

The background of the slide is a complex network diagram. It consists of numerous small, multi-colored nodes (red, blue, green, yellow, purple, cyan) connected by thin, light gray lines. These connections form a dense, interconnected web of clusters and paths, filling the entire frame. A large, semi-transparent white rectangular area is centered over the network, serving as a backdrop for the text.

Network Analysis

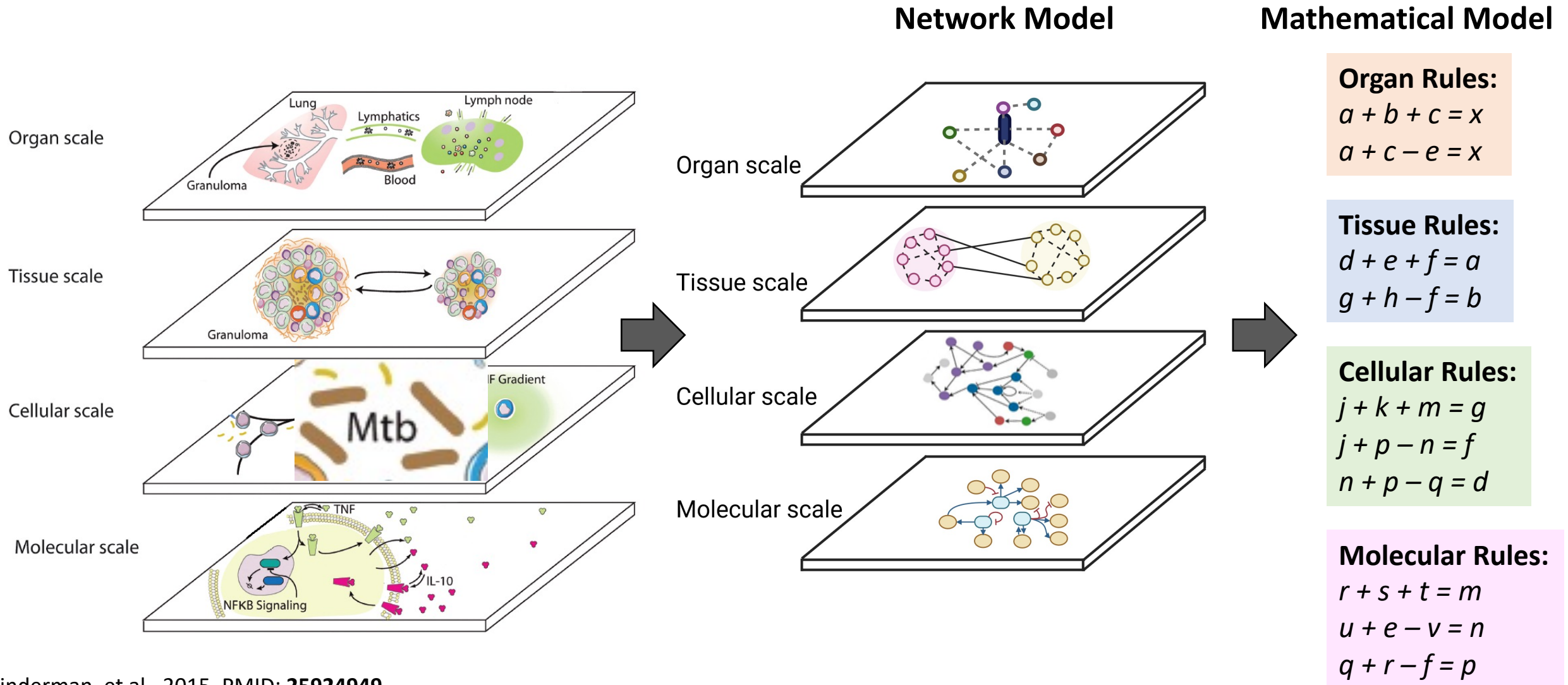
Fergal Duffy and Shuyi Ma

TB Hack Day 2023
12-13-23

Goals

- Discuss why networks are useful for analysis
- Discuss annotated vs. data-driven networks
- Method for mapping genes of interest onto network: GSEA
- Method for inferring data-driven network: WGCNA

