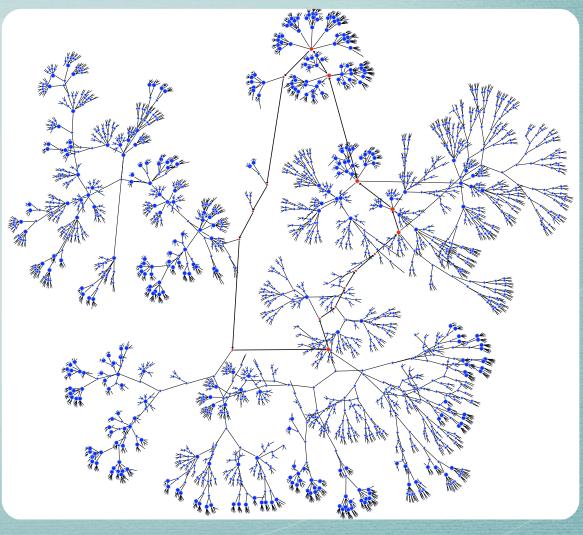
DISCRETE NETWORK DYNAMICS ANALYSIS USING NETWORK WORKBENCH

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Network Workbench http://nwb.slis.indiana.edu/



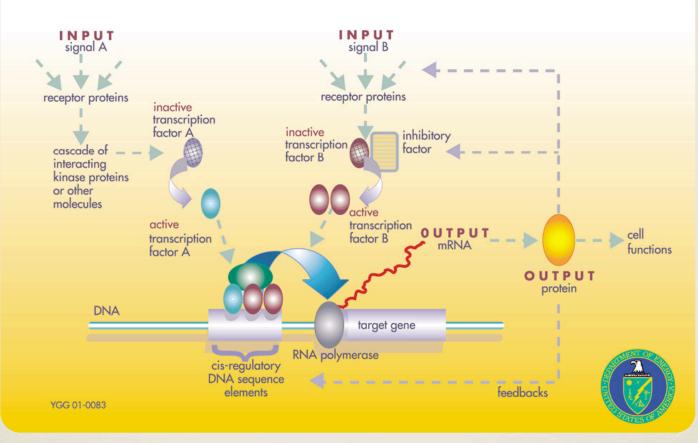
The lack of widely available tools for discrete network analysis limits the usefulness of a powerful analytical technique.

- * What is a discrete network model?
 - * How might it be applied to Bioinformatics?
- * Building a tool for analyzing discrete networks
 - * How does one analyze and construct a discrete network model for biological data?
 - * Sample application as applied to the segmentation clock

A Boolean network model is an abstract way of viewing interactions.

- * Many events can be seen as occurring or not occurring. Whether or not those events occur or do not occur influence other events.
 - * I present at the McGill Summer Sessions
 - * People listened to my presentation
 - * People were bored
 - * People found my presentation helpful or relevant
- * This same abstraction can be applied to interactions between genes, mRNAs, and proteins.

Interaction between cellular entities is complex, but we want to understand the dynamics.



A GENE REGULATORY NETWORK

Image from <u>http://genomics.energy.gov/gallery/systems_biology/detail.np/HGPI_HiRes/</u> <u>REGNET.jpg</u>

Boolean network models are powerful analysis tools.

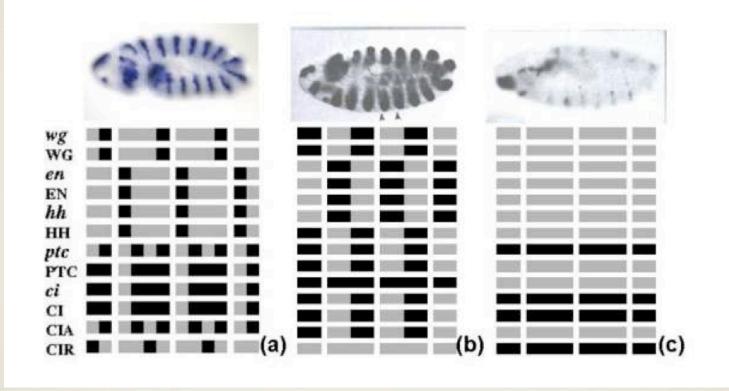


Image from M. Chaves, R. Albert, and E.D. Sontag. *Robustness and fragility of Boolean models for genetic regulatory networks*. Journal of Theoretical Biology, 2005. Vol 235.

Analyzing large networks is computationally intractable and there are few tools for analyzing smaller networks.

