

# Physical Network Models

BMI/CS 776

[www.biostat.wisc.edu/bmi776/](http://www.biostat.wisc.edu/bmi776/)

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Spring 2011

## Goals for Lecture

the key concepts to understand are the following

- physical network models
- the inference task for physical network models

# Physical Network Models

- the Bayes/module network learning task
  - given:** many measurements for each gene
  - infer:** dependencies among genes
- the physical network learning task
  - given:**
    - “known” interactions among genes
    - measurements resulting from knocking out/down selected genes
  - infer:** the subset of interactions (and perhaps their directions and signs) that account for the measured responses

## Physical Networks

- model of yeast response to osmotic and calcium stress

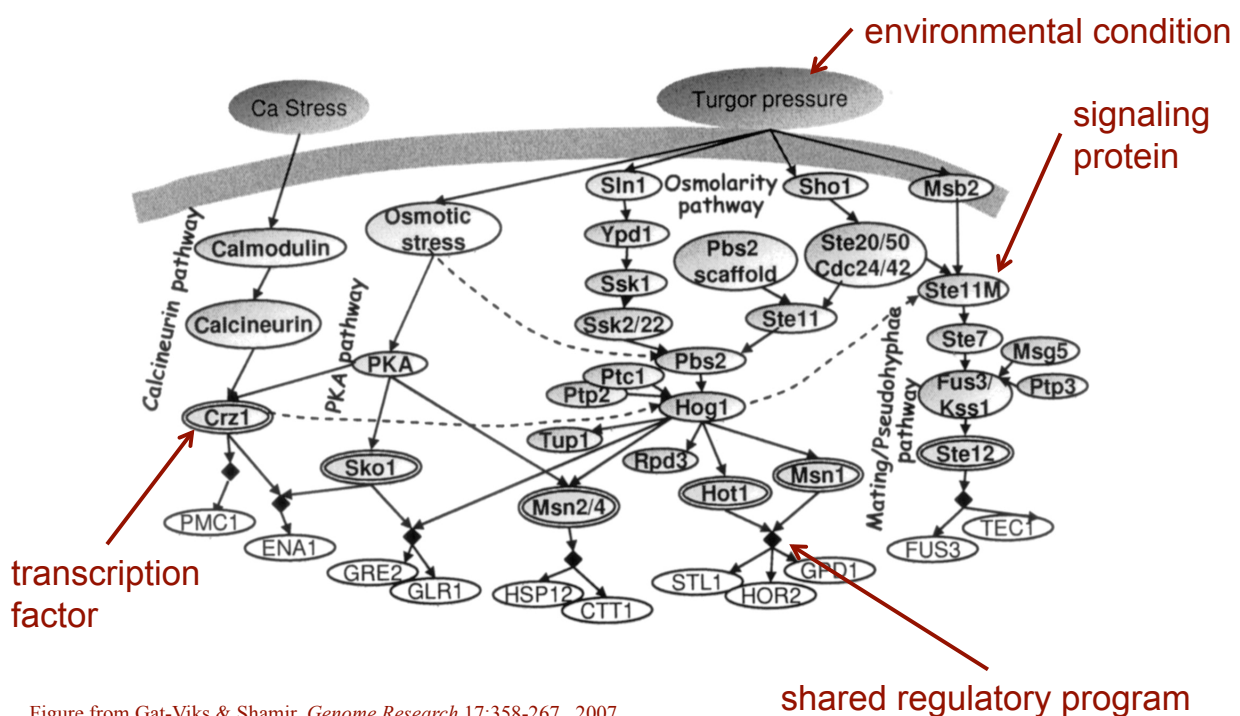
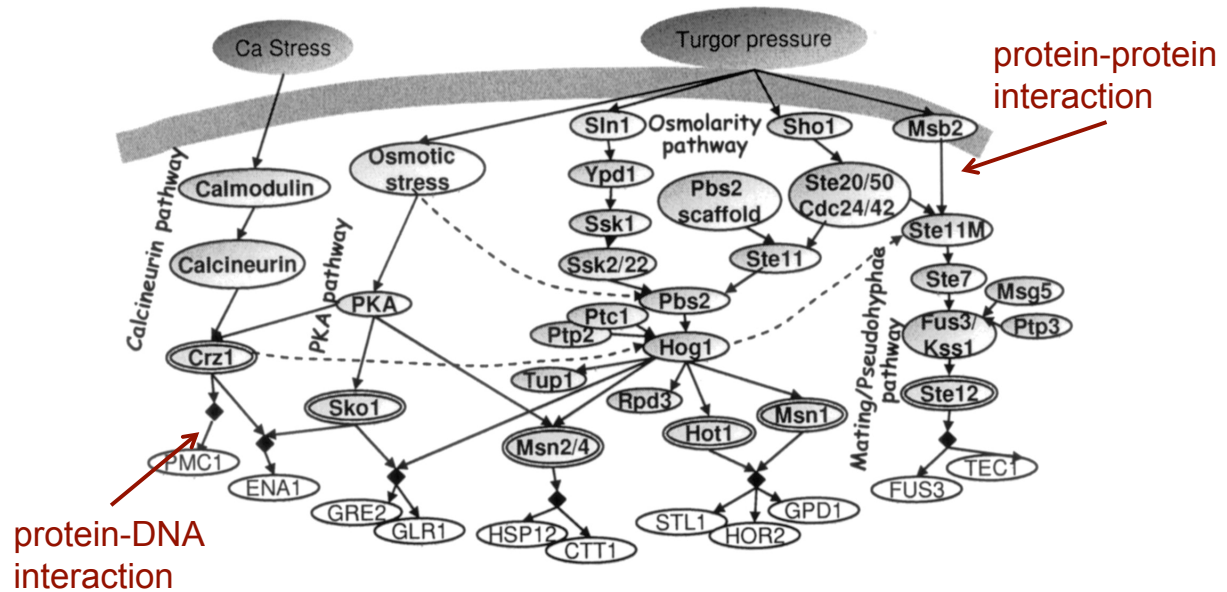


