



# Cytoscape Intro

## A) Open a network file:

1. File → Import → Network → from File... (select the TF-TF network file that you have downloaded)
2. Select “Advanced Options”, define comment character, and preview.
3. Select the source and target node, the interaction type and the edge attribute

## B) Inspect the network and experiment with some of the different visualisations.

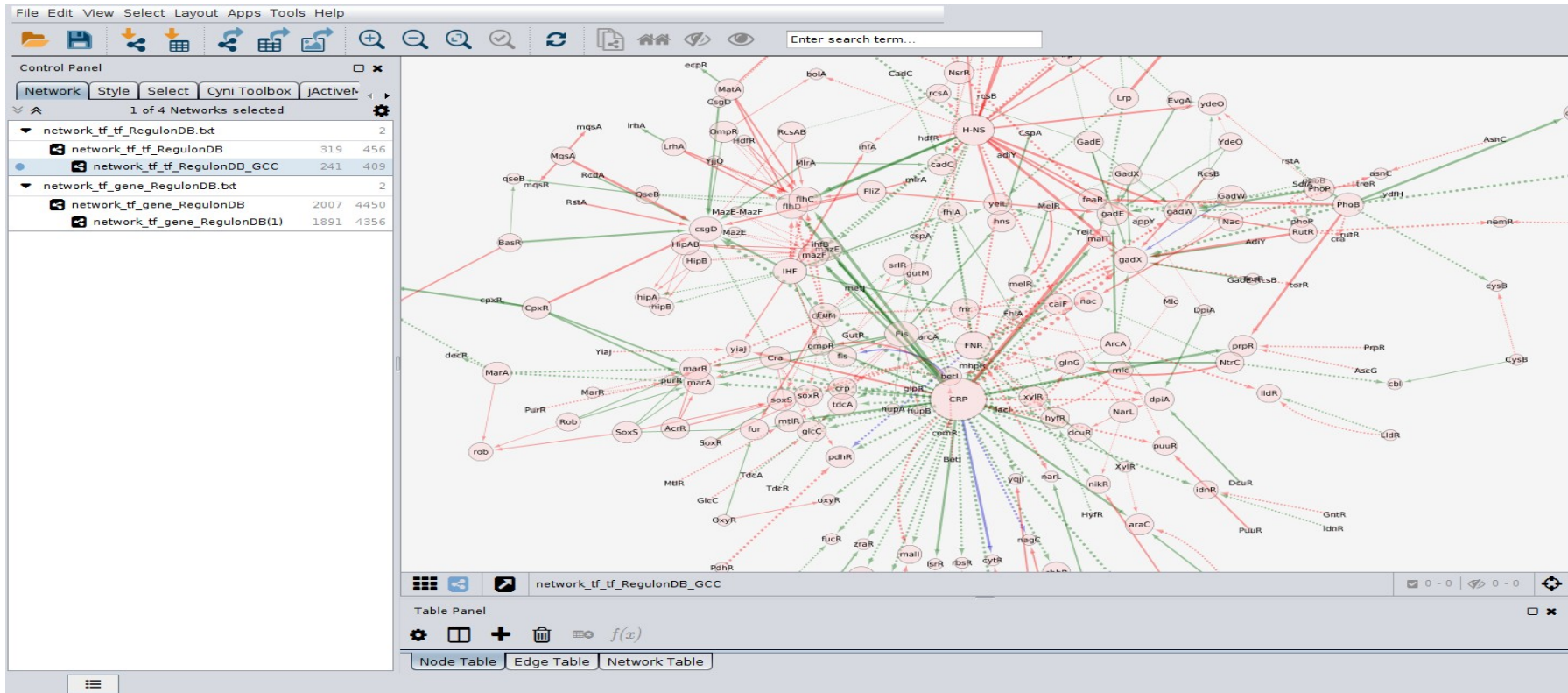


# Cytoscape Advanced.

- A) Select only the connected component (Tools → Subnetwork creation → Connected components)
- B) Analyse your network (Tools → Network Analyser)
- C) Change the nodes, edges shapes:
  - Nodes → Degrees
  - Edges → Betweenness
- D) Colour nodes, colour edges based on their activity (activating, repressing)
- E) Change edge shape based on interaction strength.