Networks can help contextualize biological complexity

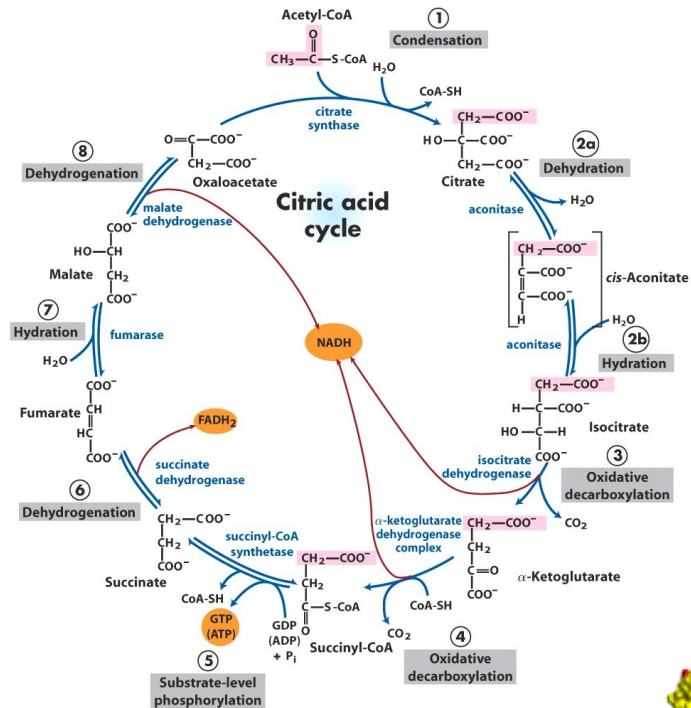


Linderman, et al., 2015, PMID: **25924949**

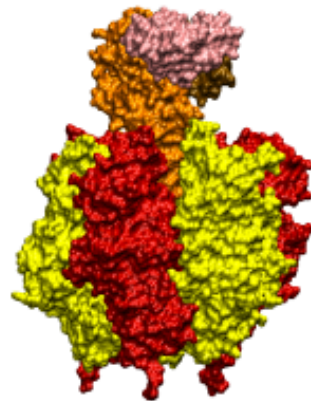
Mast et al., 2014, PMID: **25225336**

Annotated networks

Known interactions from direct characterization

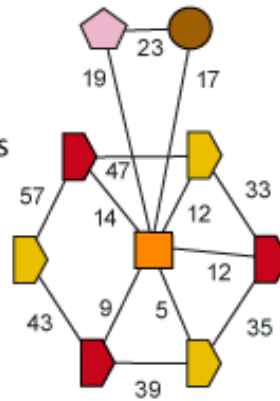


[KEGG](#)
[Reactome](#)
[Gene Ontology](#)
[STRING](#)
etc...



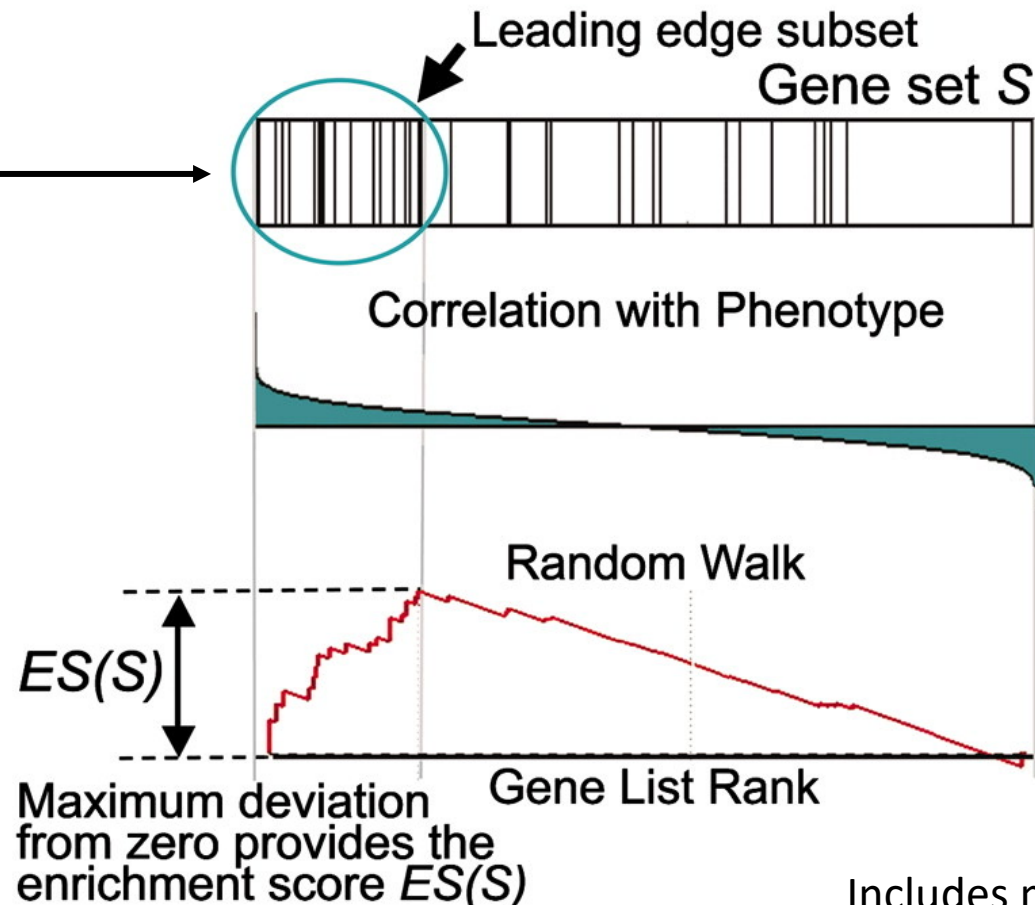
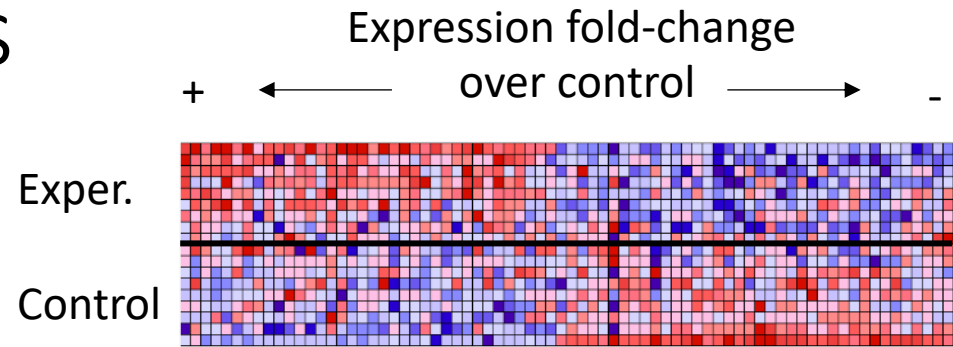
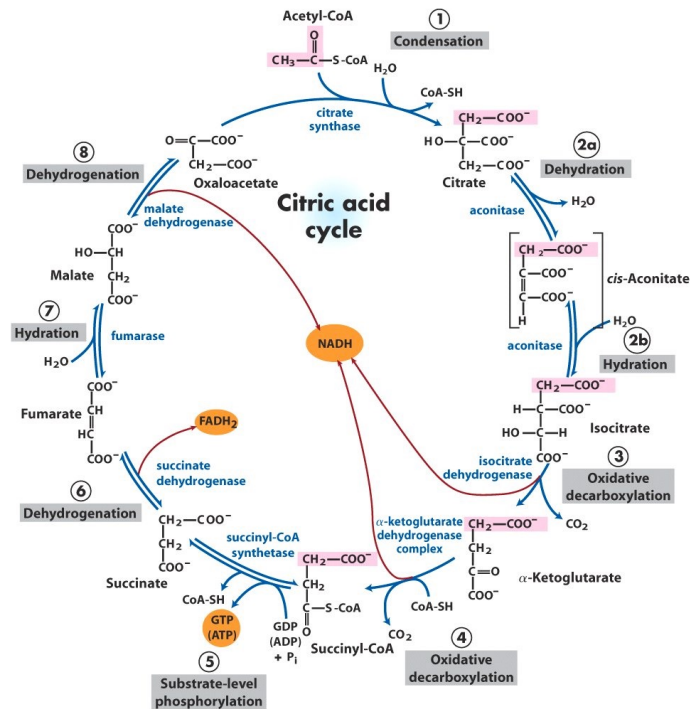
Crystallographic
structure of a complex