Analyzing the displayed network of 401 proteins on a 3.0 GHz computer would take 5.458×10^{103} years, approximately 10^{94} times longer than the age of the Earth and 4×10^{93} times longer than the age of the universe.

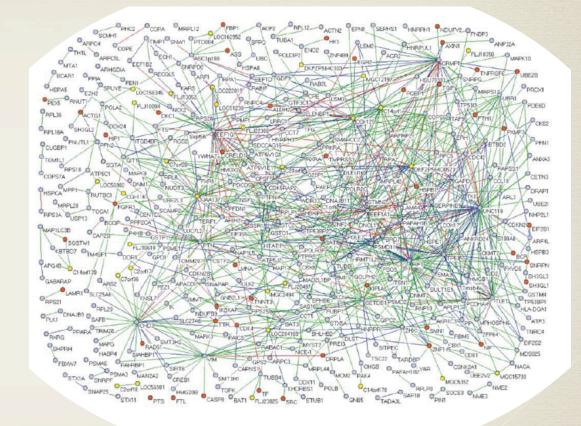
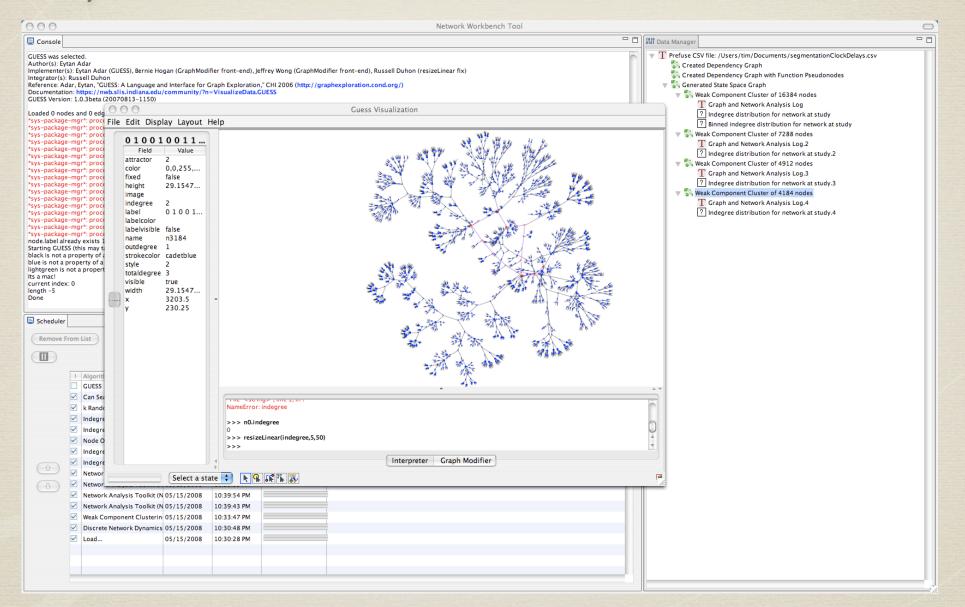


Image from A human protein-protein. interaction network: a resource for annotating the proteome. Cell, 2005. Vol 122:6.

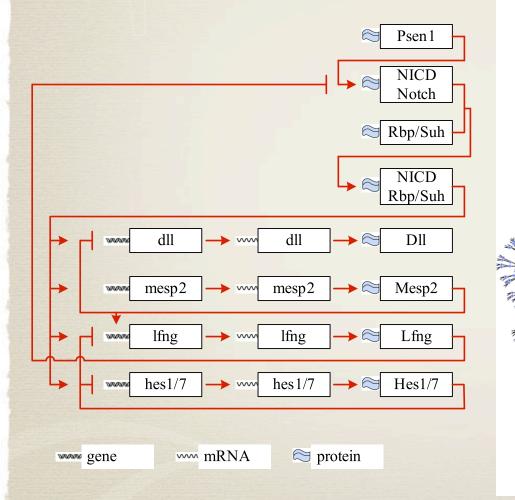
Network Workbench is a widely available tool for network analysis built on the OSGi framework.

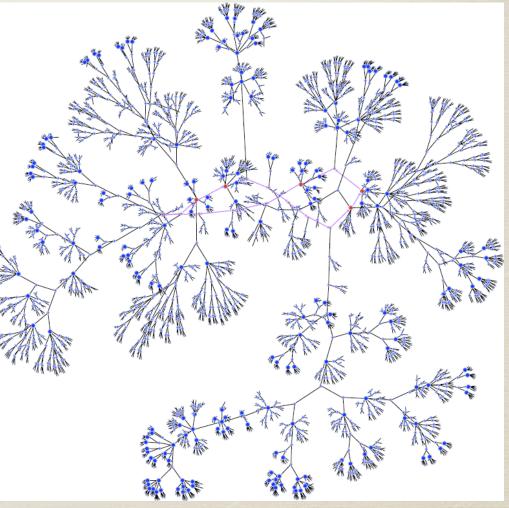


The Discrete Network Dynamics plugin allows for a large range of model analysis techniques while minimizing the computational time costs.