Figure from Gat-Viks & Shamir, *Genome Research* 17:358-267, 2007.

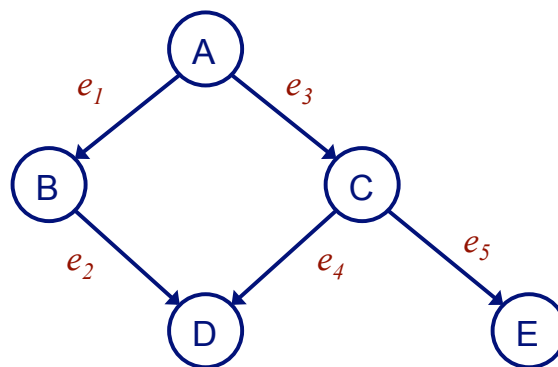
# Physical Networks

- edges represent physical interactions



## Physical Network Models

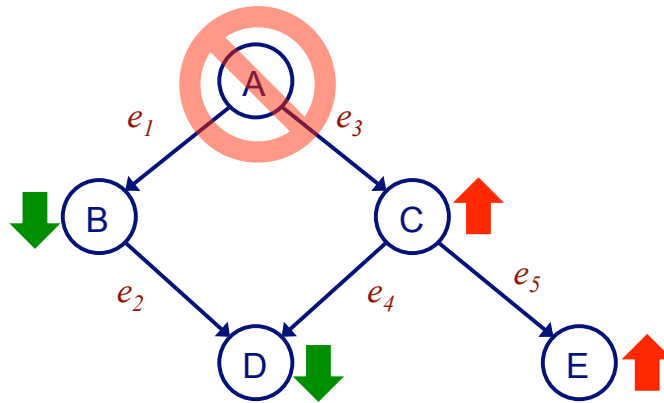
- edges in physical network models correspond to
  - protein-protein interactions
  - protein-DNA interactions