- identities
- homologies
- contacts

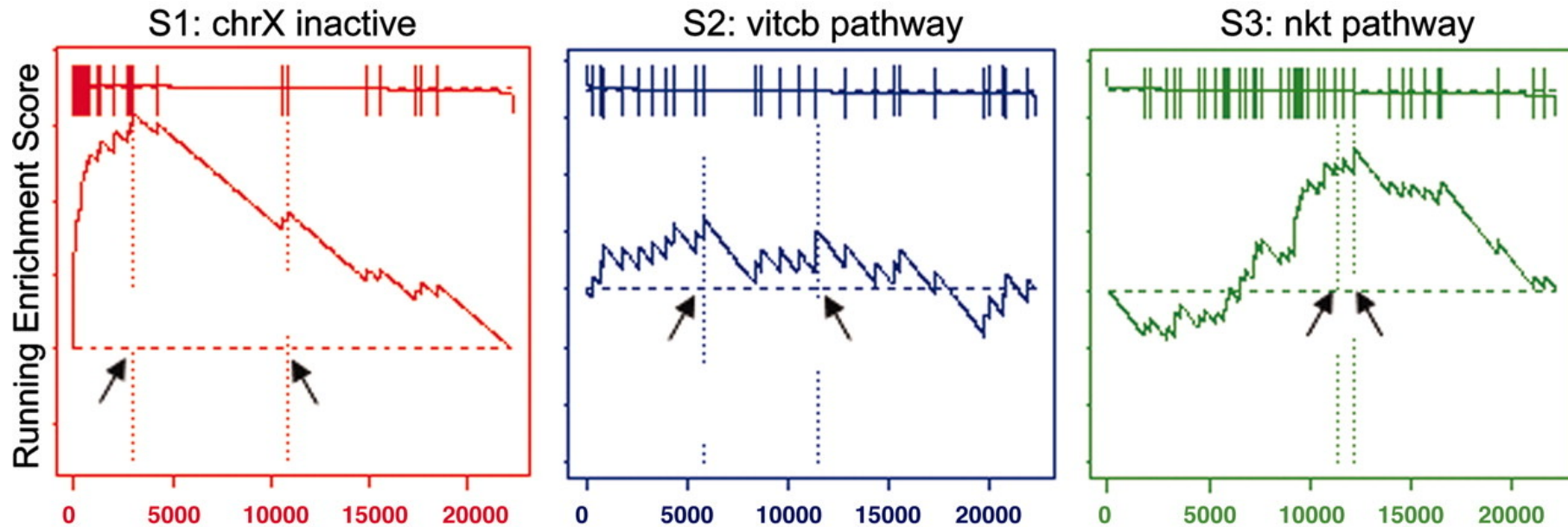


3D Complex
graph representation

Gene Set Enrichment Analysis (GSEA)

