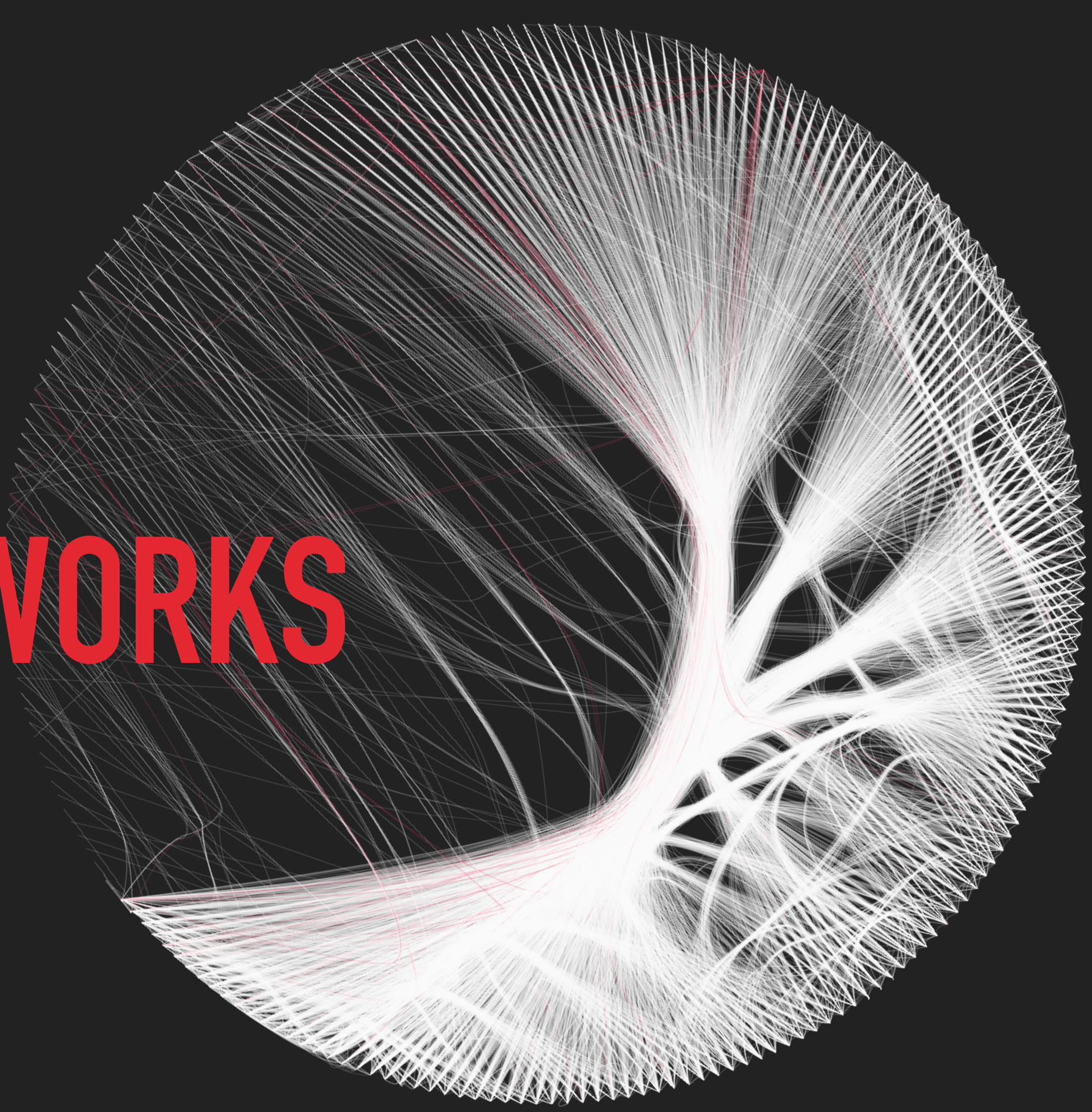
NETWORKS



NETWORK THEORY IN A NUTSHELL

Local similarity between two OTU time series: Suppose the two OTU normal transformed series are O_1 and O_2 with both of length n, i.e. $O_1 = O_{11}, O_{12}, \ldots, O_{1n}$ and $O_2 = O_{21}, O_{22}, \ldots, O_{2n}$. The positive score matrix $P_{n\times n}$ and negative score matrix $N_{n\times n}$ are calculated as follows:

(1) For $i, j = 1, \ldots, n$,
$P_{0,i} = P_{j,0} = 0$ and $N_{0,i} = N_{j,0} = 0$.

