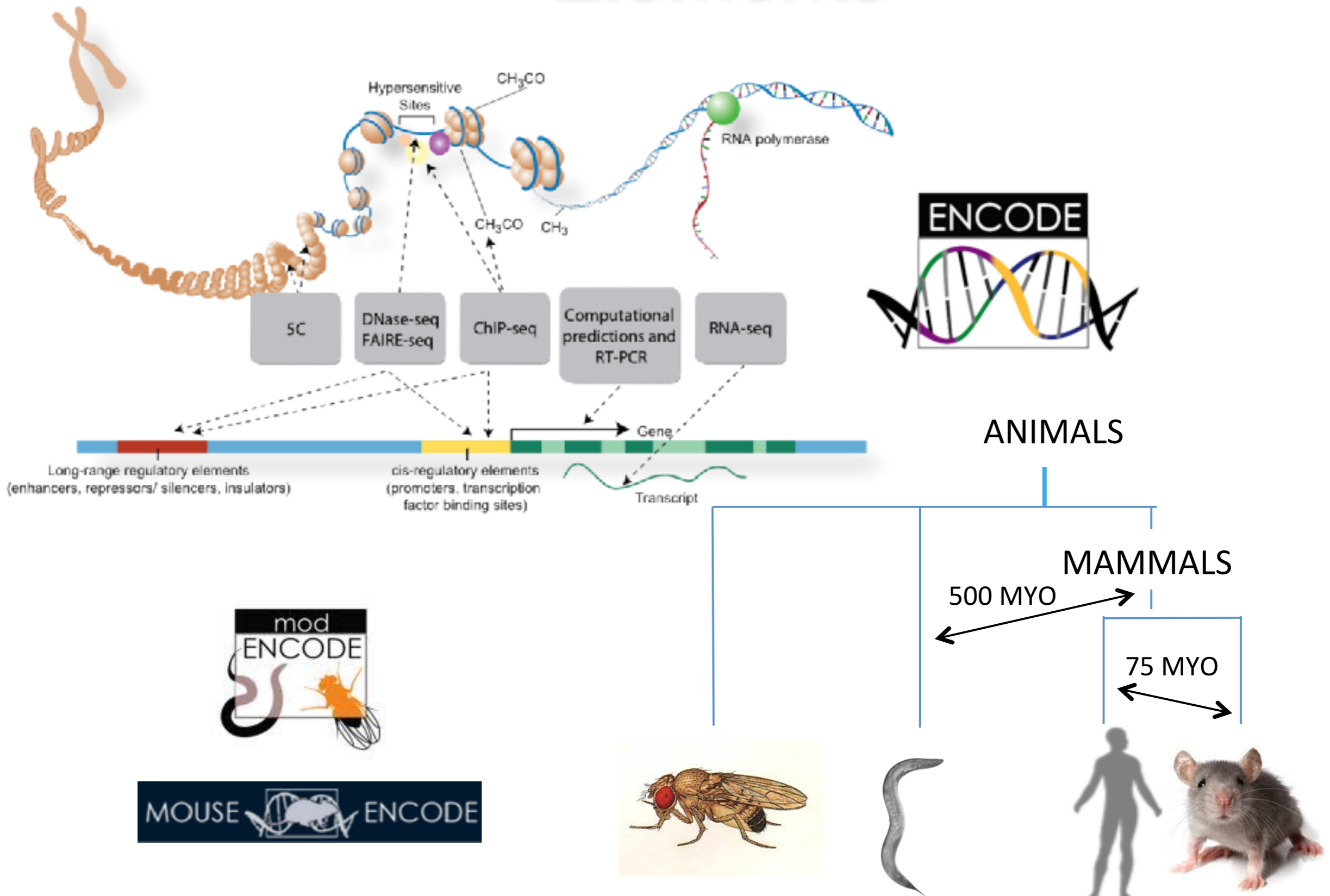


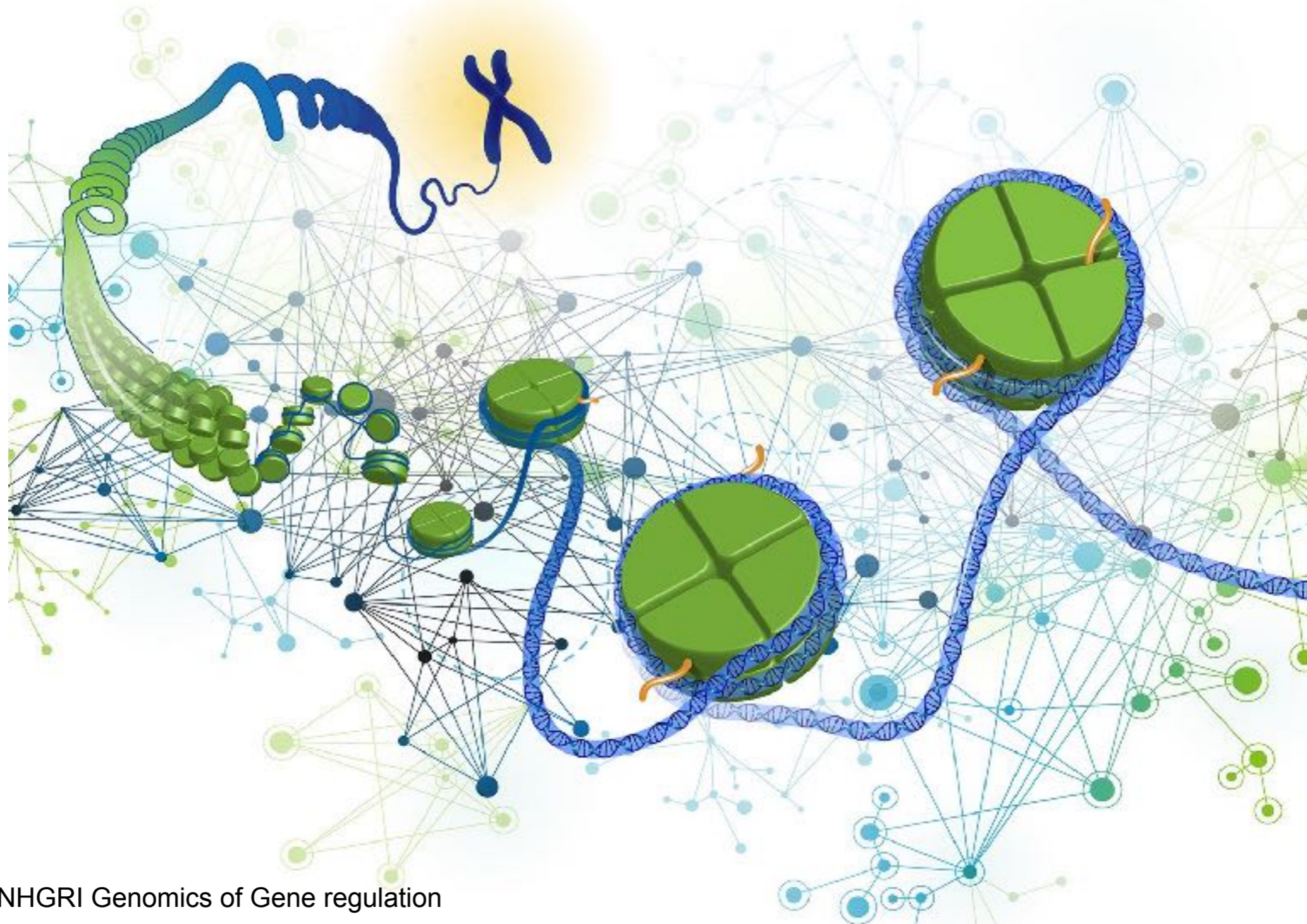
Networks

Gerstein lab

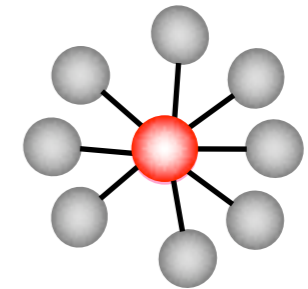
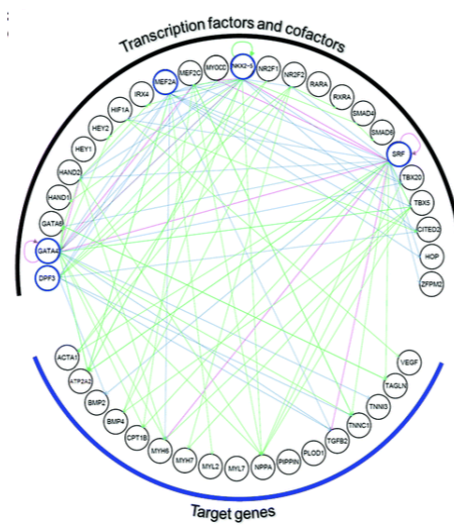
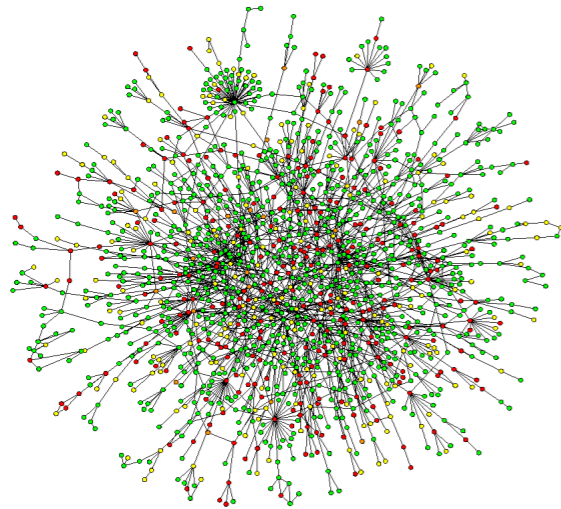