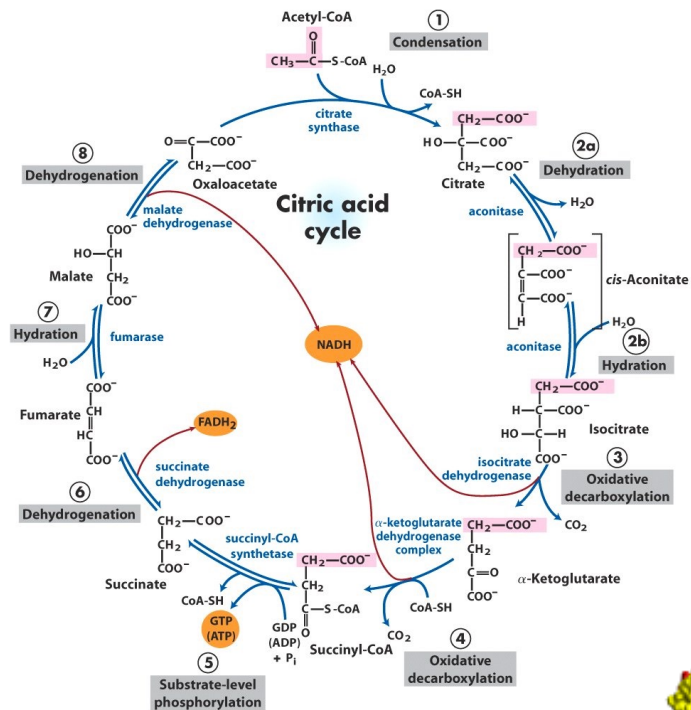


Enrichment scores measure association of gene set with phenotype

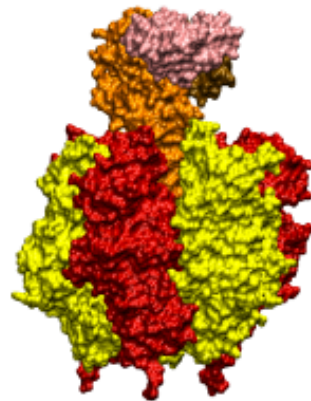


Annotated networks vs. data-driven networks

Known interactions from direct characterization

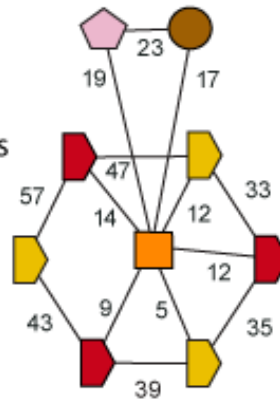