(2) For $i, j = 1, \ldots, n$ with $|i - j| \le D$,
$P_{i+1,j+1} = \max\{0, P_{i,j} + O_{1,i+1} \cdot O_{2,j+1}\}$ and
$N_{i+1,j+1} = \max\{0, N_{i,j} - O_{1,i+1} \cdot O_{2,j+1}\}$.

(3) $P(O_1, O_2) = \max_{1\le i,j\le n} P_{i,j}$ and
$N(O_1, O_2) = \max_{1\le i,j\le n} N_{i,j}$.

(4) MaxScore(O_1,O_2) = max($P(O_1,O_2)$, $N(O_1,O_2)$) and
Flag(O_1,O_2) = sgn($P(O_1,O_2) - N(O_1,O_2)$).

$$\sum_{k=K}^{\infty}\left(\frac{1}{x^2}+\frac{1}{(2k+1)^2\pi^2}\right)\exp\left(-\frac{(2k+1)^2\pi^2}{2x^2}\right) < \frac{2}{x^2}\sum_{k=K}^{\infty}\exp\left(-\frac{(2k+1)\pi^2}{2x^2}\right) \tag{4}$$

$$= \frac{2\exp\left(-\frac{(2K+1)\pi^2}{2x^2}\right)}{x^2\left(1-\exp\left(-\frac{2\pi^2}{2x^2}\right)\right)}.$$

Thus, for an error threshold β, we can choose K so that

$$\frac{16\exp\left(-\frac{(2K+1)\pi^2}{2x^2}\right)}{x^2\left(1-\exp\left(-\frac{2\pi^2}{2x^2}\right)\right)} \le \beta. \tag{5}$$

Then we approximate $P(R_n/(\sigma\sqrt{n}) \ge x)$ by

$$1 - 8\sum_{k=0}^{K-1}\left(\frac{1}{x^2}+\frac{1}{(2k+1)^2\pi^2}\right)\exp\left(-\frac{(2k+1)^2\pi^2}{2x^2}\right). \tag{6}$$

Trump Connections

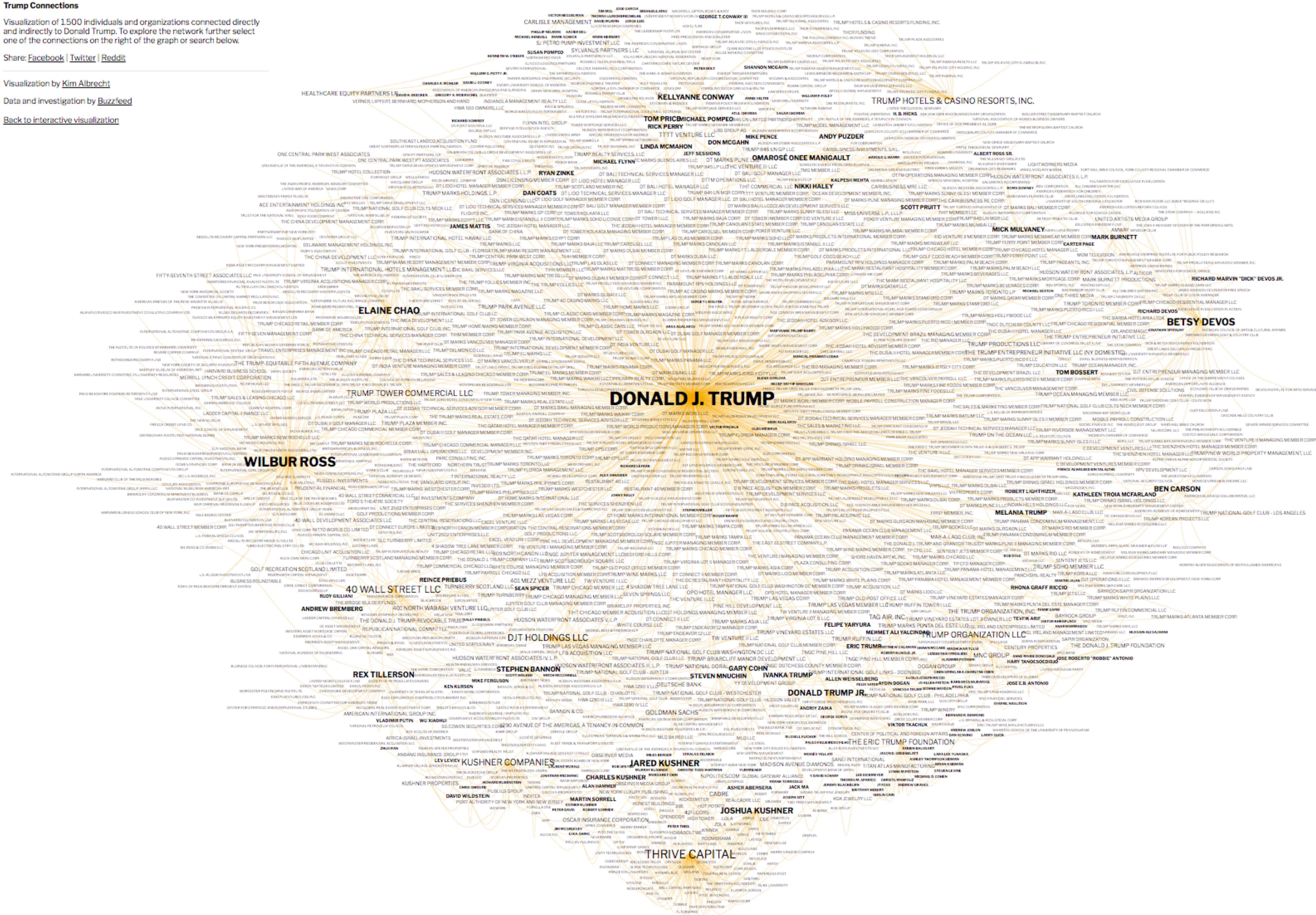
Visualization of 1.500 individuals and organizations connected directly and indirectly to Donald Trump. To explore the network further select one of the connections on the right of the graph or search below.

