

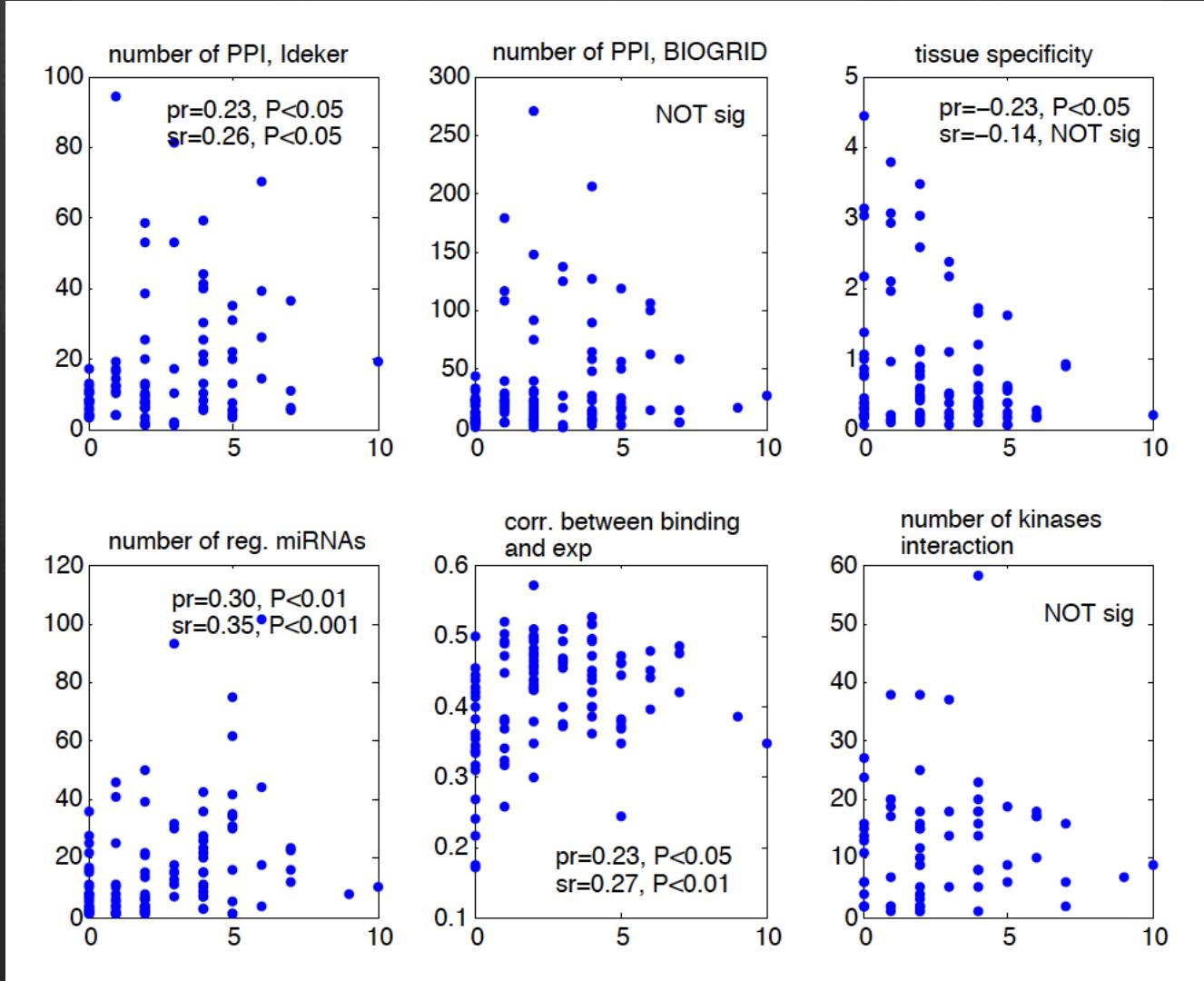
Update of the ENCODE network

6/16/2011

The Network

- 428 ChIP-Seq tracks, with 119 unique transcription factors, in different cell lines or under different conditions
- Target identification based on Chao's probabilistic framework, with q-value 0.01
- 7 TFs are removed: CTCF, EP300, TAF1, TAF7, TBP, WRNIP1, XRCC4
- TF network: 112 TFs, and 309 edges (compare with the previous version: 67 TFs, 1000 edges)
- Properties of TFs: number of physical interacting partners (Ideker, BIOGRID), tissue specificity, number of regulating miRNAs, correlation of binding signals vs expression, number of kinase interactions, ... (structural properties: disorder etc, evolutionary ...)