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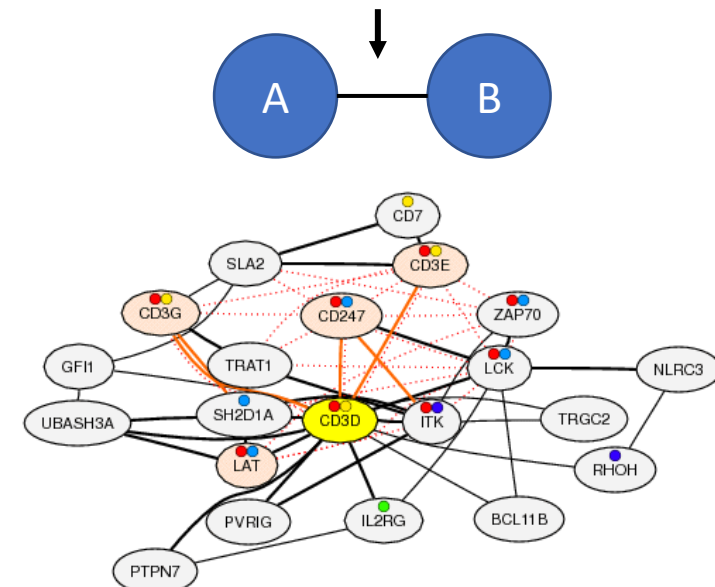
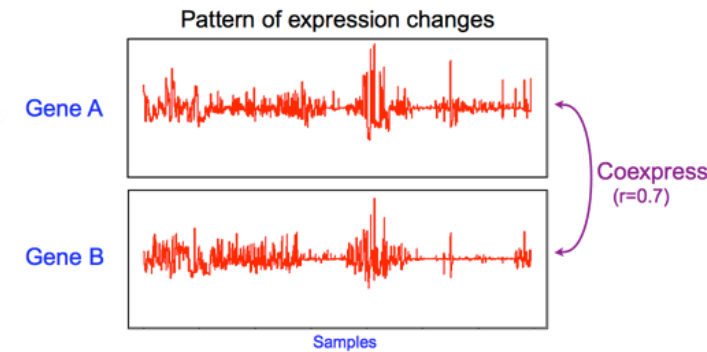
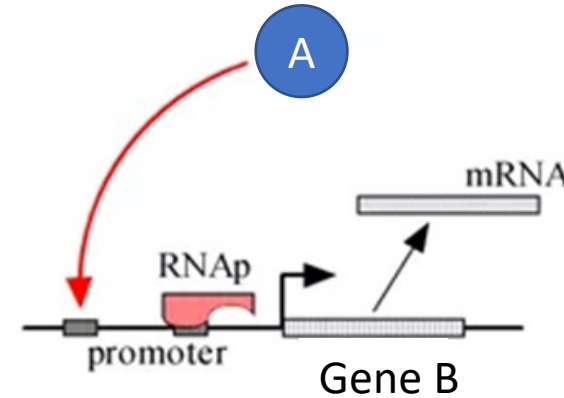
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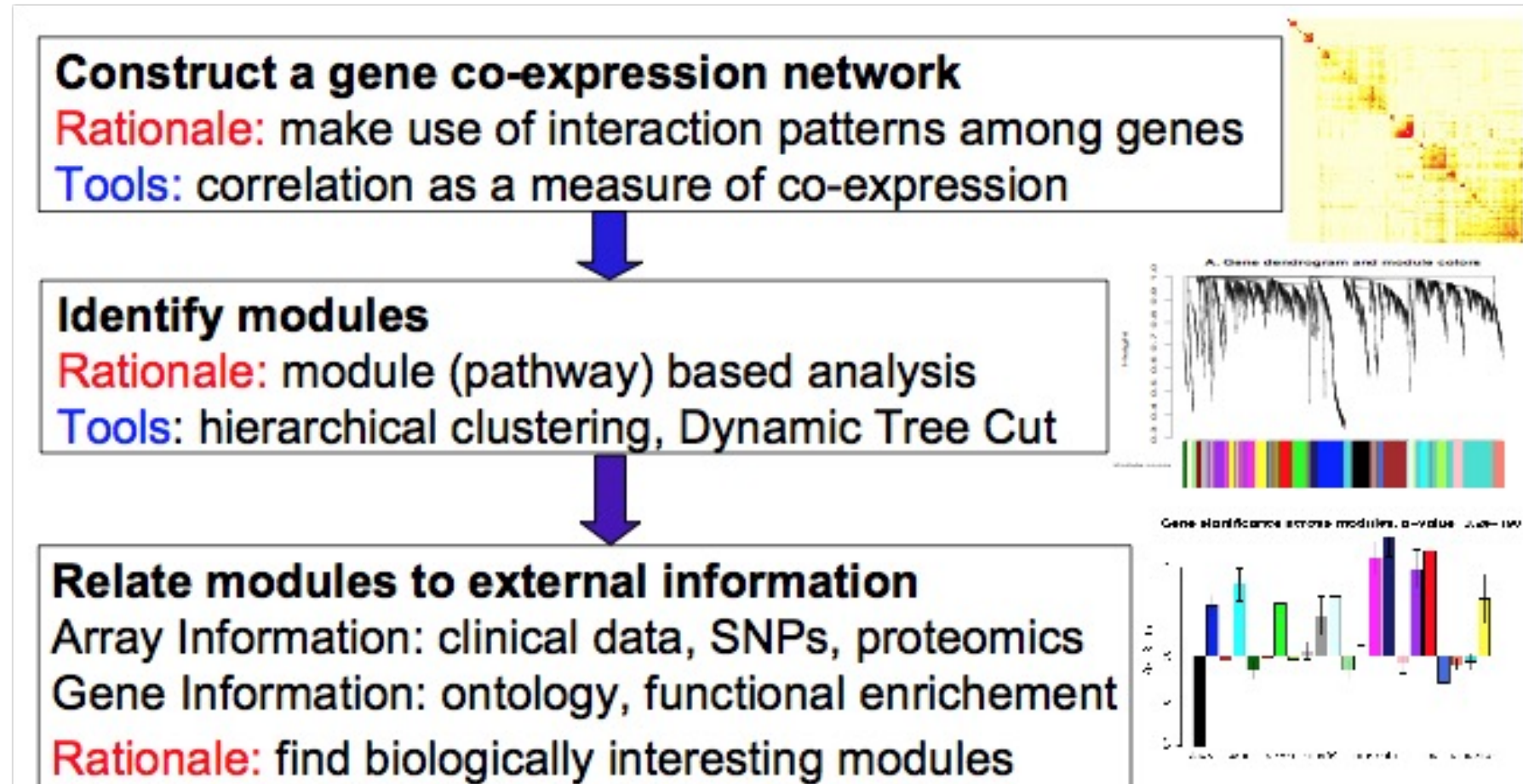
3D Complex
graph representation

