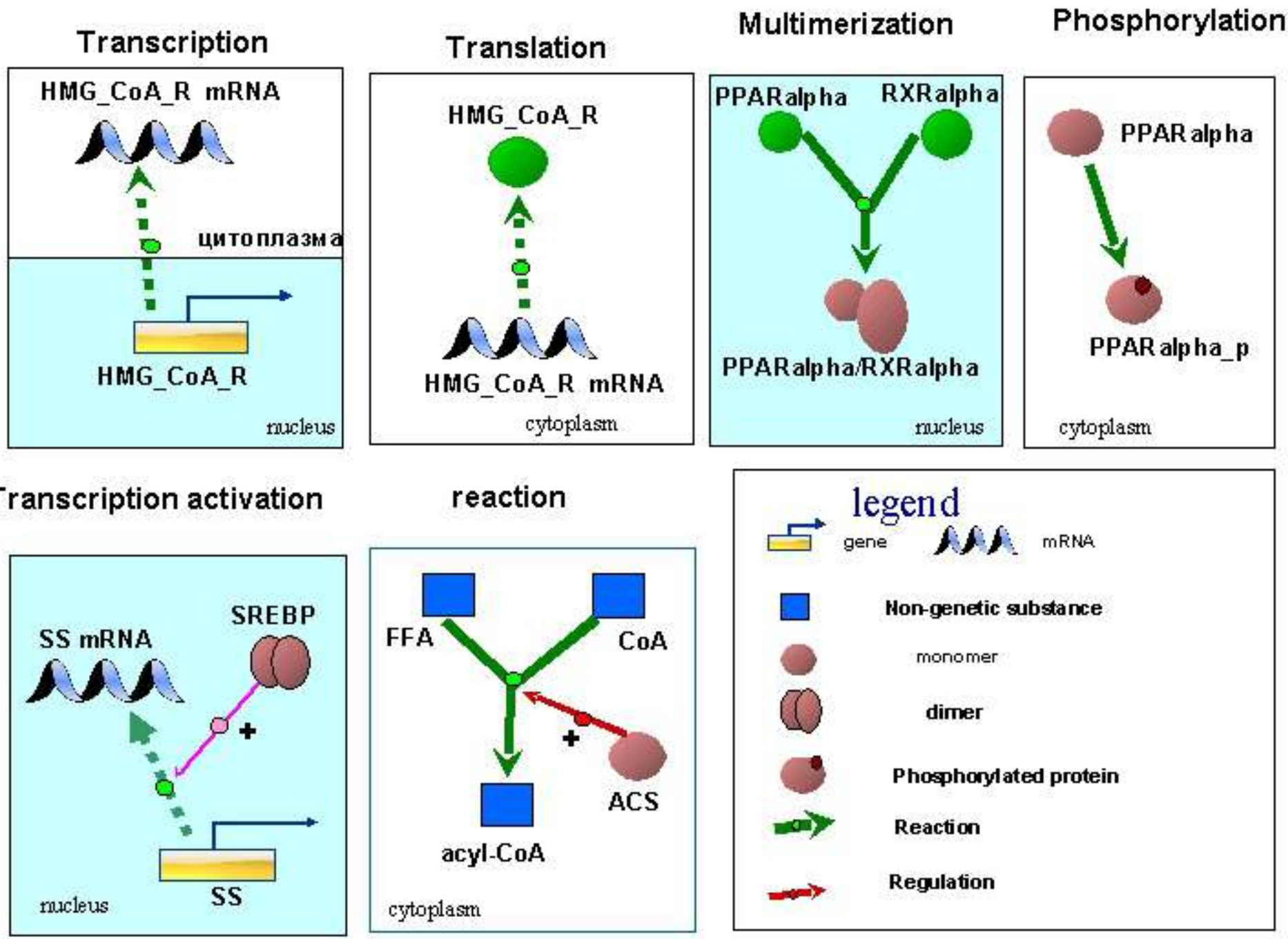
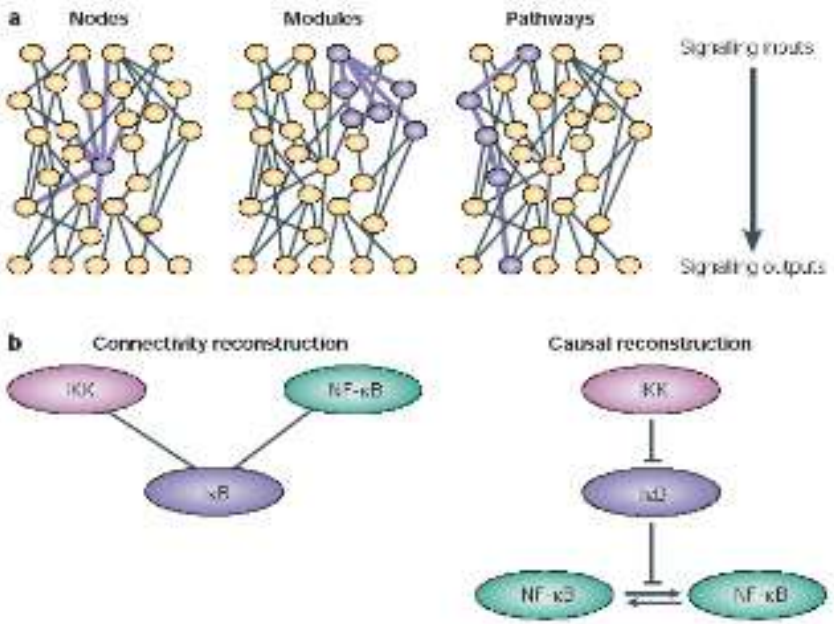
The elementary processes in GENENET database