# Single Gene

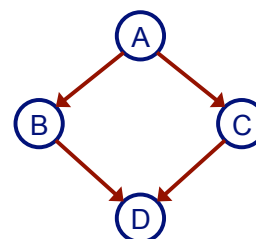
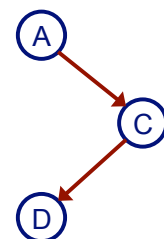
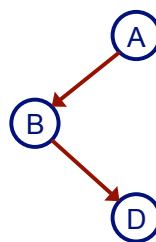
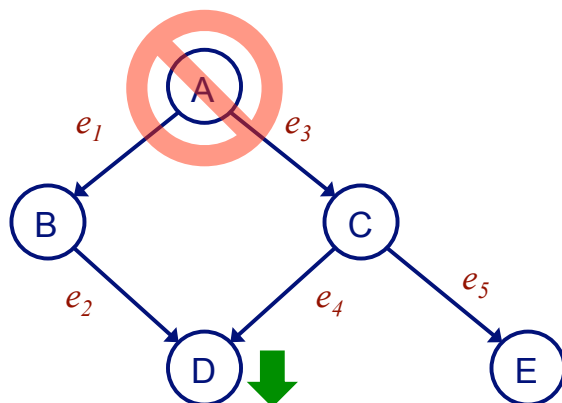
## Knockout/Knockdown Experiments

- consider an experiment in which we
  - manipulate a gene by knocking it out (disabling it) or knocking it down (lowering its expression)
  - then measure the effect of this manipulation on the expression levels of other genes



## Physical Network Model Example

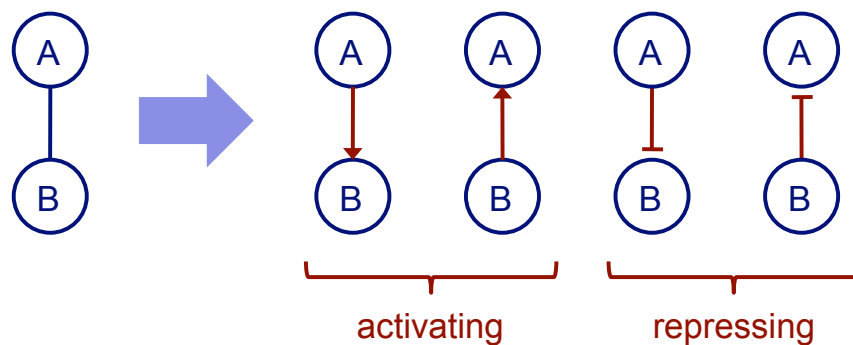
- suppose we knock out gene A and observe that the expression of gene D goes down
- there are three possible explanations for this causal relationship



# Physical Network Models

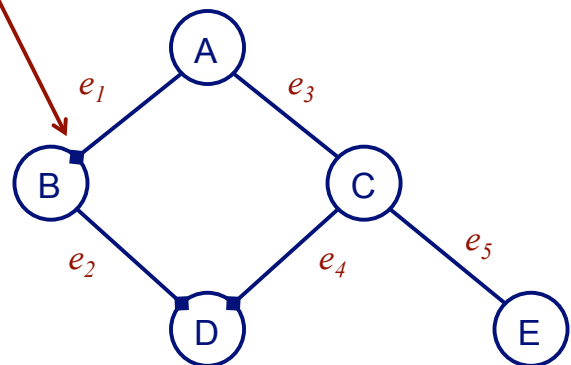
- thus for each edge we are uncertain about its *presence* (is the interaction involved in the condition being analyzed)
- for some edges we also have uncertainty about
  - *direction*
  - *sign* (is the interaction activating or repressing)

e.g. 4 ways this interaction could be interpreted in explanations



# Physical Network Models

to indicate edges for which we know the direction, but not the sign, we'll use arrowheads like this