Inferred interactions from shared behavior



<https://coxpresdb.jp/static/overview.shtml>

Weighted Gene Co-expression Network Analysis (WGCNA)

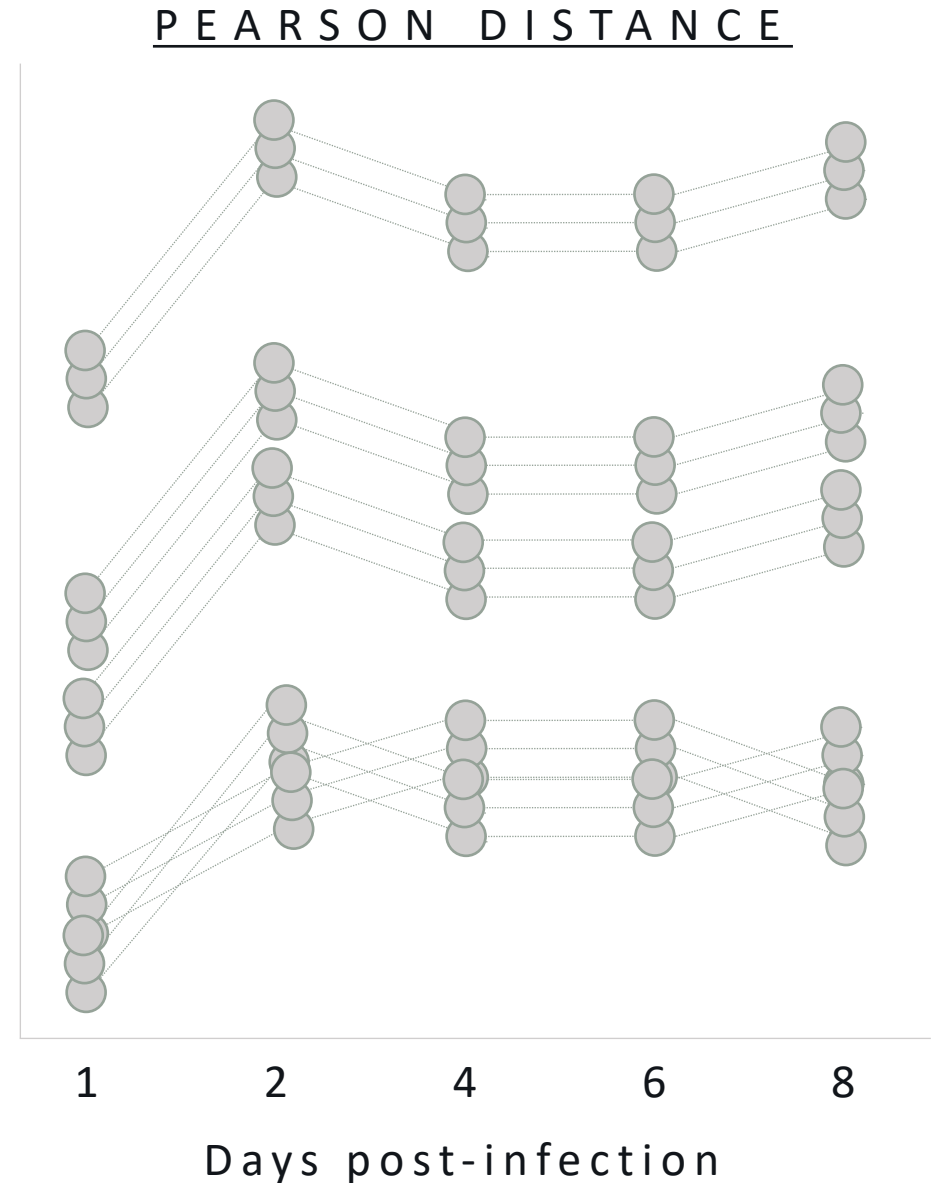
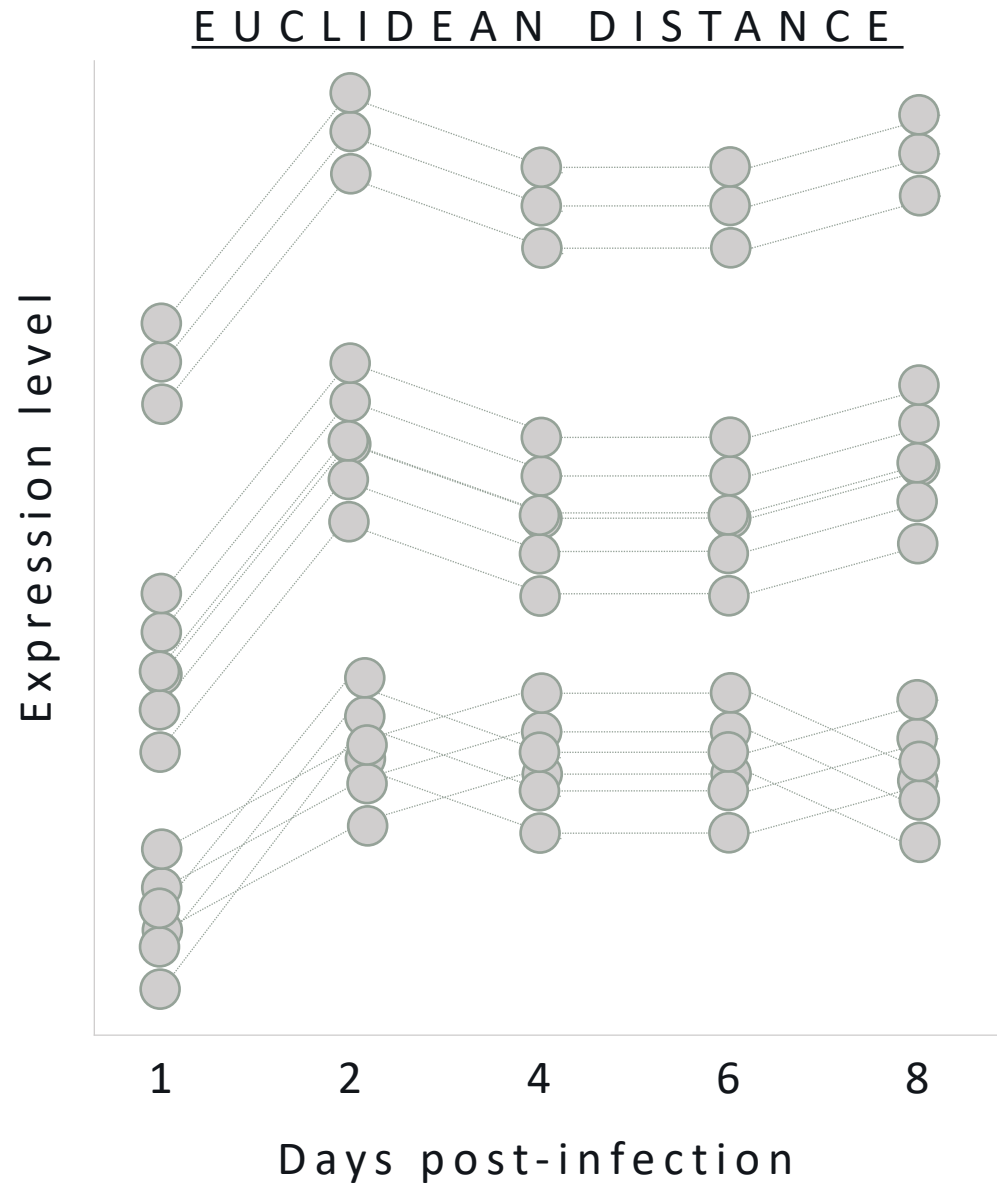


Clustering using WGCNA - Bioinformatics Team (BiolTeam) at the University of Texas - UT Austin Wikis (utexas.edu)