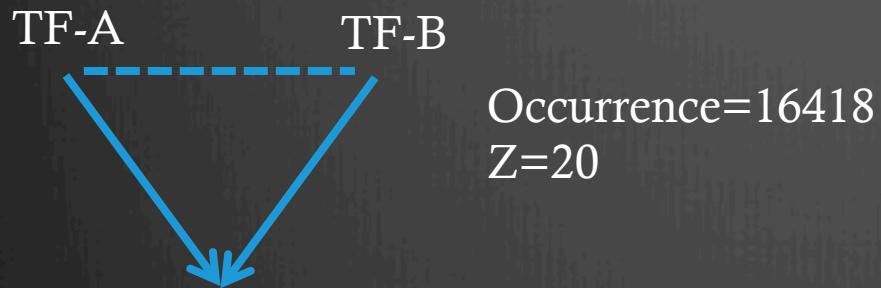
Correlating TF properties with network out-degree



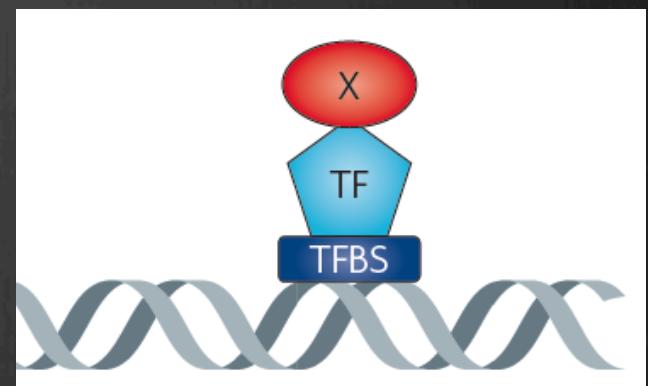
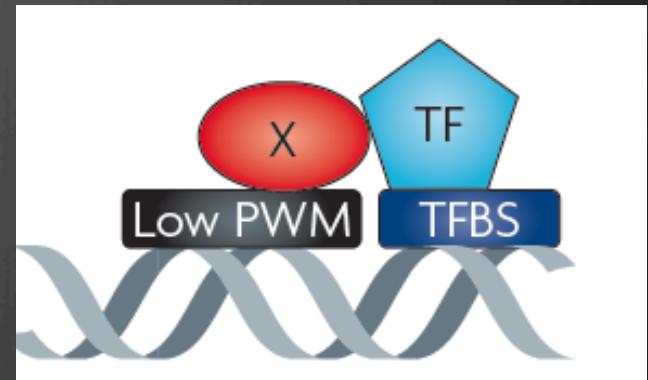
Remarks:

- Previous version: K562, 67 TFs, 1000 edges, we didn't observe the correlations
- NO correlation between TF properties and its in-degree (in-deg is not a genome-wide property)
- Individual nodes -> pairwise correlation -> modules (motifs) -> global (hierarchy)

Integrate with PPI data



- Look at individual motifs, distinguish the two scenarios
- Using information content of the PWMs, identify master regulators, and tissue specific guys
- The filtered network might do a better job for this analysis