Reconstructing a gene network



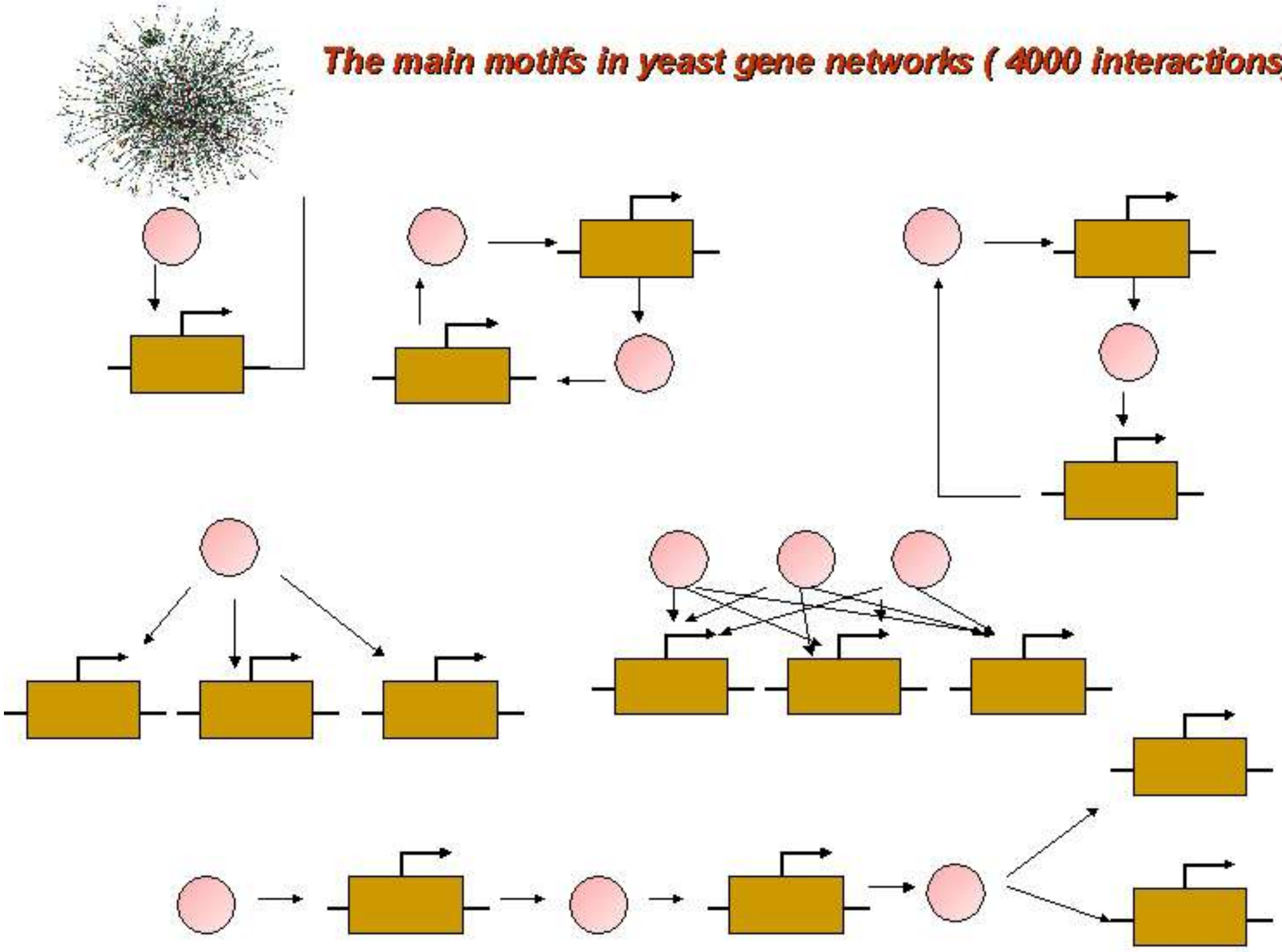
Compounds	Reactions			
	R_1	R_2	R_3	R_4
IKK	−1	+1	0	0
IKK complex	+1	−1	0	0
IκBpp–NF-κB	0	+1	−1	0
IκBpp (degraded)	0	0	+1	0
NF-κB (cytoplasm)	0	0	+1	−1
IκB–NF-κB	−1	0	0	0
ATP	−2	0	0	0
ADP	0	+2	0	0
NF-κB (nucleus)	0	0	0	+1