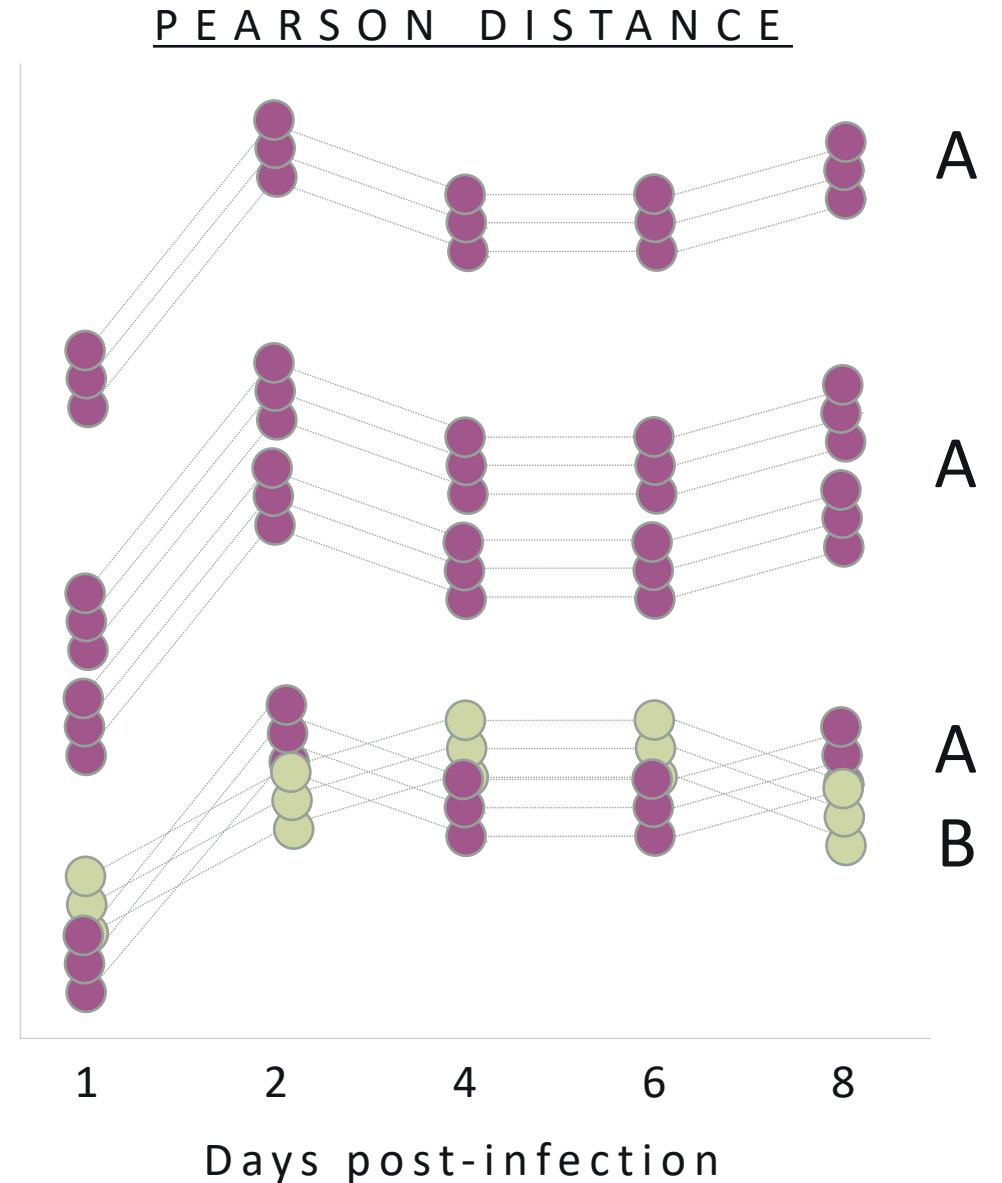
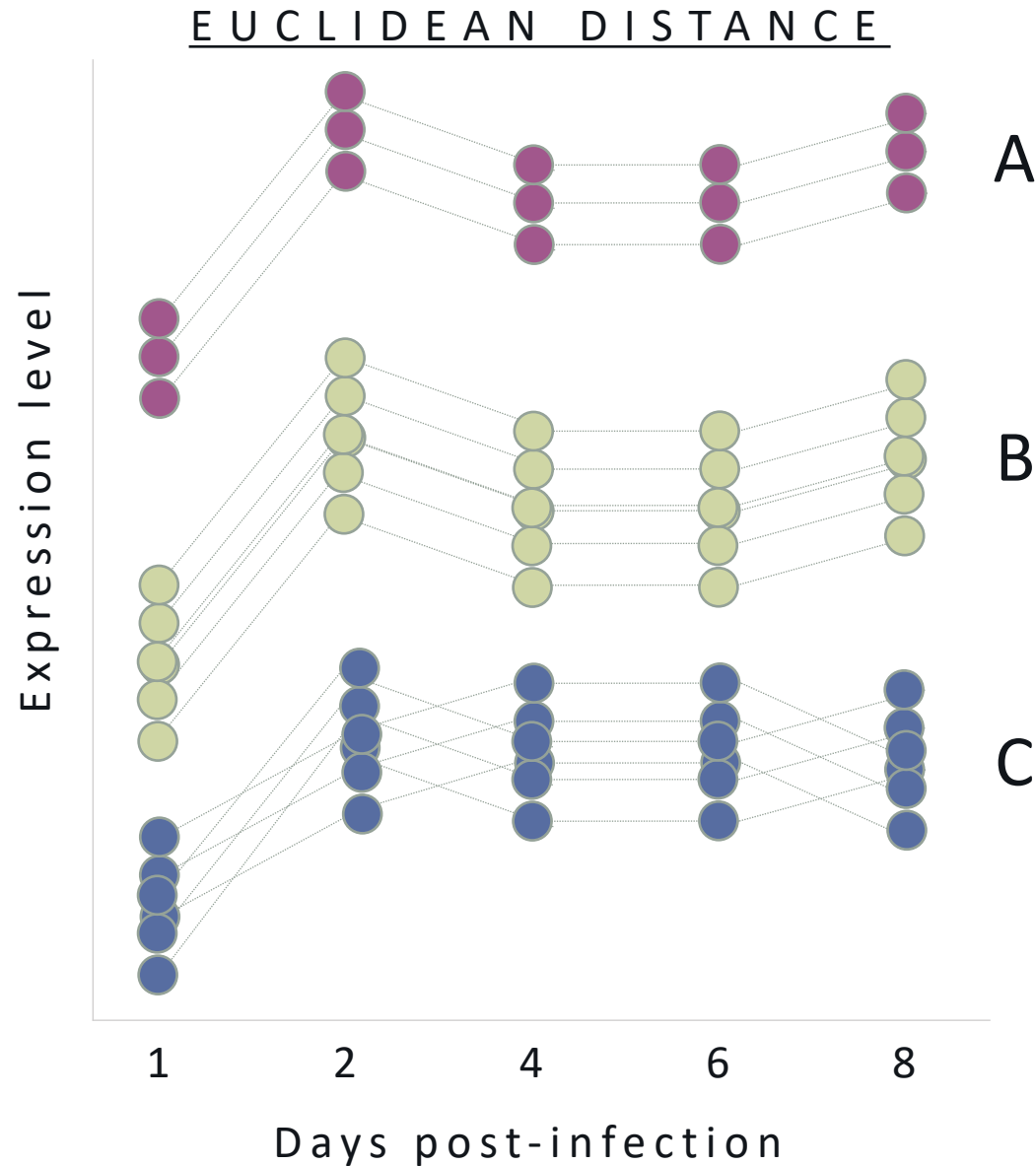
<https://bioinformaticsworkbook.org/tutorials/wgcna.html>

