

True topology

Topology tested

A → B

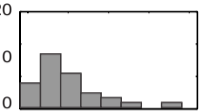
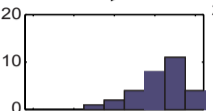
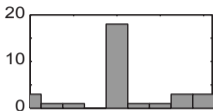
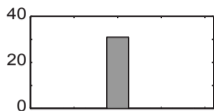
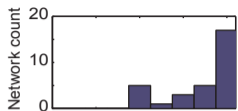
A ⊣ B

A B

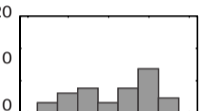
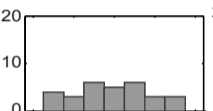
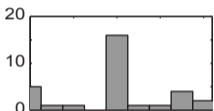
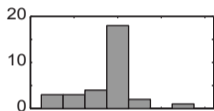
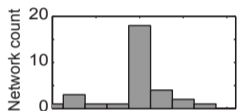
A ⊣ B

A ⊣ X ⊣ B

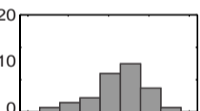
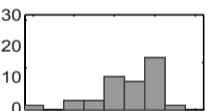
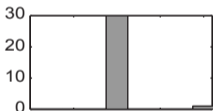
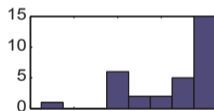
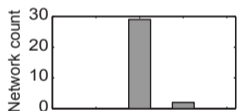
A → B



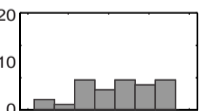
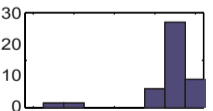
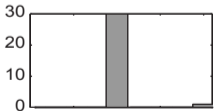
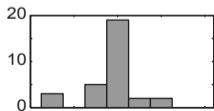
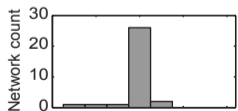
B → A



A ⊣ B



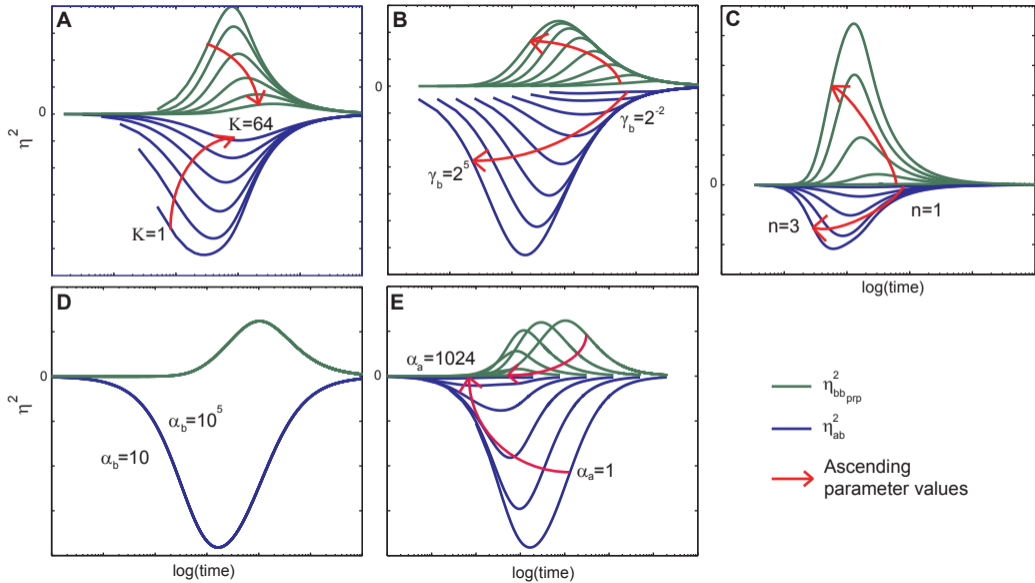
B ⊣ A



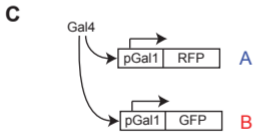
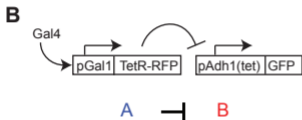
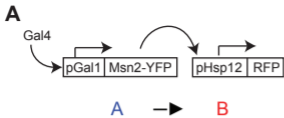
Correlation score

■ correct topology ■ incorrect topology

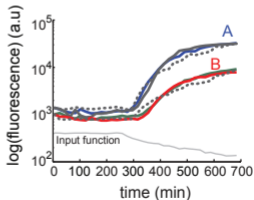
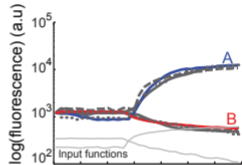
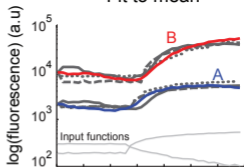
Dynamic noise propagation