# Physical Network Models

separate binary variables represent edge

- presence

$$X_{\bar{E}_G} = \{x_{e_1}, x_{e_2}, x_{e_4}\}$$

$$X_{\bar{E}_G} = \{x_{e_3}, x_{e_5}\}$$

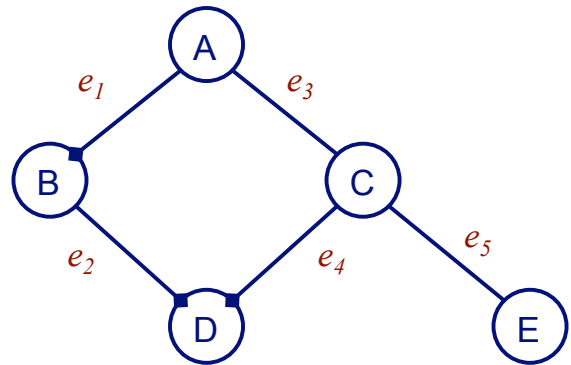
- direction

$$D_{\bar{E}_G} = \{d_{e_3}, d_{e_5}\}$$

- sign

$$S_{\bar{E}_G} = \{s_{e_1}, s_{e_2}, s_{e_4}\}$$

$$S_{\bar{E}_G} = \{s_{e_3}, s_{e_5}\}$$



## Inference in Physical Network Models

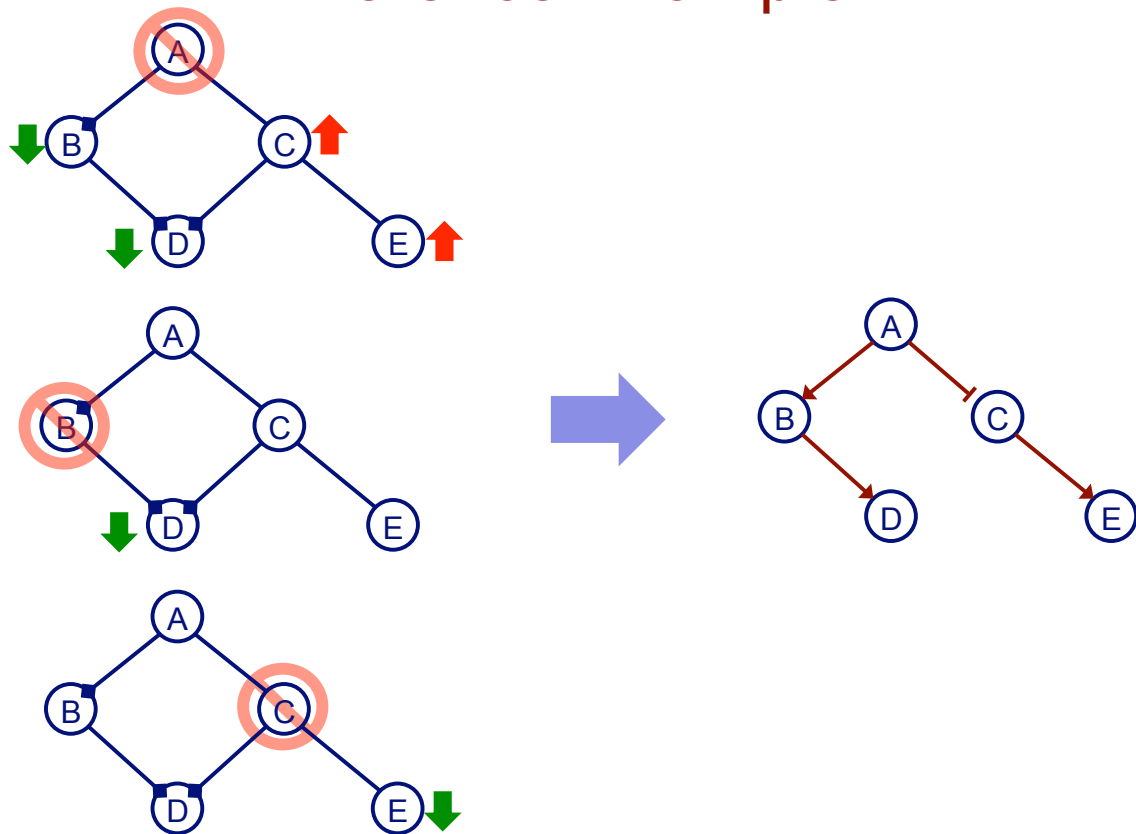
**given**

- a set of knockout experiments in some condition of interest

**infer**

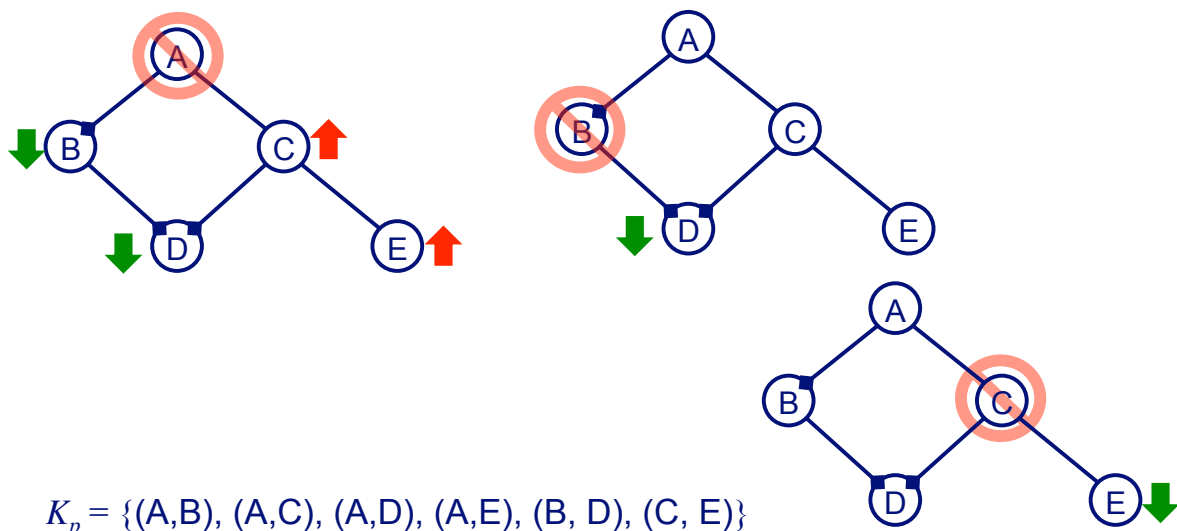
- an assignment of values to the variables such that they provide a coherent explanation for the experiments

## Inference Example



## Physical Network Models

- let  $K_p$  be the set of *significant* knockout effects
- for the following experiment effects, we have...



$$K_p = \{(A,B), (A,C), (A,D), (A,E), (B,D), (C,E)\}$$

# Physical Network Models

additional variables

- set of *actual* knockout effects

$$K = \{k_{ij} : (i, j) \in K_p\}$$