https://rstudio-pubs-static.s3.amazonaws.com/687551_ed469310d8ea4652991a2e850b0018de.html

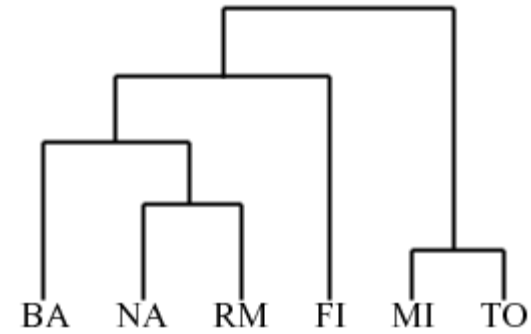
Comparing Distance Metrics for Co-expression



Comparing Distance Metrics for Co-expression



Grouping by distance with clustering



Grouping by distance with clustering

	BA	FI	MI	NA	RM	TO
BA	0	662	877	255	412	996
FI	662	0	295	468	268	400
MI	877	295	0	754	564	138
NA	255	468	754	0	219	869
RM	412	268	564	219	0	669
TO	996	400	138	869	669	0



Grouping by distance with clustering

	BA	FI	MI	NA	RM	TO
BA	0	662	877	255	412	996
FI	662	0	295	468	268	400
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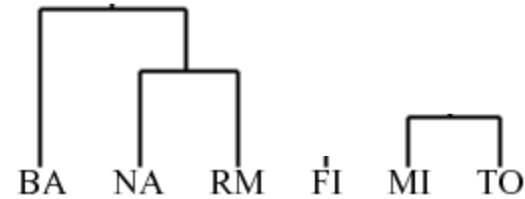
Grouping by distance with clustering

	BA	FI	MI/TO	NA	RM
BA	0	662	877	255	412
FI	662	0	295	468	268
MI/TO	877	295	0	754	564
NA	255	468	754	0	219
RM	412	268	564	219	0



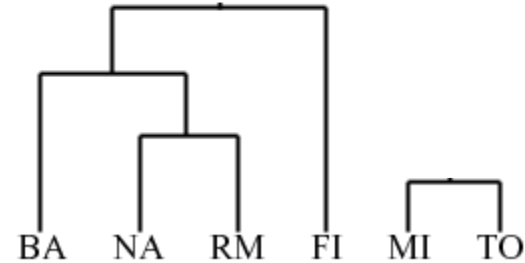
Grouping by distance with clustering

	BA	FI	MI/TO	NA/RM
BA	0	662	877	255
FI	662	0	295	268
MI/TO	877	295	0	564
NA/RM	255	268	564	0



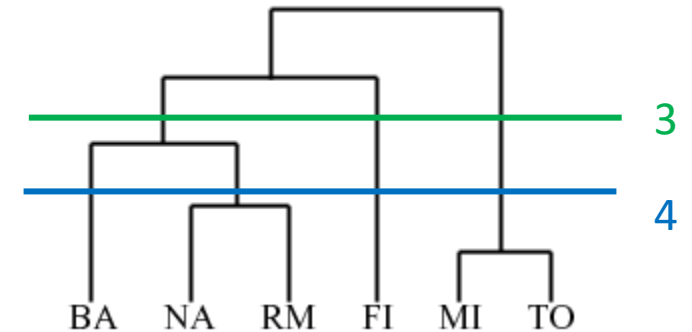
Grouping by distance with clustering

	BA/NA/RM	FI	MI/TO
BA/NA/RM	0	268	564
FI	268	0	295
MI/TO	564	295	0



Grouping by distance with clustering

	BA/FI/NA/RM	MI/TO
BA/FI/NA/RM	0	295
MI/TO	295	0



* Height of bar corresponds to how distant samples are from each other

** Choice of distance cutoff determines number of modules