ENCODE: Encyclopedia of DNA Elements



Network is a powerful framework for data integration



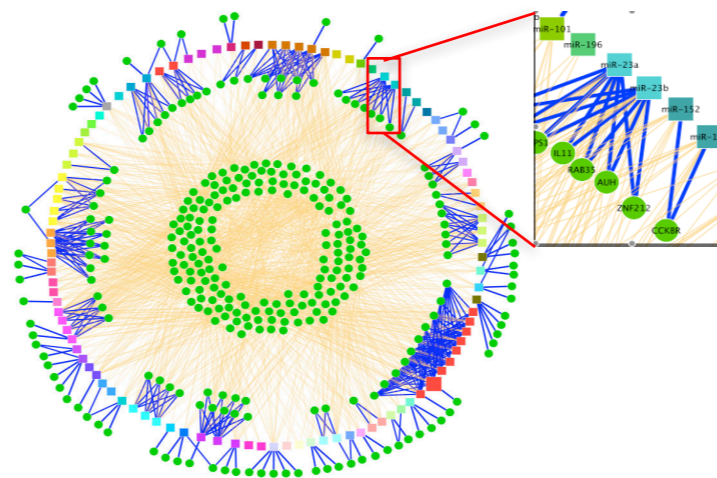
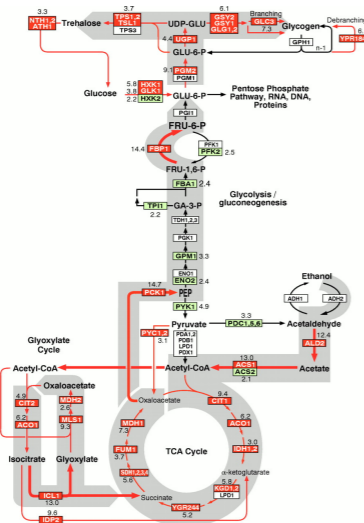
Common biological networks