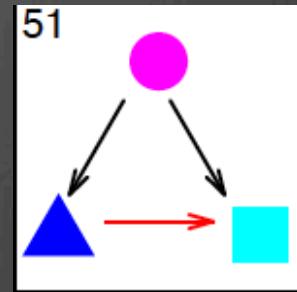
Enriched motifs



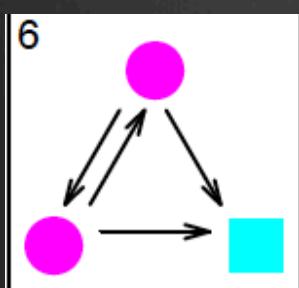
N=40, z=6.96



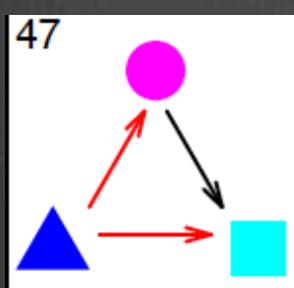
Not sig



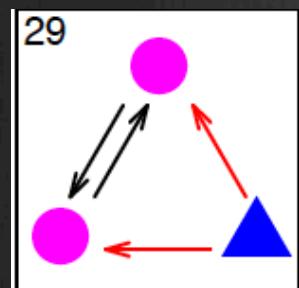
Not sig



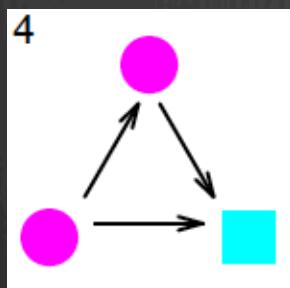
N=4203



z=2.65



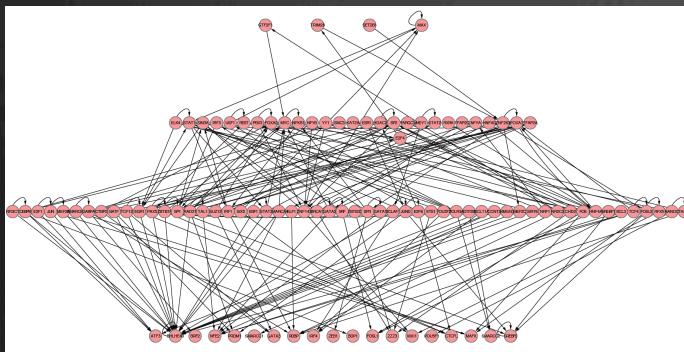
N=110



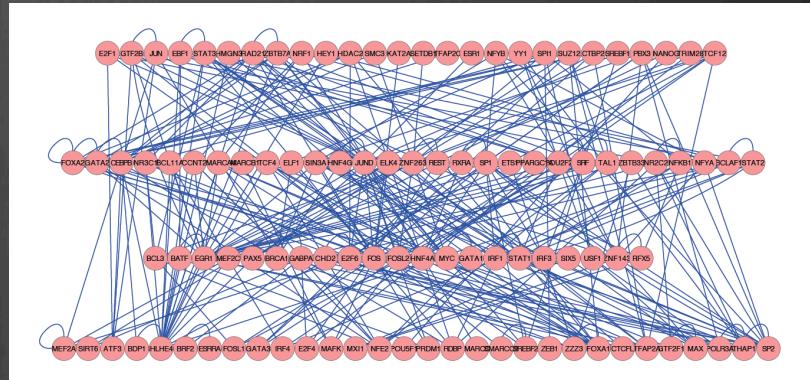
z=28

Zoo of Hierarchies

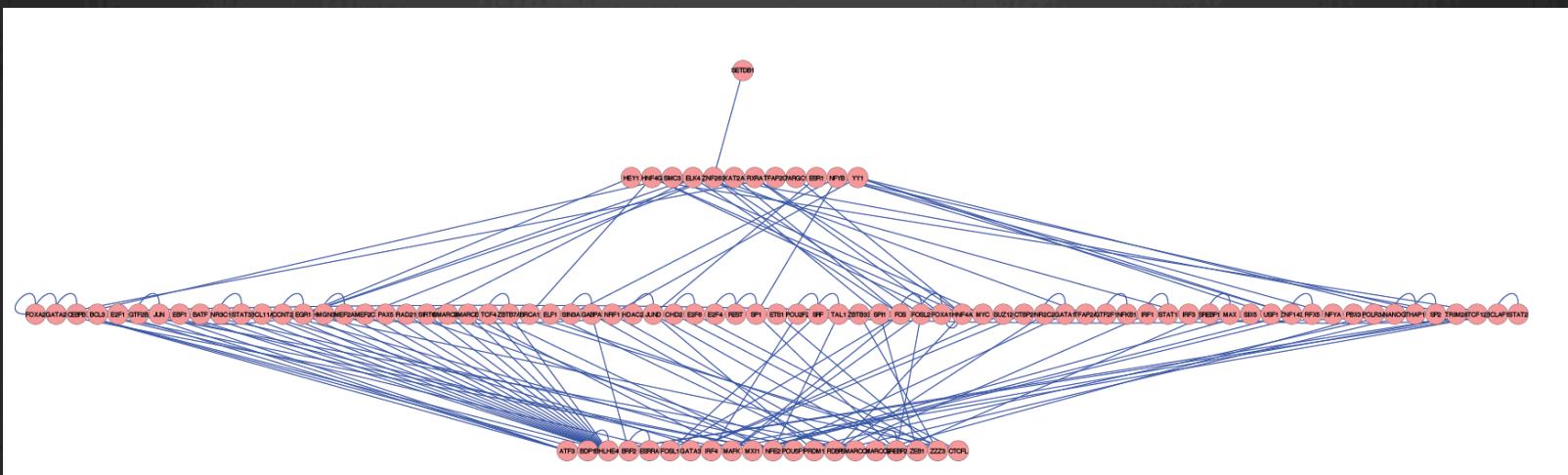
Leaf removal algorithm



Minimize feedback



Breadth first search



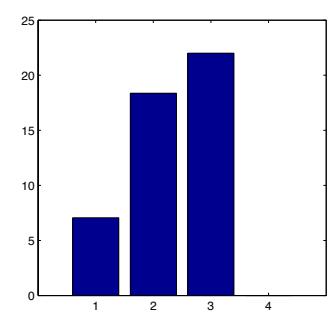
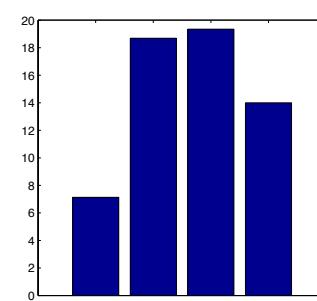