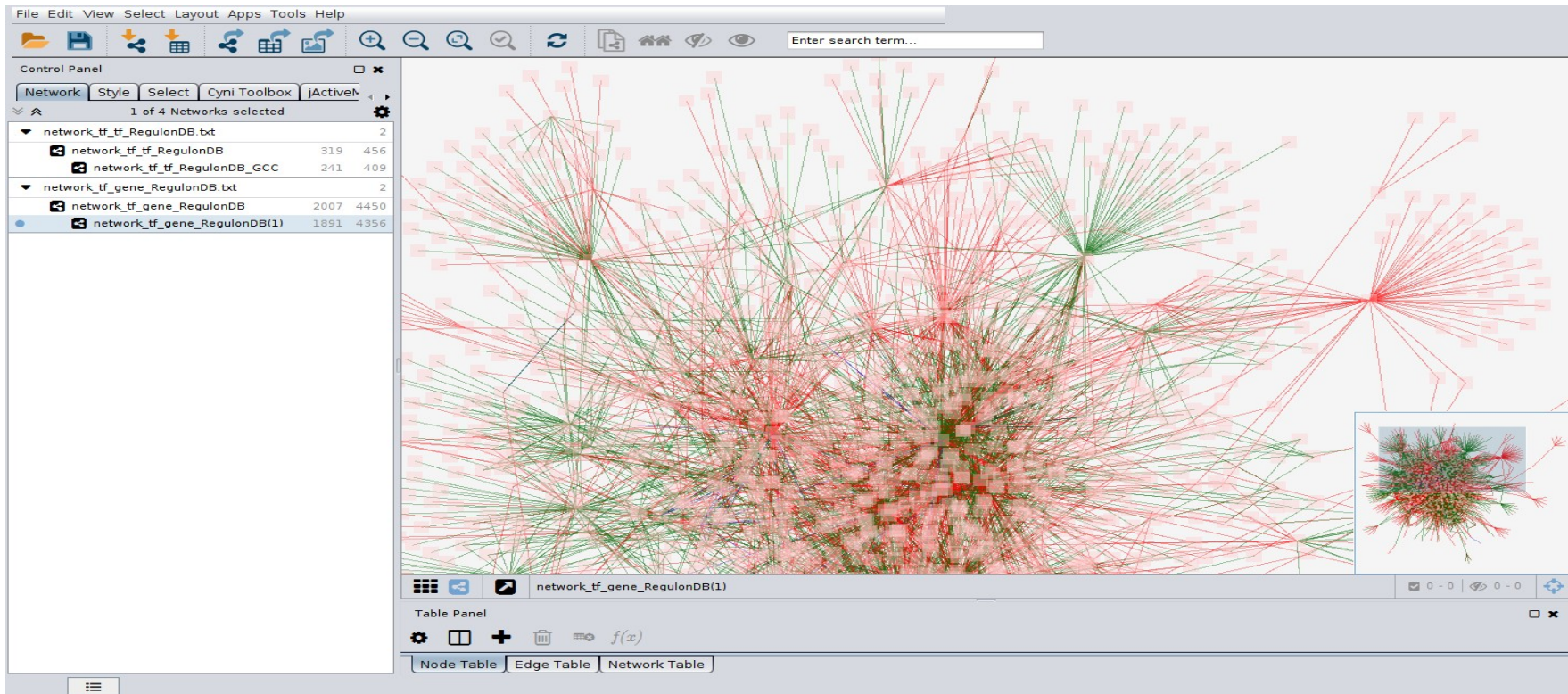
# Cytoscape Advanced II

Hopefully you will get an image like the following:



# Cytoscape final

- Replicate the analysis for the TF-genes network.
- Can you identify global activators? repressors?



# Back to RegulonDB

- 1) Choose your TF/gene of interest
- 2) Go back to RegulonDB and choose “regulon list”
- 3) Find *everything* you want for each TF.