Share: Facebook | Twitter | Reddit

Visualization by Kim Albrecht

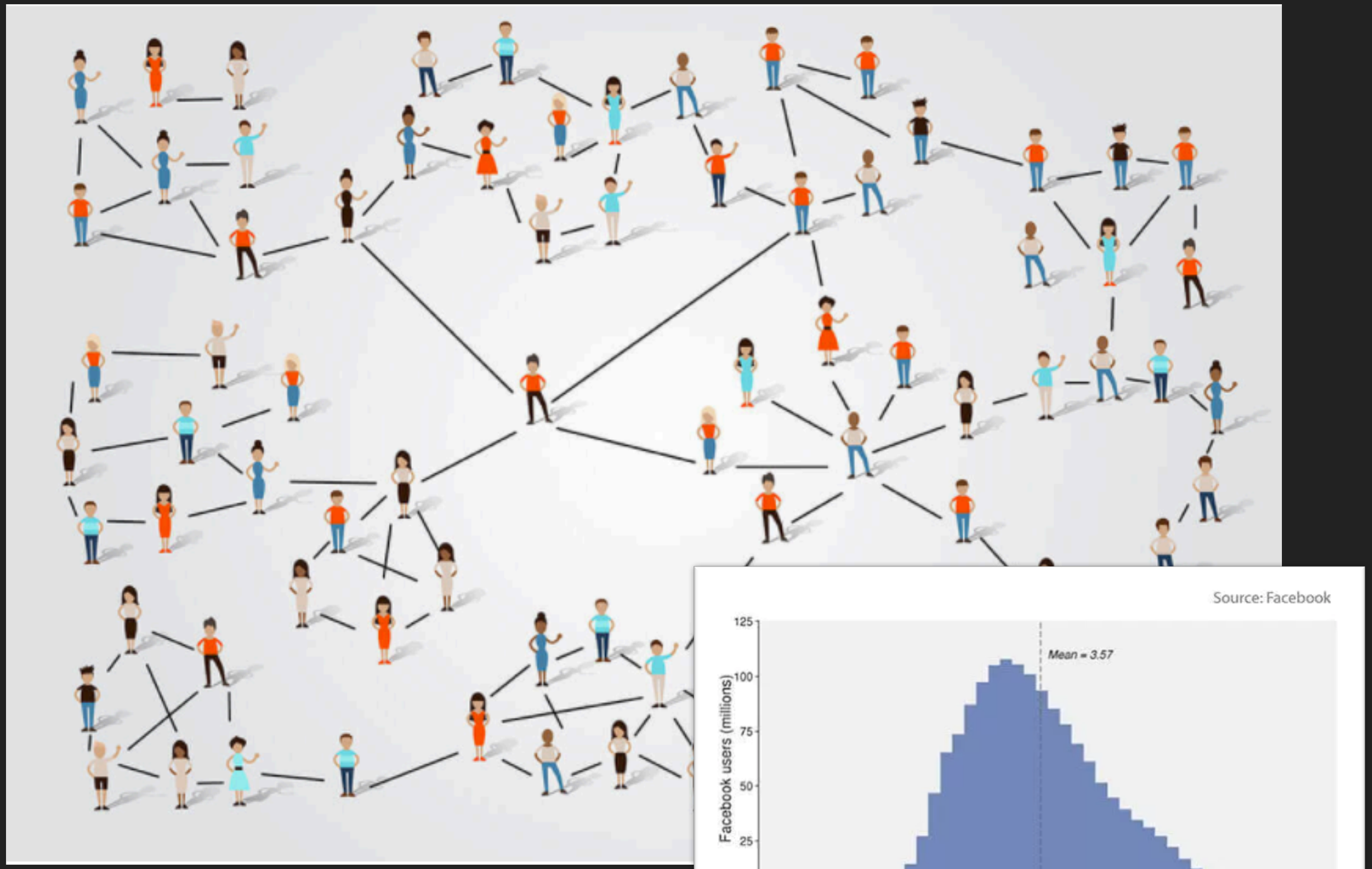