$$k_{ij} = \begin{cases} +1 & \text{if knocking out } i \text{ causes } j \text{ to go up} \\ 0 & \text{if knocking out } i \text{ has no effect on } j \\ -1 & \text{if knocking out } i \text{ causes } j \text{ to go down} \end{cases}$$

- measurements of gene expression in knockouts  
(think of  $o_{ij}$  as a noisy measurement of  $k_{ij}$ )

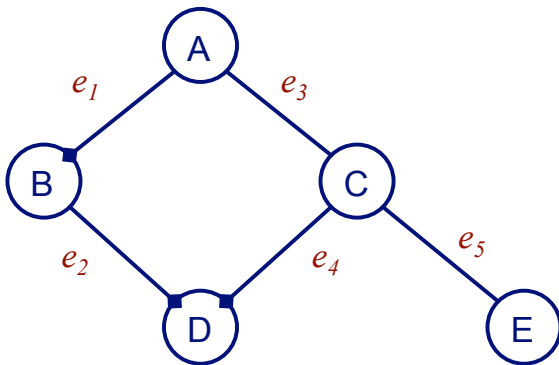
$$O = \{o_{ij} : (i, j) \in K_p\}$$

# Physical Network Models

additional variables

- path selection variables

$$\Sigma = \{\sigma_{ija} : (i, j) \in K_p \text{ sth } a \text{ is a valid path btwn } i \text{ and } j\}$$



$$\sigma_{AD1} = \text{A} \xrightarrow{e_1} \text{B} \xrightarrow{e_2} \text{D}$$

$$\sigma_{AD2} = \text{A} \xrightarrow{e_3} \text{C} \xrightarrow{e_4} \text{D}$$



# Inference in Physical Network Models

- inference task: determine assignment of values to the  $X, S, D$  variables to maximize

$$P(X_{\bar{E}_G}, S_{\bar{E}_G}, X_{\bar{E}_G}, S_{\bar{E}_G}, D_{\bar{E}_G}, K, \Sigma \mid Y_{\bar{E}_G}, Y_{\bar{E}_G}, O_K)$$