The most signalling network reconstructions focus on particular nodes, modules or pathways in given network. Network "nodes" describe the many interactions that a given compound (for example transcription factor NF-kB) participates in. Network "modules" consist of a group of related reaction that often incorporate feedback mechanisms.Network "pathways"connect a signalling input to signalling output.

There are there levels of resolution in reconstruction of NF-kB activation.

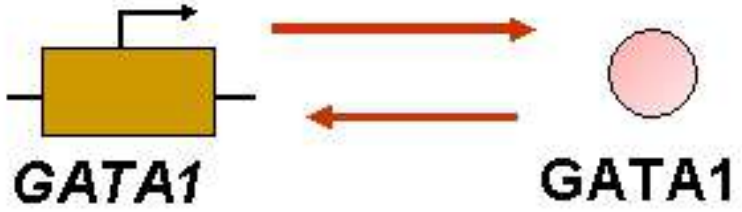
Papin J.A. et al., Nature review, 2005

The main motifs in yeast gene networks (4000 interactions)

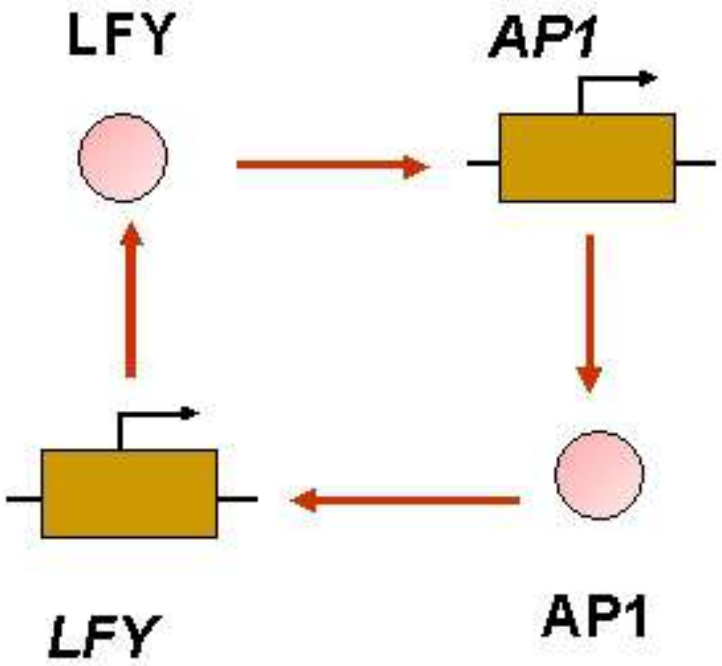


Lee T.I. et al., 2002