Functional conformation	Function	Promoter	Sigma factor	Central Rel-Pos	Distance to first Gene	Genes	Sequence	LeftPos	RightPos	Evidence (Confirmed, Strong, Weak)	References
LexA	repressor	chop	Sigma70	-0.5	-23.5	cho	ccgcctgttcaCTGCTATATAAACCACTtccggagtc	1823482	1823501	[ABSCS], [HBSCS]	[1], [2], [3], [4]
LexA	repressor	dinBp	Sigma70	-6.5	-24.5	dinB, ynfQ, ynfP	accctgaatCAGTGTATACCTTTACCACTtggaggtg	250864	250883	[ABSCS], [HBSCS], [BCWHO]	[1], [2], [3], [4], [5]
LexA	repressor	dinDp	nd	8.5	-53.5	dinD	agatactcacAAGTGTATATAAACCACTTtagagattac	3817697	3817716	[ABSCS], [GEA], [HBSCS]	[1], [3], [4], [6], [7]
LexA	repressor	dinGp	Sigma70	-27.5	-24.5	dinG	aattgccacaTATTCTCTTTATACAGTtttcagggtt	833036	833055	[ABSCS], [BPP], [GEA]	[8], [9]
LexA	repressor	dinIp	Sigma70	-7.5	-29.5	dinI	aggttttttTACCTGTATAAATAACCACTTattcaacag	1121507	1121526	[ABSCS], [BPP], [GEA], [HBSCS], [HBCS], [SM]	[1], [3], [4], [6], [10]
LexA	repressor	dinJp	Sigma70	89.5	-24.5	dinJ, ynfQ	ctacaattcaAAGTGTATAAATAATACACACagagagatac	246517	246536	[ABSCS], [GEA]	[6], [11]
LexA	repressor	dinOp	Sigma70	-29.5	-223.5	dinO	tgcaggagTCTCTGTATATAACCTTCatgactgttat	3648002	3648021	[HBSCS]	[12]
LexA	repressor	dinQp	Sigma70	-7.5	-201.5	dinQ	aectgcgatTACTGTATATATTCCAGTtagctctgag	3647980	3647999	[ABSCS], [GEA], [HBSCS]	[1], [12]
LexA	repressor	ftsKp1	Sigma70	-0.5	-86.5	ftsK	ttgattacacTCTCTGTATAATCCATACACacagactgg	933128	933147	[ABSCS], [BPP], [GEA]	[6], [8], [13]
LexA	repressor	ftsLp2	nd	3.0	-18.5	ftsL, ftsL, murE, murF, murG, murH, ftsV, murG, murC, ddiB, ftsQ, ftsA, ftsZ, lpxC	cgtagttcagTCTCTGTATTTCAGAGAGacgaatgcat	91004	91023	[HBSCS]	[14], [15]

Showing 1 to 10 of 45 entries

First Previous 1 2 3 4 5 Next Last

## Alignment and PSSM for LexA TFBSs

Aligned TFBS of LexA

Show 10 entries

Search:

CTGCTATATAAACCACTC  
TCTCTCTCTCAATACCAAG  
AAGCTAATAATATACACA  
CACTGTATACCTTTACCACT  
ACCAATATACATAATAT  
CACTGTATATAAACCACT  
AACTATATAAACCACTC  
AACTGTATATAAACCACT  
CCTCTCTCTAATACCACT  
TACTGTATAAACCACTT

Sequence

Showing 1 to 10 of 40 entries

First Previous 1 2 3 4 Next Last

Position weight matrix (PWM).

A	16	26	1	2	0	6	30	1	31	16	33	18	25	16	23	1	37	4	2	21
C	6	4	39	1	1	3	5	3	1	4	0	7	1	9	16	38	1	0	12	4
G	1	7	0	0	0	39	8	0	5	6	2	1	5	3	1	1	0	35	7	7
T	17	3	0	37	0	23	5	31	2	14	5	14	9	12	0	0	2	1	19	8

PWM logo



# Transcription regulation is **ONLY ONE** aspect of Network Biology

- Networks everywhere in biology:
  - ✓ Ecological (food web) networks
  - ✓ Neuronal networks (cognition).
  - ✓ Protein interaction networks.
  - ✓ miRNA, RNAbps and other post-transcriptional regulation networks.
  - ✓ Disease – symptoms – mutations networks.
  - ✓ ... the list is endless BUT

You now know how to analyse them all with **Cytoscape** and table files!

- There is a series of very well made “official” tutorials for Cytoscape, you can access them here:

<http://opentutorials.cgl.ucsf.edu/index.php/Portal:Cytoscape3>