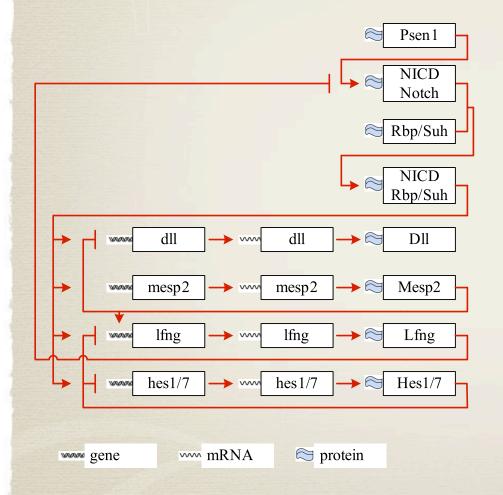
000 N	etwork Description		💿 🔘 📄 segmentationClockDelay
	Blah		<pre>"orignialModel","Names","clockFunctions" "f1=x11+~x13","g_dll","f1=x11*~x13"</pre>
Function Label	clockFunctions	÷ 0	"f2=x11","g_mesp2","f2=x11" "f3=x11+x13+~x15","g_lfng","f3=x11+x13*~
Number of States per Node	2	Q	"f4=x11+~x15","g_hes1/7","f4=x11*~x15" "f5=x1","m_dll","f5=x1"
Input Function Format	Polynomial	÷ 0	"f6=x2","m_mesp2","f6=x2" "f7=x3","m_lfng","f7=x3"
State Space Specification	All trajectories	÷ 0	"f8=x4","m_hes1/7","f8=x4" "f9=x9","P_senl","f9=x9"
Updating Scheme	Synchronous	÷ 0	"f10=x9+~x14","p_Notch/NICD","f10=x9*~x14" "f11=x10","p_NICD/Rbp/Suh","f11=x10"
Node Label	Names	÷ 0	"f12=x5","p_dll","f12=x5" "f13=x6","p_mesp2","f13=x6" "f14_x7" "p_fpp" "f14_x7"
Enter update schedule sepa	rated by space	Q	"f14=x7","p_lfng","f14=x7" "f15=x8","p_hes1/7","f15=x8"
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Analyzing the state space of the segmentation clock using the Discrete Network Dynamics plugin reveals that the network topology drives oscillations.