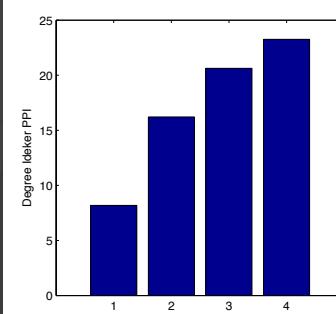
TF properties wrt levels

MF

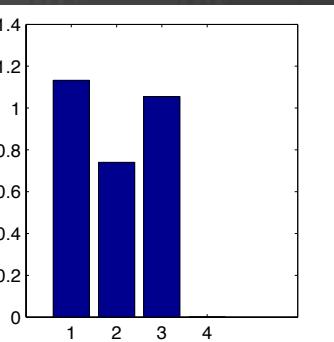
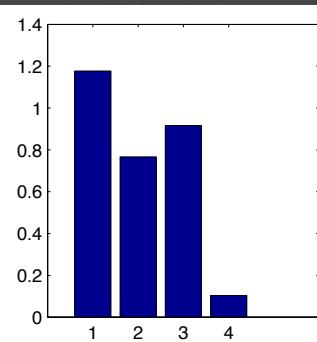
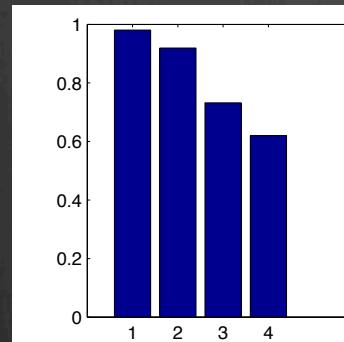
LR

BFS

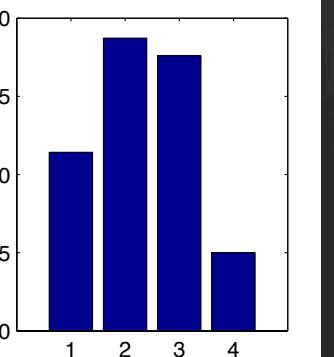
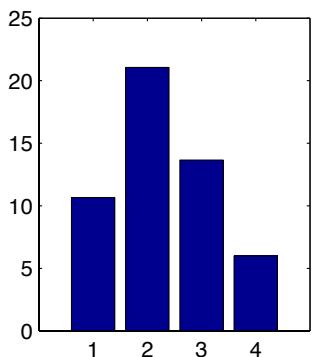
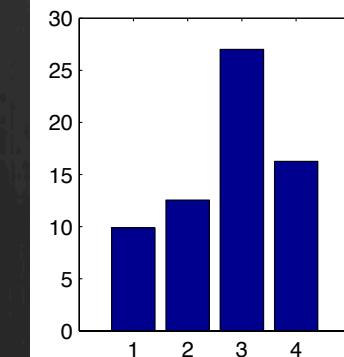
Number of PPI
partners



Tissue specificity



Num. of miRNA
regulators



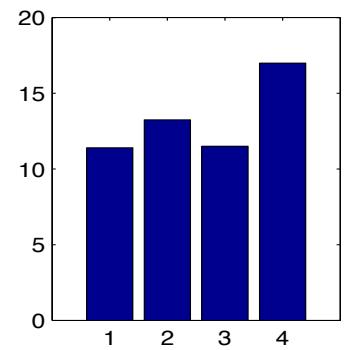
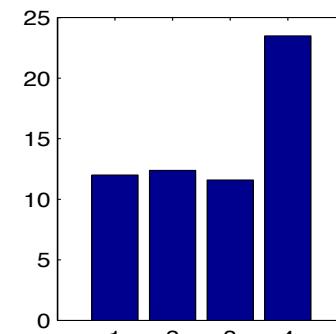
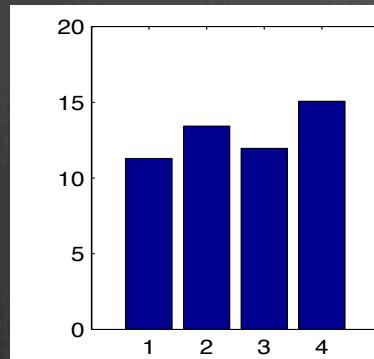
TF properties wrt levels

MF

LR

BFS

Num of regulating kinases



Corr. With exp