Network



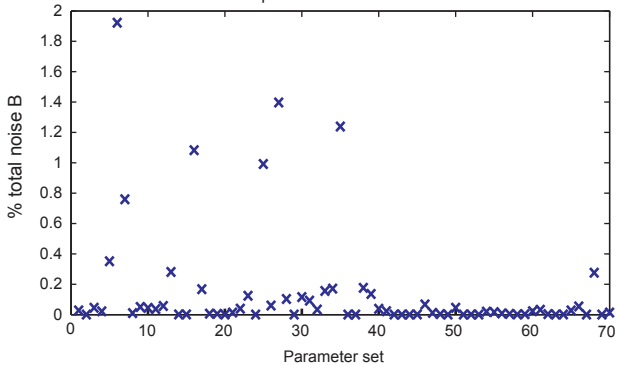
Fit to mean



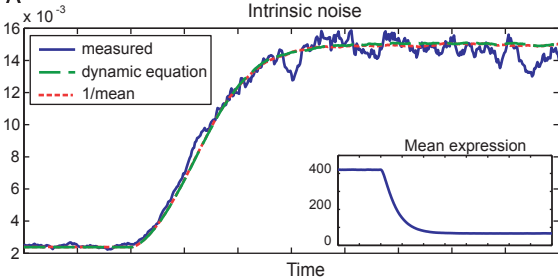
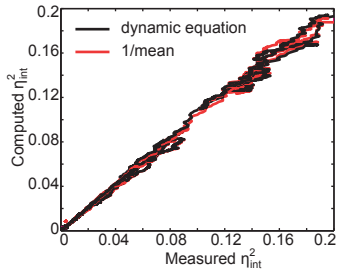
Fitted model:

- Regulation by gene A or B
- - - A and B co-regulated: activation
- · · · A and B co-regulated: inhibition

Percent improvement with second moment



$\times \frac{(\text{difference of predictions})}{\eta_{bb}^2}$

A**B**

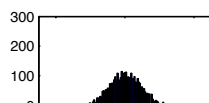
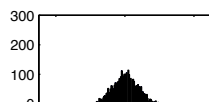
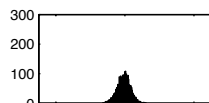
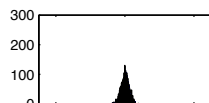
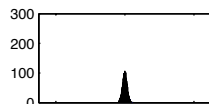
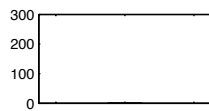
Network

 $A \rightarrow B$

Network

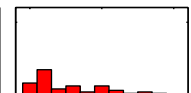
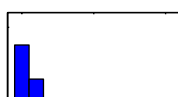
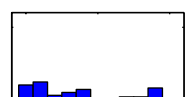
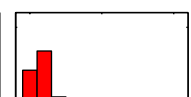
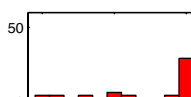
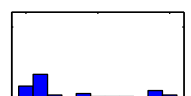
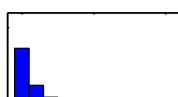
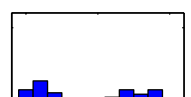
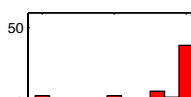
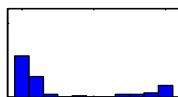
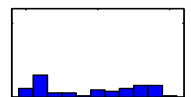
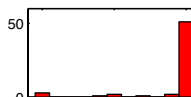
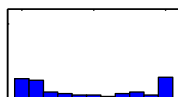
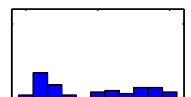
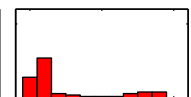
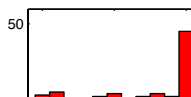
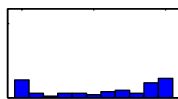
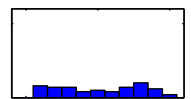
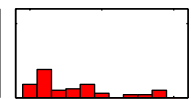
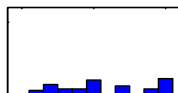
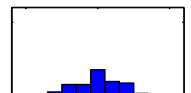


Global noise



-200 0 200

Topology tested

 $A \rightarrow B$ $B \rightarrow A$  $A \rightarrow B$ $B \rightarrow A$ 

Correlation

Network

$A \rightarrow B$

Network



Sampling rate

Topology tested

$A \rightarrow B$

$B \rightarrow A$

Topology tested

$A \rightarrow B$

$B \rightarrow A$