Undirected

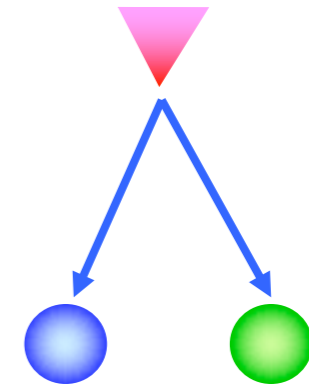
Protein-protein Interaction networks

TF-target-gene Regulatory networks



Metabolic pathway networks

miRNA-target networks



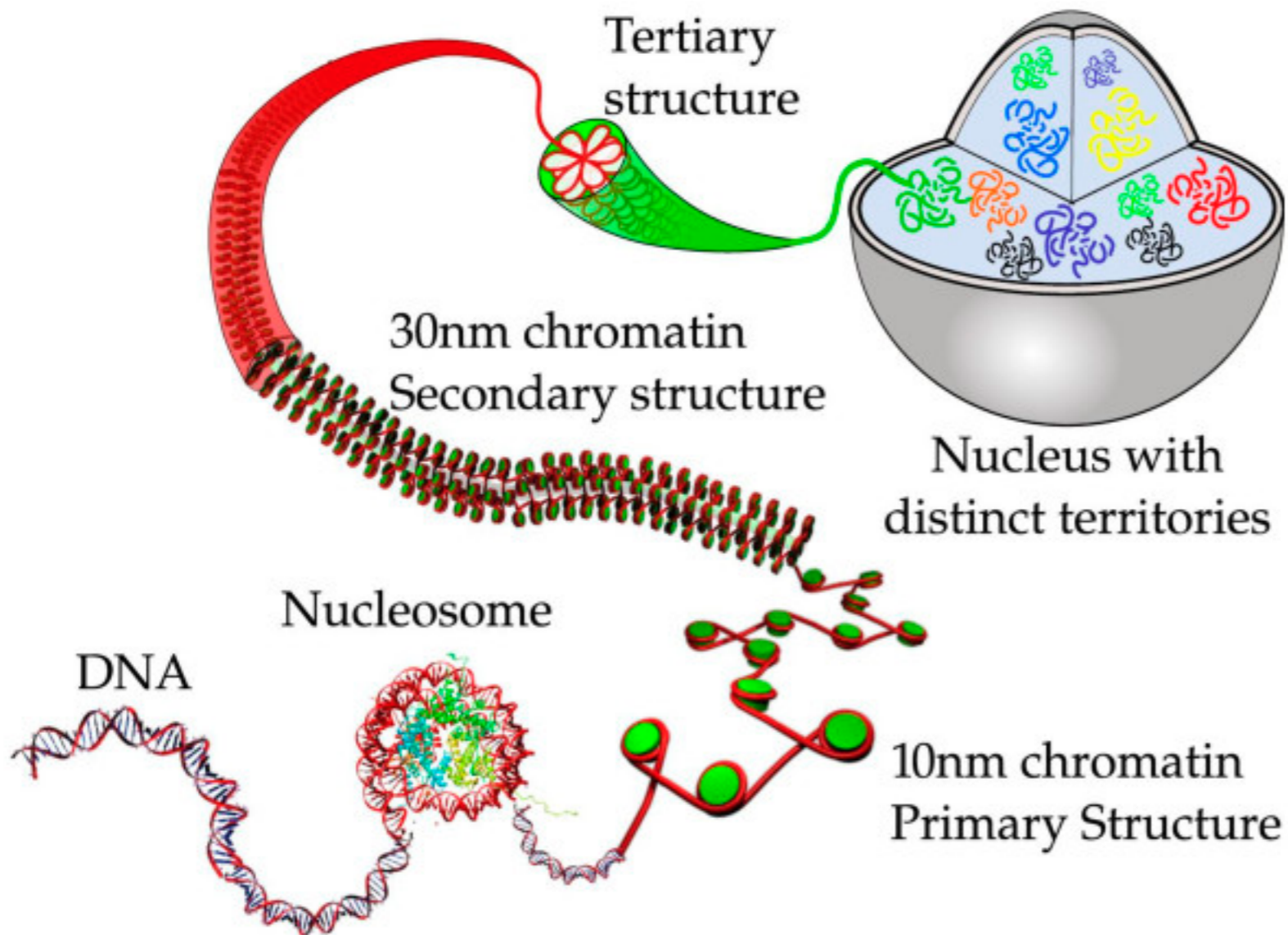
Directed

Example: 3D organization of genome



"We finished the genome map, now we can't figure out how to fold it."

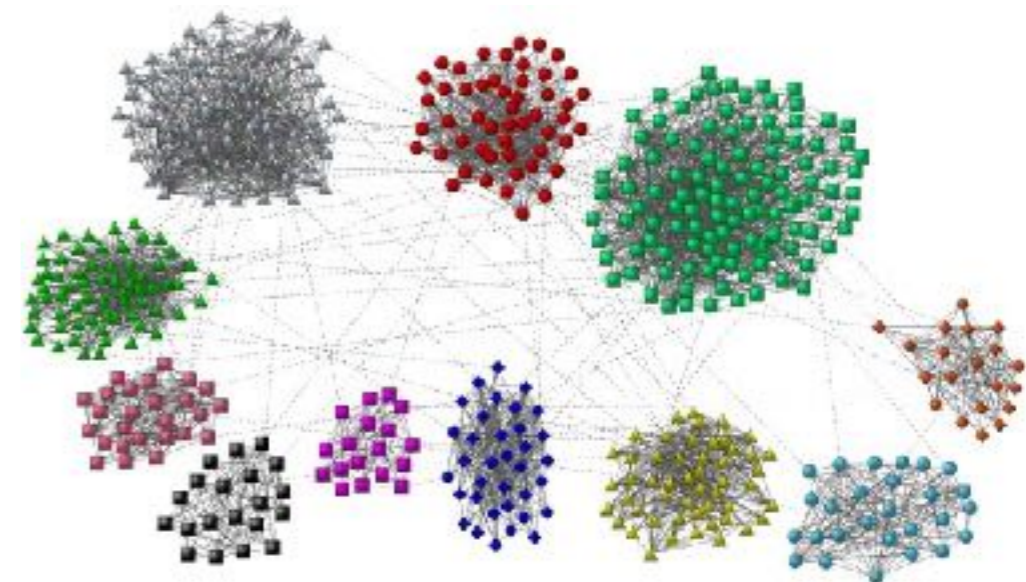
Example: 3D organization of genome



Topologically associating domains (TADs)



Network communities



Example: 3D organization of genome

The screenshot shows the GitHub interface for the repository 'gersteinlab / MrTADFinder'. At the top, there are navigation links for Personal, Open source, Business, Explore, Pricing, Blog, and Support. A search bar and 'Sign in'/'Sign up' buttons are also present. The repository name 'gersteinlab / MrTADFinder' is displayed, along with 'Watch 2', 'Star 0', and 'Fork 0' buttons. Below this, there are tabs for Code, Issues (0), Pull requests (0), Projects (0), Pulse, and Graphs. A note states 'No description or website provided.' The repository statistics show 30 commits, 1 branch, 0 releases, and 1 contributor. A 'Branch: master' dropdown and a 'New pull request' button are visible. A 'Find file' button and a 'Clone or download' button are also present. The commit history shows a commit by Koon-Kiu Yan of group gerstein, titled 'fix broken functions', with the latest commit 'ca63b98' 26 days ago. The file list includes 'data', 'MrTADFinder.jl', 'README.md', and 'run_MrTADFinder.jl'. The 'README.md' file is selected, showing the title 'MrTADFinder' and the description: 'MrTADFinder aims to identify topologically associating domains (TADs) in multiple resolutions.' Under the heading 'INPUT FILES:', it states: 'MrTADFinder takes an whole-genome-to-whole genome contact map as an input. The contact map should be a'.

Personal Open source Business Explore Pricing Blog Support This repository Search Sign in Sign up

gersteinlab / MrTADFinder Watch 2 Star 0 Fork 0

Code Issues 0 Pull requests 0 Projects 0 Pulse Graphs

No description or website provided.