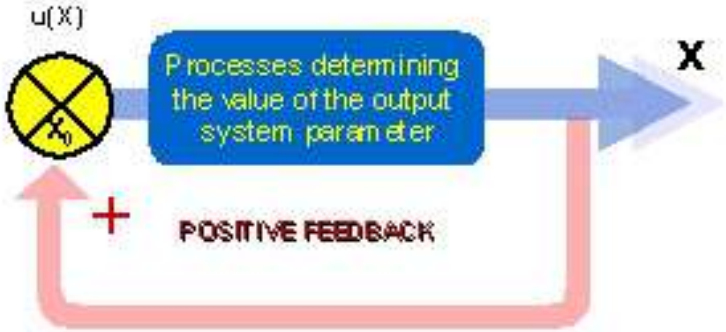
Positive feedbacks



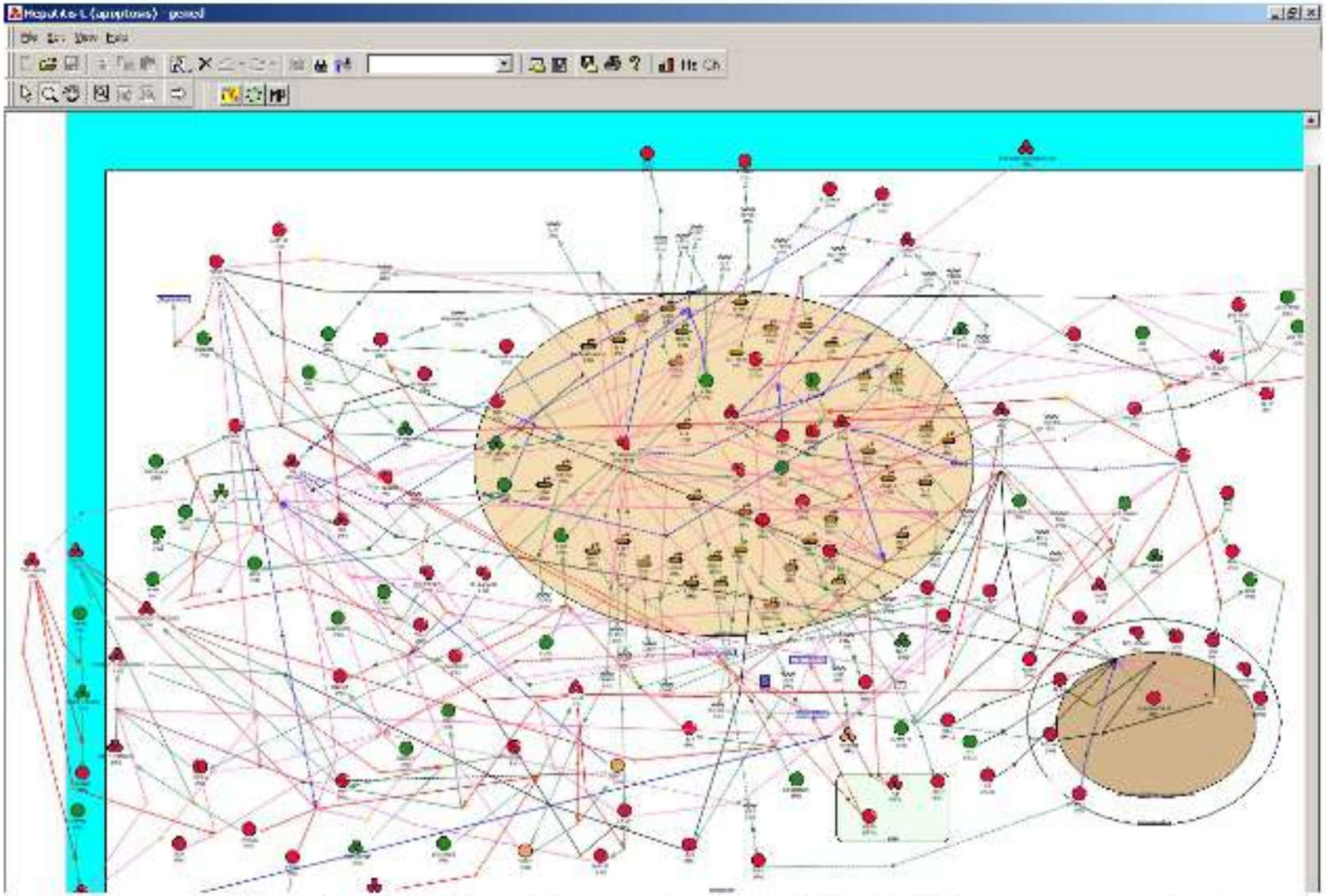
Transcription factor activates its own gene



Cross effect of transcription factors with positive feedback



Apoptosis gene network in hepatitis C



Apoptosis plays a significant role in the pathogenesis of hepatitis C. This process may be viewed as a host defense mechanism against viral infection and hepatocarcinogenesis. Hepatitis C virus (HCV)-regulated gene network in apoptosis was reconstructed on the basis
of the data extracted from 273 experimental papers. The 157 negative and positive autoregulatory circuits are clustered due to the coalescing nodes NF-κB/IκB, c-FLIP, TRAF2, and caspase 3.