- Yeang et al. use an *undirected graphical model* approach to do this inference

# Inference in Physical Network Models

$$P(X_{\bar{E}_G}, S_{\bar{E}_G}, X_{\bar{E}_G}, S_{\bar{E}_G}, D_{\bar{E}_G}, K, \Sigma \mid Y_{\bar{E}_G}, Y_{\bar{E}_G}, O_K) \propto$$

$$\prod_{\bar{e}_i \in \bar{E}_G} \phi_{\bar{e}_i}(x_{\bar{e}_i}; y_{\bar{e}_i}) \times$$

$$\prod_{\bar{e}_i \in \bar{E}_G} \phi_{\bar{e}_i}(x_{\bar{e}_i}; y_{\bar{e}_i}) \times$$

$$\prod_{(i,j) \in K_p} \phi_{ij}(k_{ij}; o_{ij}) \psi_{ij}(X_{ij}, D_{ij}, S_{ij}, \Sigma_{ij}, k_{ij})$$

# The Model Potentials

- three of the potentials relate values of variables to their corresponding measurements

$$\phi_{\bar{e}_i}(x_{\bar{e}_i}; y_{\bar{e}_i}) \quad \phi_{\bar{e}_i}(x_{\bar{e}_i}; y_{\bar{e}_i}) \quad \phi_{ij}(k_{ij}; o_{ij})$$

- these potential functions have the general form

$$\phi_{\bar{e}_i}(x_{\bar{e}_i}; y_{\bar{e}_i}) = \left[ \frac{P(y_{\bar{e}_i} \mid x_{\bar{e}_i} = 1)}{P(y_{\bar{e}_i} \mid x_{\bar{e}_i} = 0)} \right]^{x_{\bar{e}_i}}$$

# The Model Potentials

- consider the potential for a single path, whose set of edges is denoted by  $E_a$

$$\psi_{ija}(X_a, D_a, S_a, k_{ij}) =$$

$$\prod_{e \in E_a} I(x_e = 1) \times$$

are all edges present?

$$I\left(\prod_{e \in E_a} s_e = -k_{ij}\right) \times$$

are the signs of the edges consistent with the KO effect?

$$\prod_{e \in \bar{E}_a} I(d_e = \hat{d}_e)$$

are undirected edges going in the right direction?

- $I(\bullet)$  is an indicator function returning 1 if the given condition is satisfied, 0 otherwise

# The Model Potentials

- now take into account the path selection variable

$$\psi_{ija}(X_a, D_a, S_a, k_{ij}, \sigma_{ija}) = \varepsilon + (1 - \varepsilon) I(\sigma_{ija} = 1) \psi_{ija}(X_a, D_a, S_a, k_{ij})$$

- because our knowledge of interactions is incomplete, have the potential be nonzero even when the path is not selected

# The Model Potentials

- now specify the (soft) condition that at least on candidate path is selected to explain  $k_{ij}$

$$\psi_{ij}(X_{ij}, D_{ij}, S_{ij}, \Sigma_{ija}, k_{ij}) = \left[ \varepsilon + (1 - \varepsilon) \left( 1 - \prod_a I(\sigma_{ija} = 0) \right) \right] \times \prod_a \psi_{ija}(X_a, D_a, S_a, \sigma_{ija}, k_{ij})$$

# The Model Potentials Summarized

- experimental noise in measurements is taken into account
- each knockout effect is explained by at least one path
- to explain an effect, the edges of a path must
  - be “present”
  - be going in the the right direction
  - have their signs be consistent with the effect
- also the path must
  - be shorter than some predefined upper bound
  - end in a protein-DNA interaction

## Empirical Evaluation

- mating response pathway experiment
  - 149 knockout effect pairs from 13 experiments
  - 106 pairs in 9 experiments are connected by paths  $\leq 5$
- run inference procedure on all data
  - all effects are explained by solution found
  - only 21 effects are trivially explained by direct protein-DNA binding
- leave out some effects in a cross-validation experiment; see what error rate is in predicting effects

TABLE 2. CROSS VALIDATION ON  
KNOCK-OUT PAIRS

<i># hold-outs</i>	<i># trials</i>	<i>% error</i>
1	106	2.83%
5	200	3.5%
20	200	5.9%

# Discussion

- approach looks for consistent explanations for cases in which we have
  - “known” interactions among genes
  - measurements resulting from knocking out/down selected genes
- predictive accuracy is high for a small, densely connected network
- incomplete knowledge of interactions may make approach less viable in larger networks
  - only 1,091 out of 23,766 pairs are connected by valid paths in a genome-wide data set