30 commits 1 branch 0 releases 1 contributor

Branch: master New pull request Find file Clone or download

Koon-Kiu Yan of group gerstein fix broken functions Latest commit ca63b98 26 days ago

data	fix broken functions	26 days ago
MrTADFinder.jl	fix broken functions	26 days ago
README.md	new distance	3 months ago
run_MrTADFinder.jl	fix broken functions	26 days ago

README.md

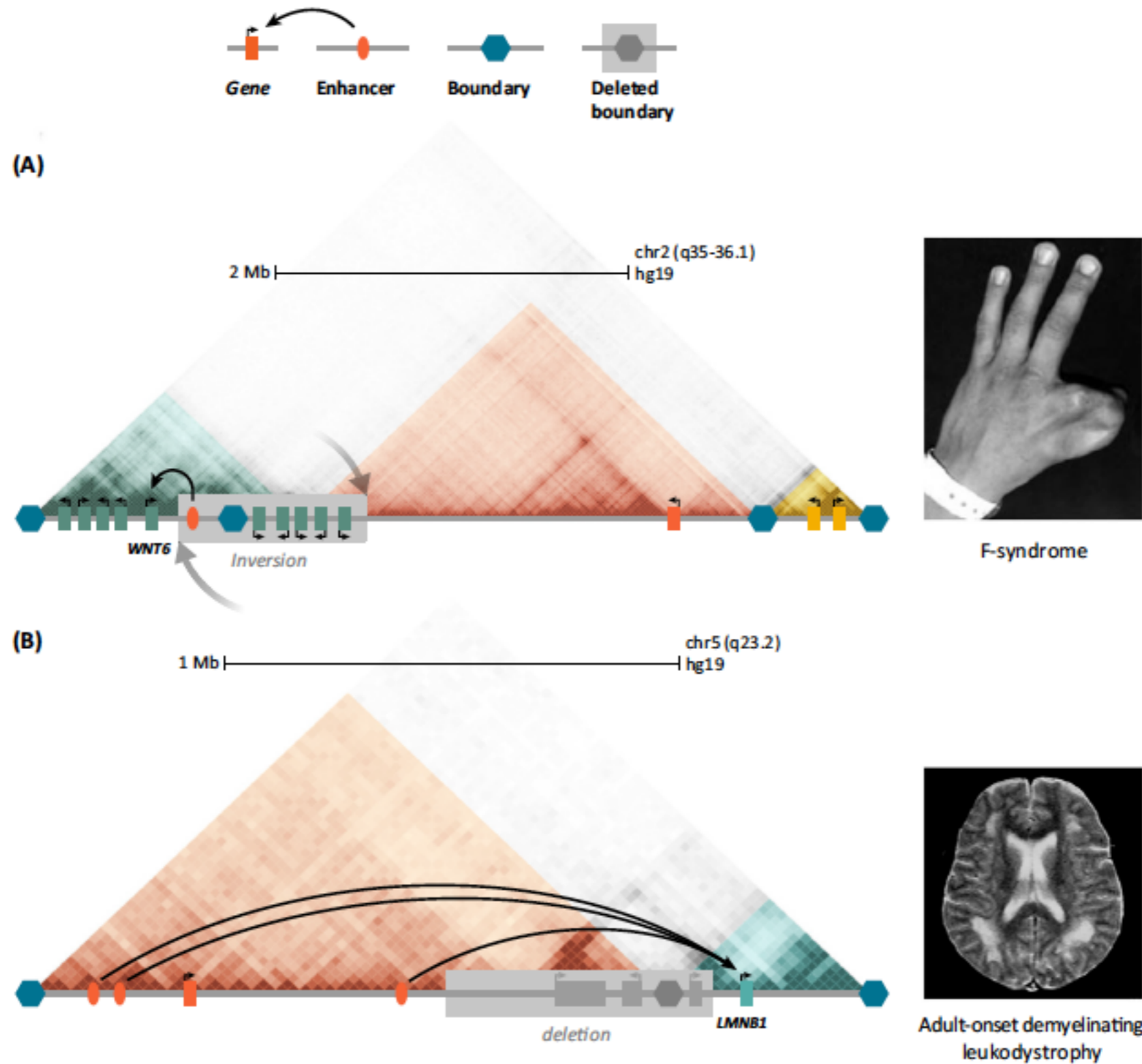
MrTADFinder

MrTADFinder aims to identify topologically associating domains (TADs) in multiple resolutions.

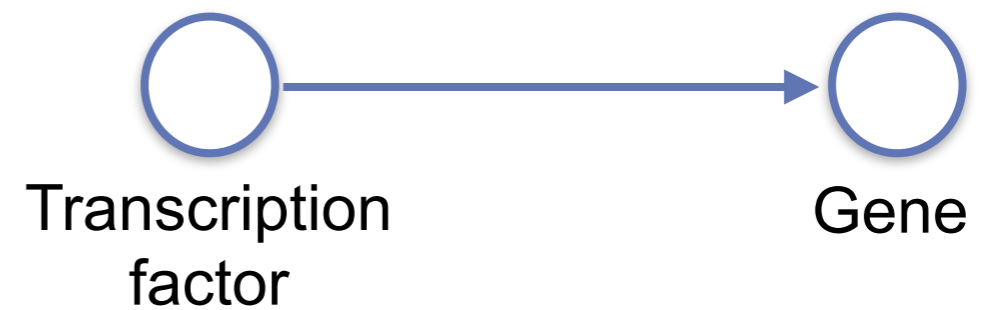
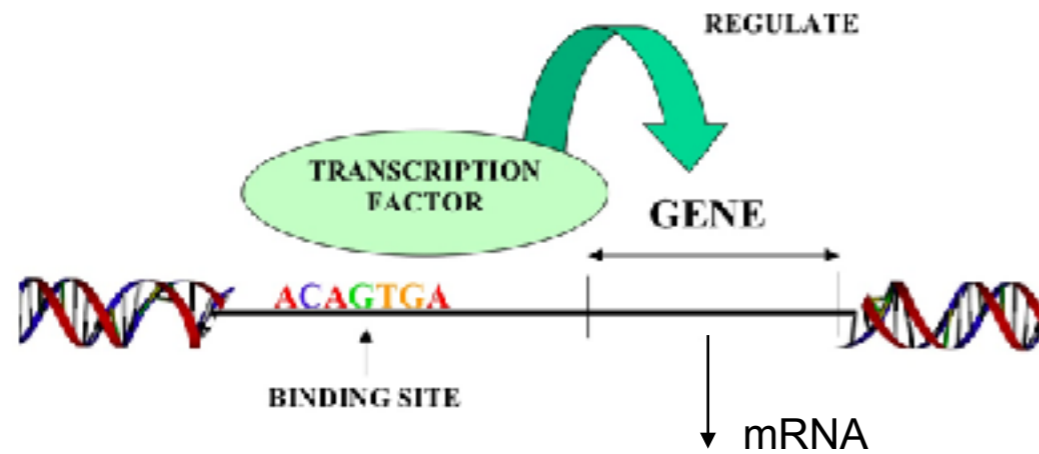
INPUT FILES:

