnetworks within Cells

- *metabolic*: describe reactions through which enzymes convert substrates to products
- regulatory (genetic): describe interactions that control expression of particular genes
- *signaling*: describe interactions among proteins and (sometimes) small molecules that relay signals from outside the cell to the nucleus
- note: these networks are linked together and the boundaries among them are not crisp



Part of the E. coli Regulatory Network



A Signaling Network

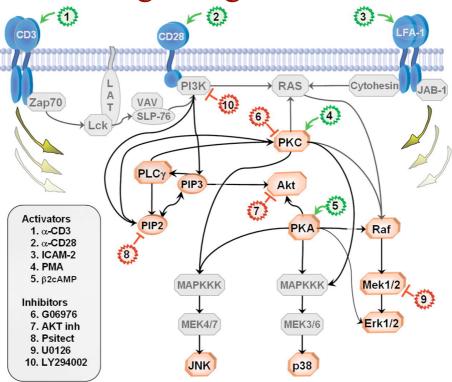


Figure from Sachs et al., Science 2005

Two Key Tasks

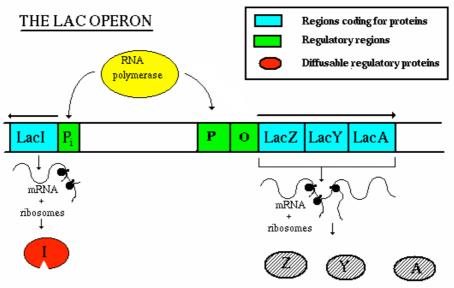
- *learning*: given background knowledge and high-throughput data, try to infer the (partial) structure/parameters of a network
- *inference*: given a (partial) network model, use it to predict an outcome of biological interest (e.g. will the cells grow faster in medium x or medium y?)
- both of these are challenging tasks because typically
 - data are noisy
 - data are incomplete characterize a limited range of conditions
 - important aspects of the system not measured some unknown structure and/or parameters

Representations for Network Models

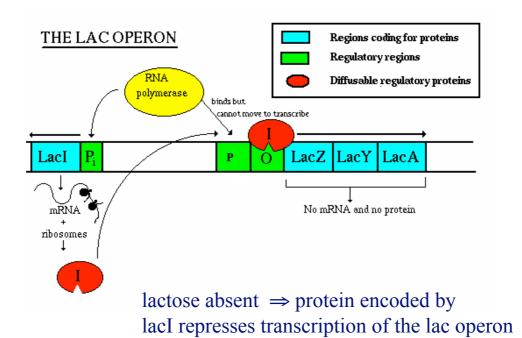
- directed graphs
- Boolean networks
- Bayesian networks
- differential equations
- systems of constraints + linear programs
- logic programs
- etc.

Transcriptional Regulation Example: the lac Operon in *E. coli*

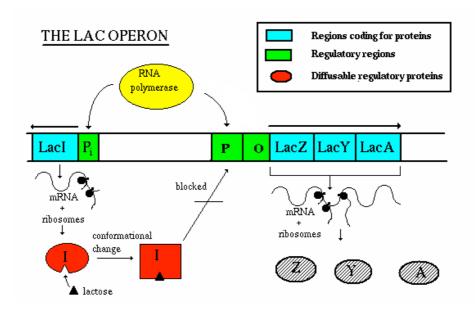
E. coli can use lactose as an energy source, but it prefers glucose. How does it switch on its lactose-metabolizing genes?



The lac Operon: Repression by LacI

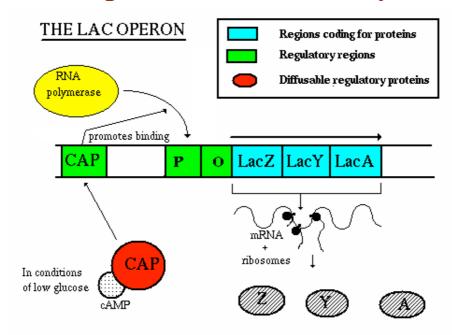


The lac Operon: Induction by LacI



lactose present ⇒ protein encoded by lacI won't bind to the operator (O) region

The lac Operon: Activation by Glucose



glucose absent ⇒ CAP protein promotes binding by RNA polymerase; increases transcription