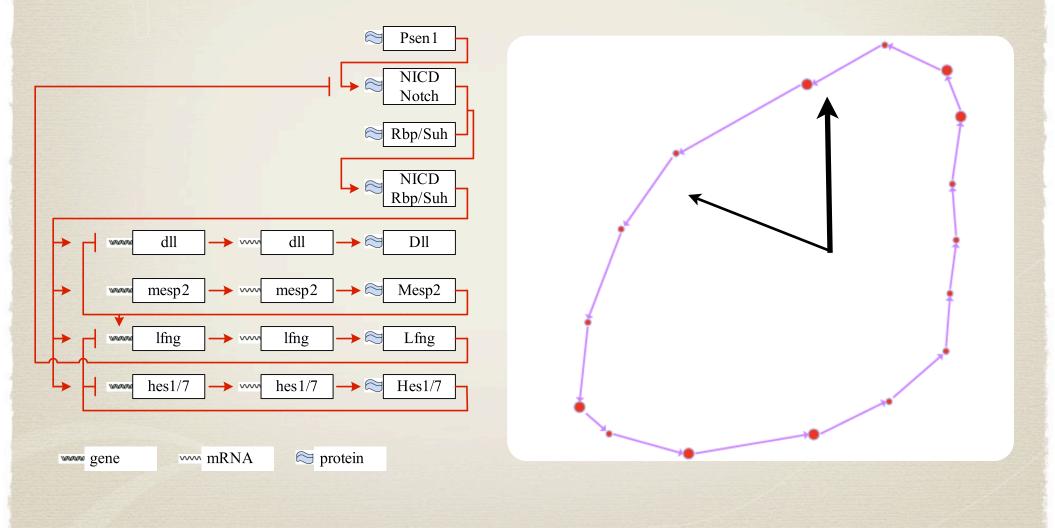




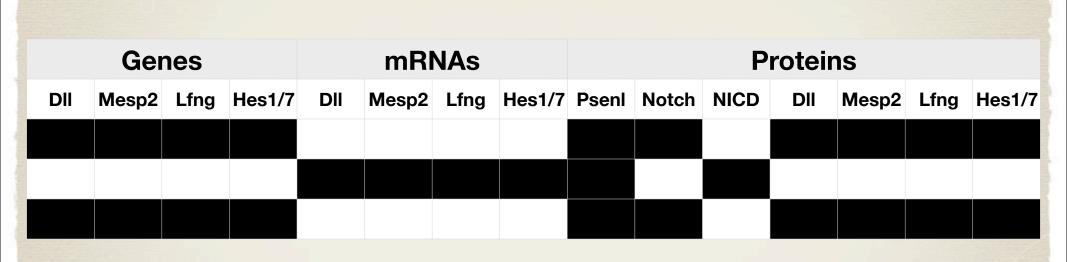
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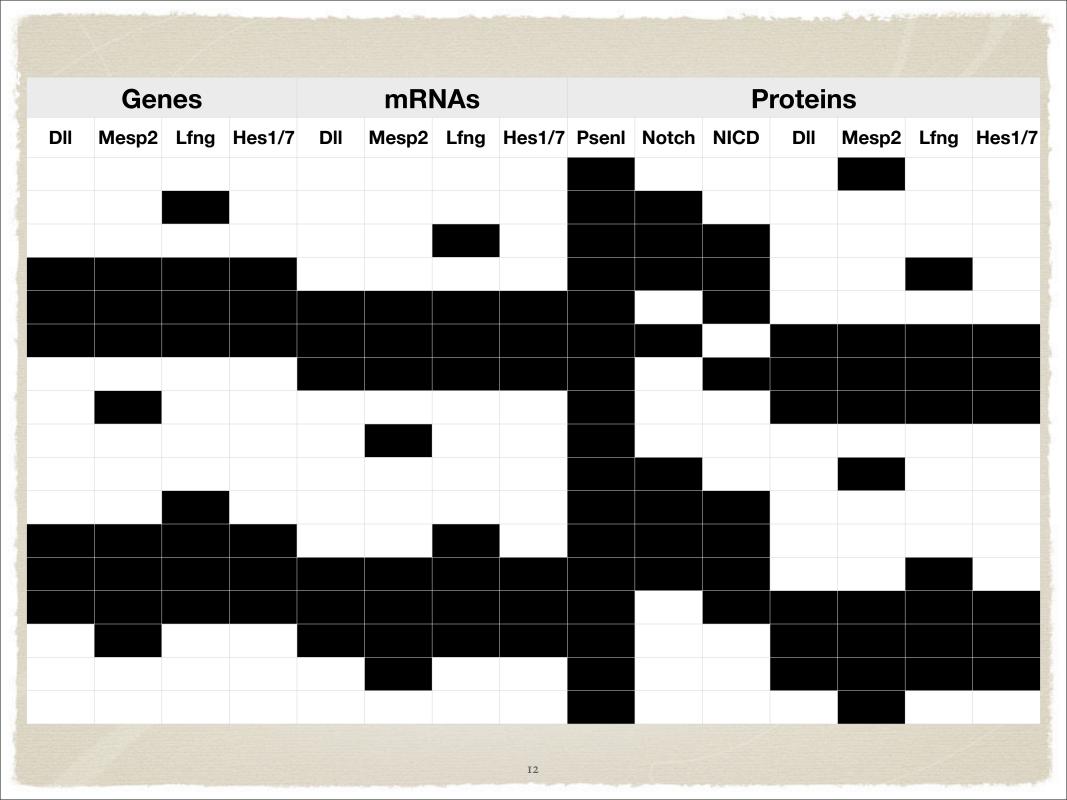
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	Ger	nes		mRNAs				Proteins						
DII	Mesp2	Lfng	Hes1/7	DII	Mesp2	Lfng	Hes1/7	Psenl	Notch	NICD	DII	Mesp2	Lfng	Hes1/7
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DII	Mesp2	Lfng	Hes1/7	Psenl	Notch	NICD	DII	Mesp2	Lfng	Hes1/7	
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	Gei	nes		Proteins							
DII	Mesp2	Lfng	Hes1/7	Psenl	Notch	NICD	DII	Mesp2	Lfng	Hes1/7	
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					14						

	Ger	nes		Proteins							
DII	Mesp2	Lfng	Hes1/7	Psenl	Notch	NICD	DII	Mesp2	Lfng	Hes1/7	
					15						