MrTADFinder takes an whole-genome-to-whole genome contact map as an input. The contact map should be a

Disruption of domain structure causes congenital disease



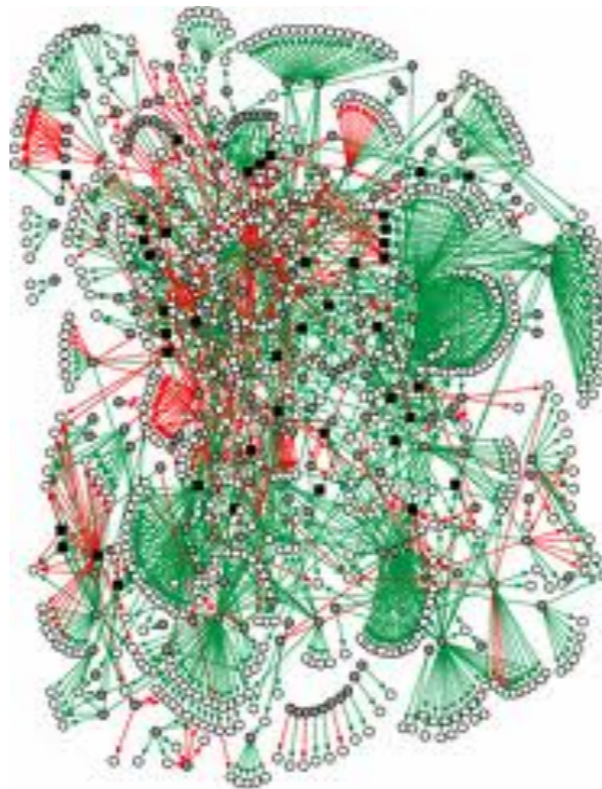
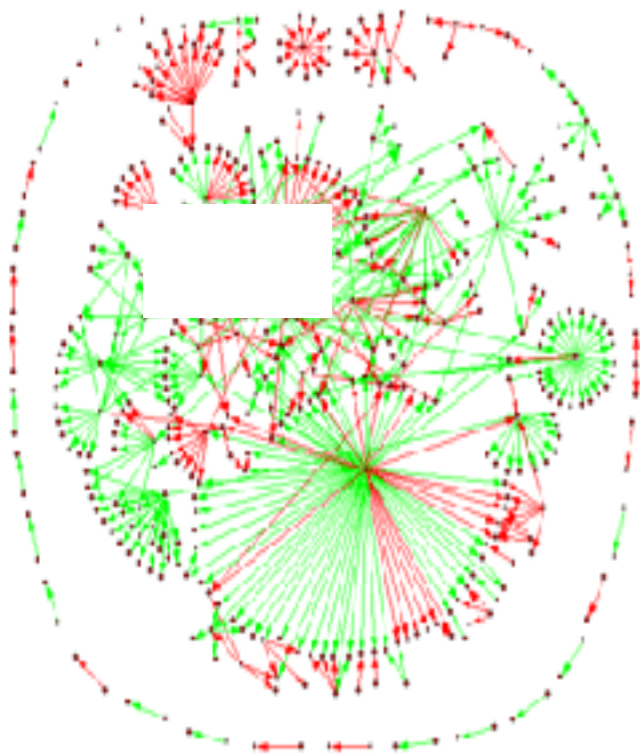
Example: Transcriptional regulatory network



Bacteria
E. coli: 100 TFs, 4000 genes

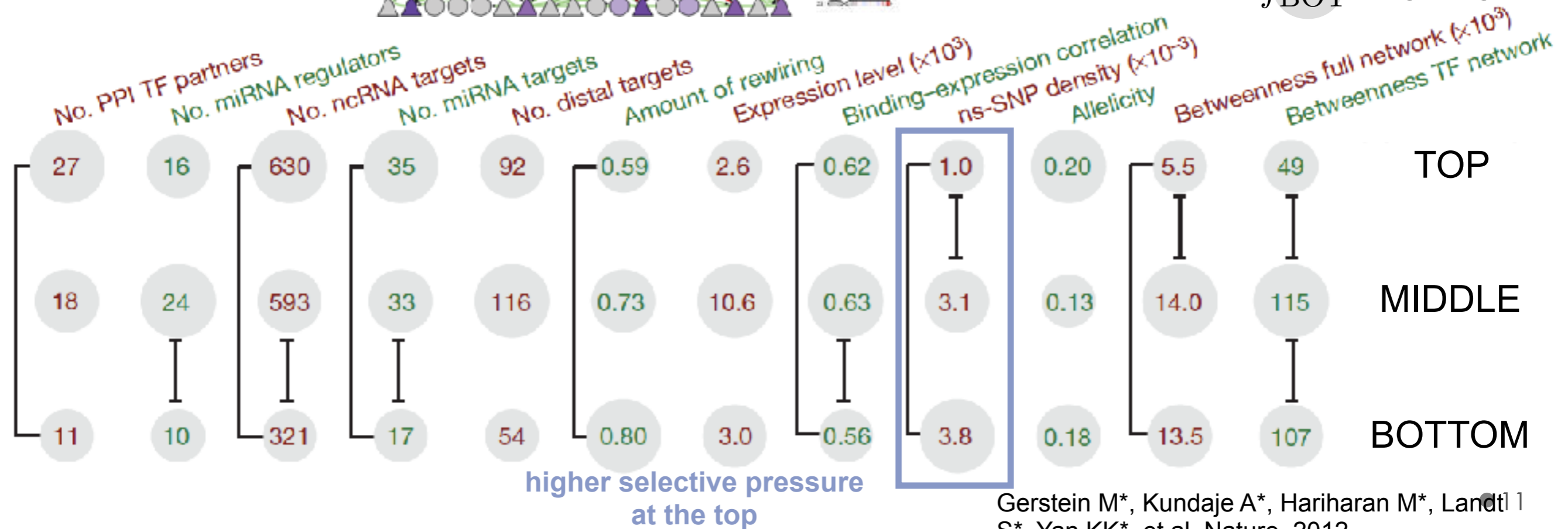
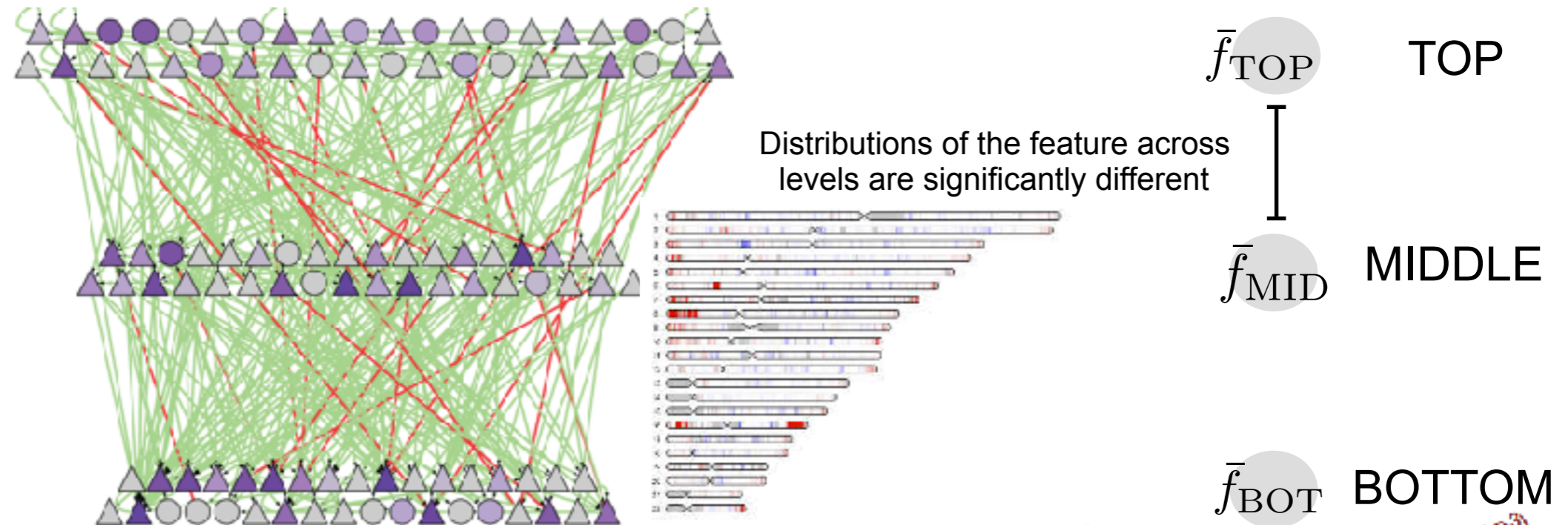
Single-celled eukaryotes
Baker's yeast: 200 TFs, 6000 genes

Complex eukaryotes
Human: 1400 TFs, 20000 genes

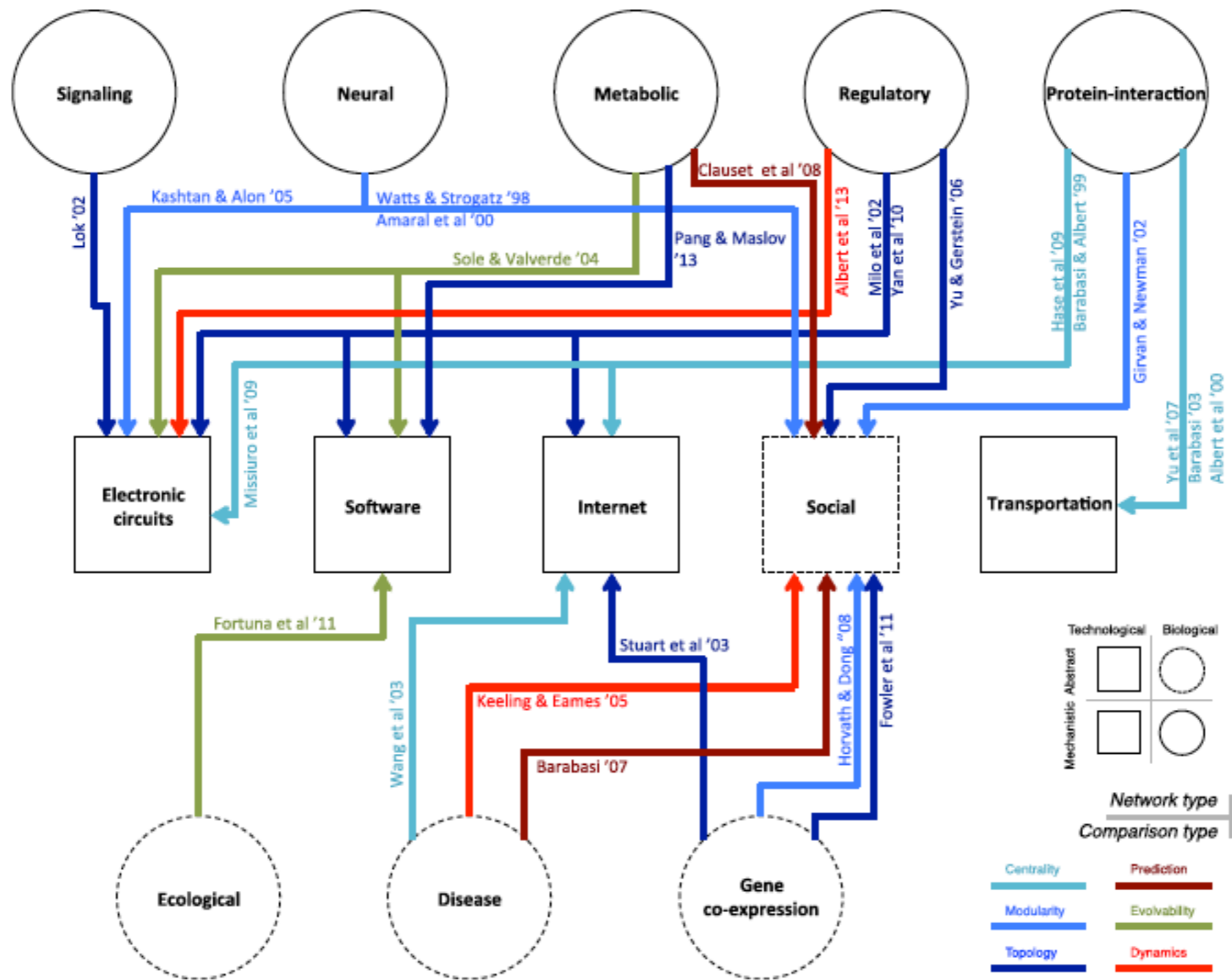


?

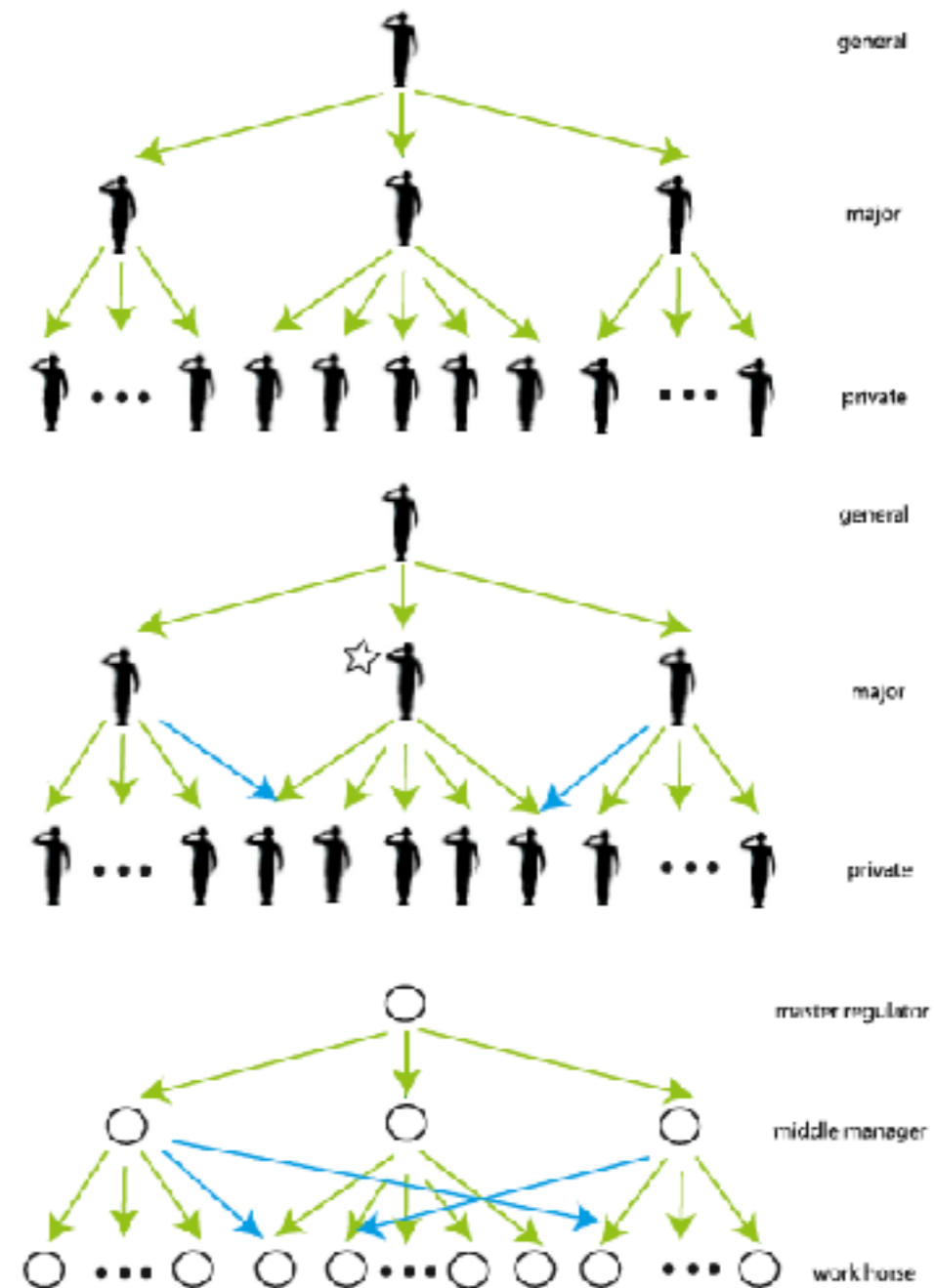
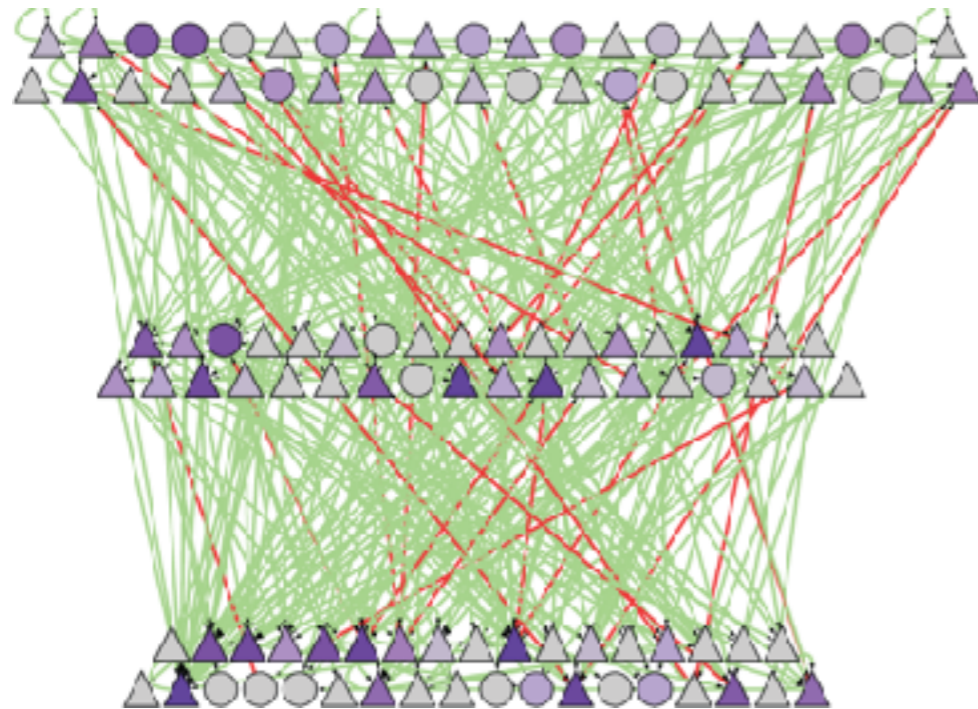
Example: Hierarchical organization of human transcriptional regulatory network



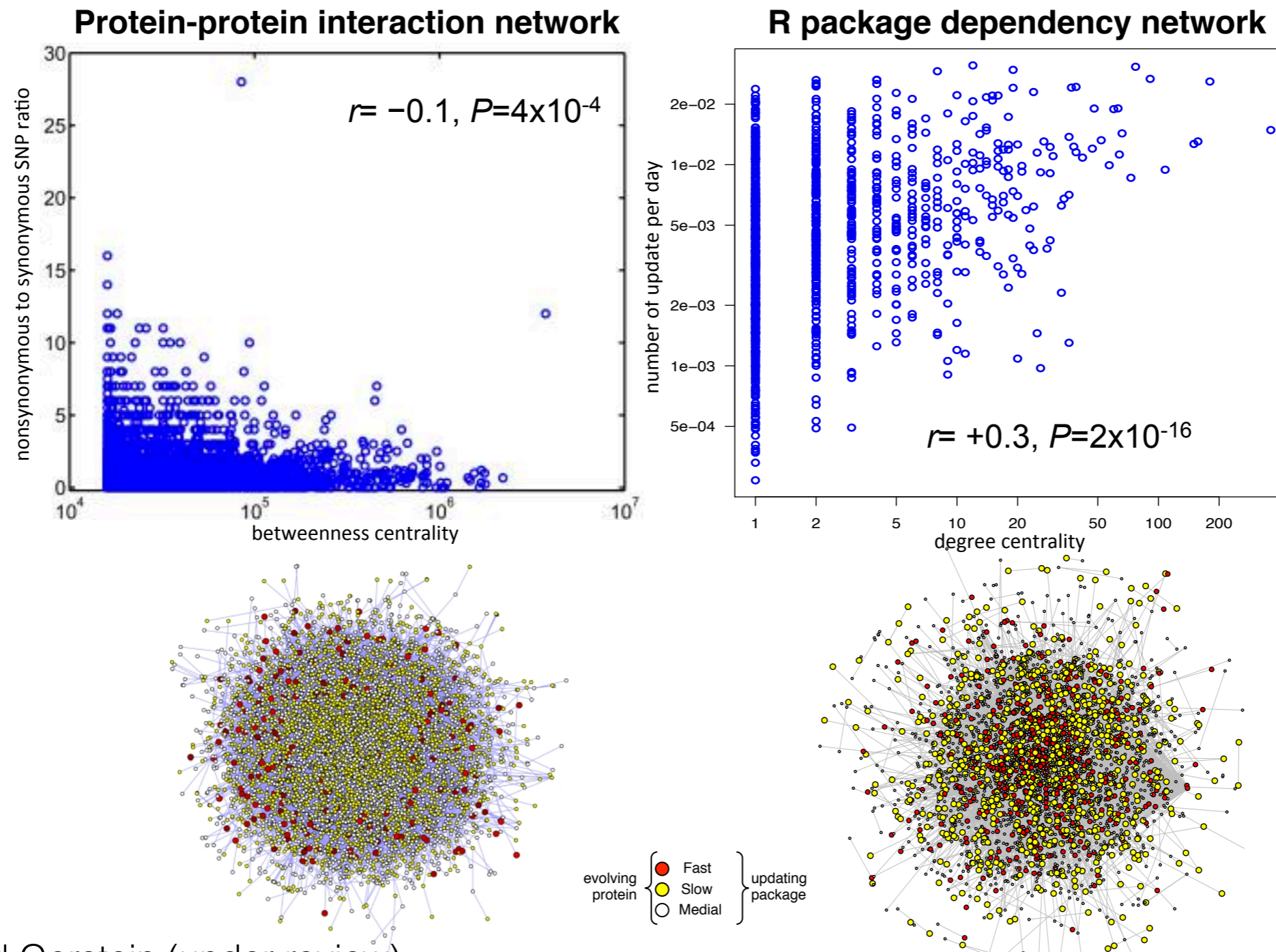
Example: Network comparison



Example: human transcriptional regulatory network versus chain-of-command hierarchy

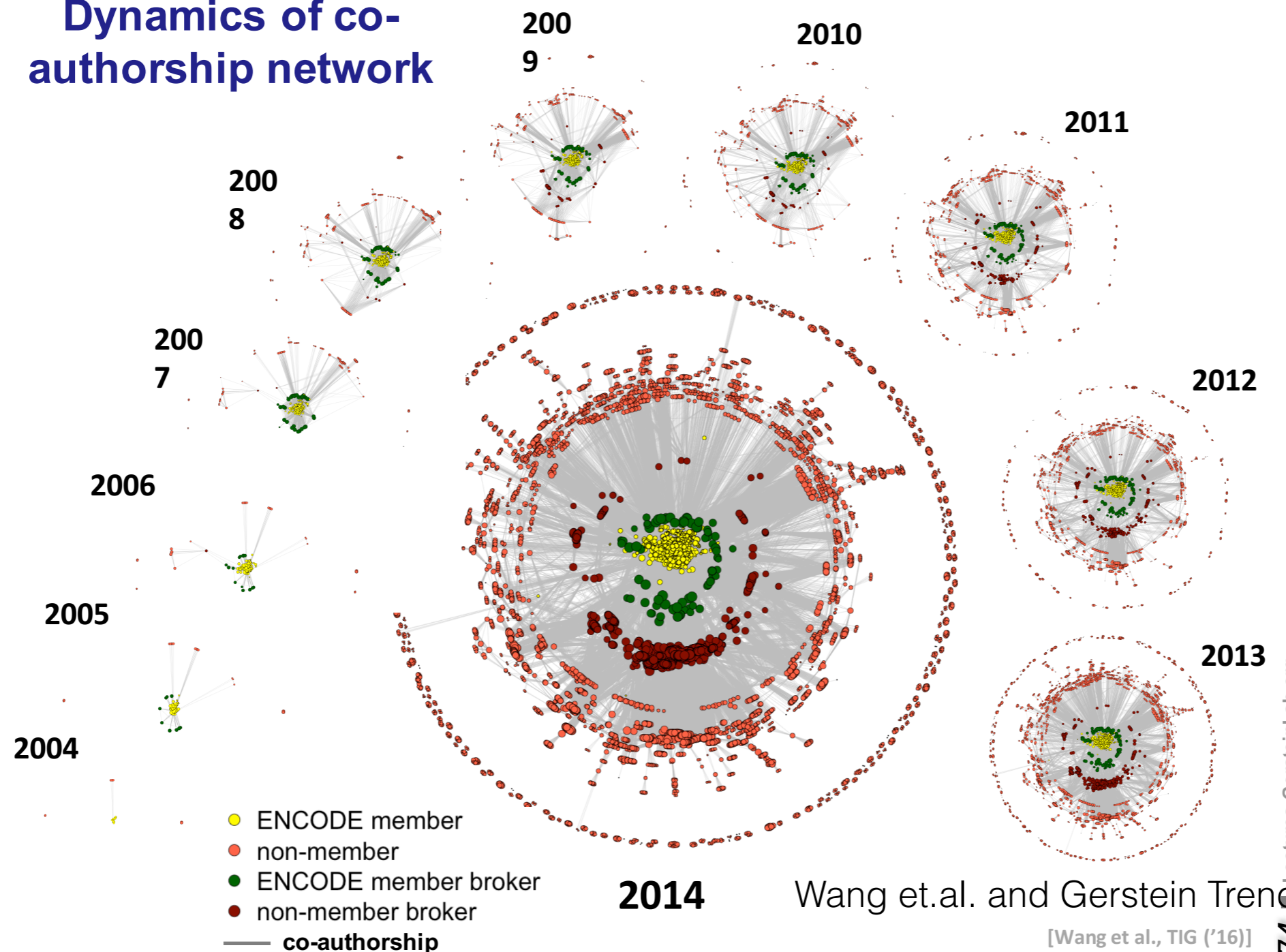


Example: Protein-protein interaction network versus software package dependency network



Example: Collaboration network in a scientific consortium

Dynamics of co-authorship network



Wang et.al. and Gerstein Trends in Genetics 2016

[Wang et al., TIG ('16)]