Data and investigation by Buzzfeed

Back to interactive visualization

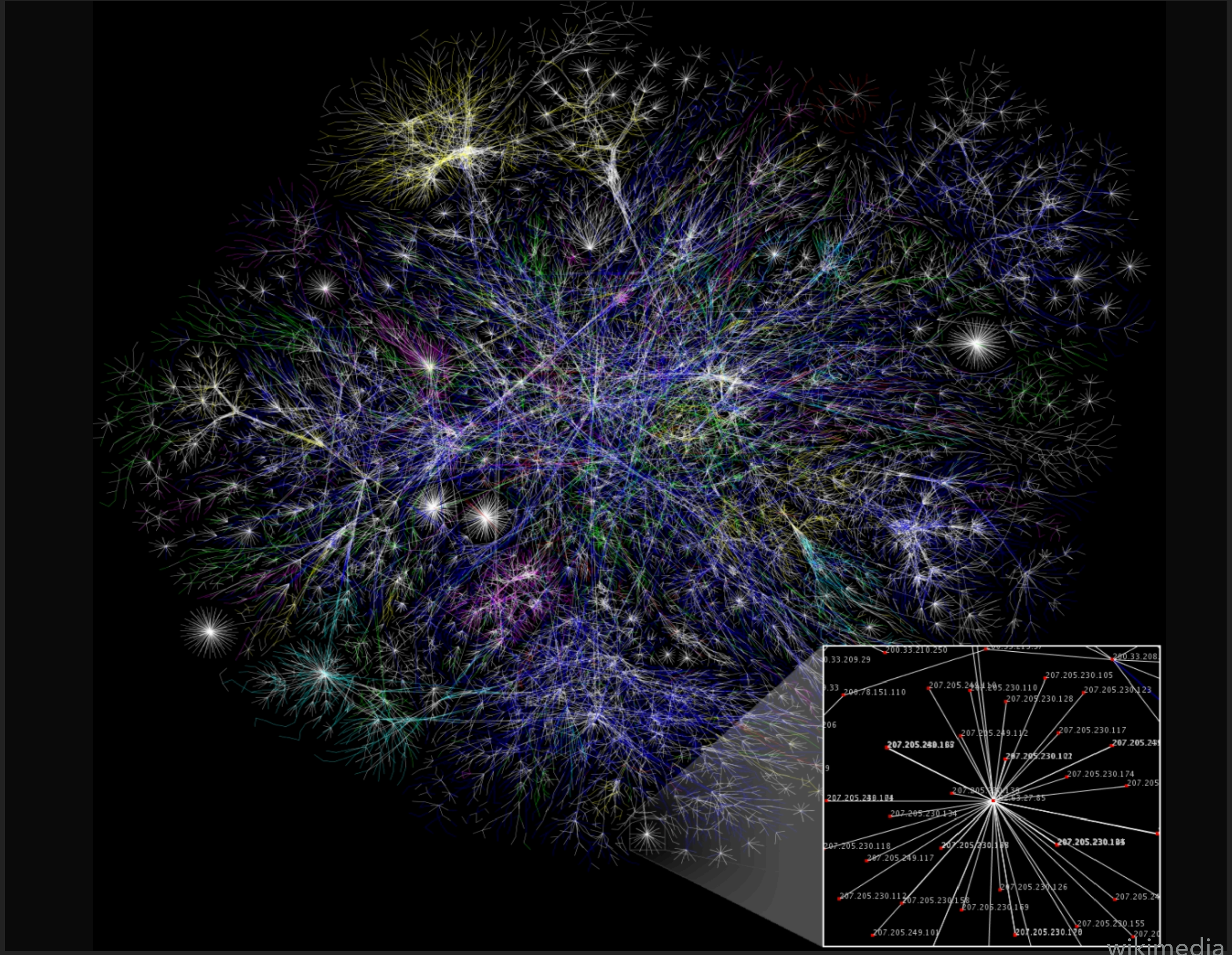


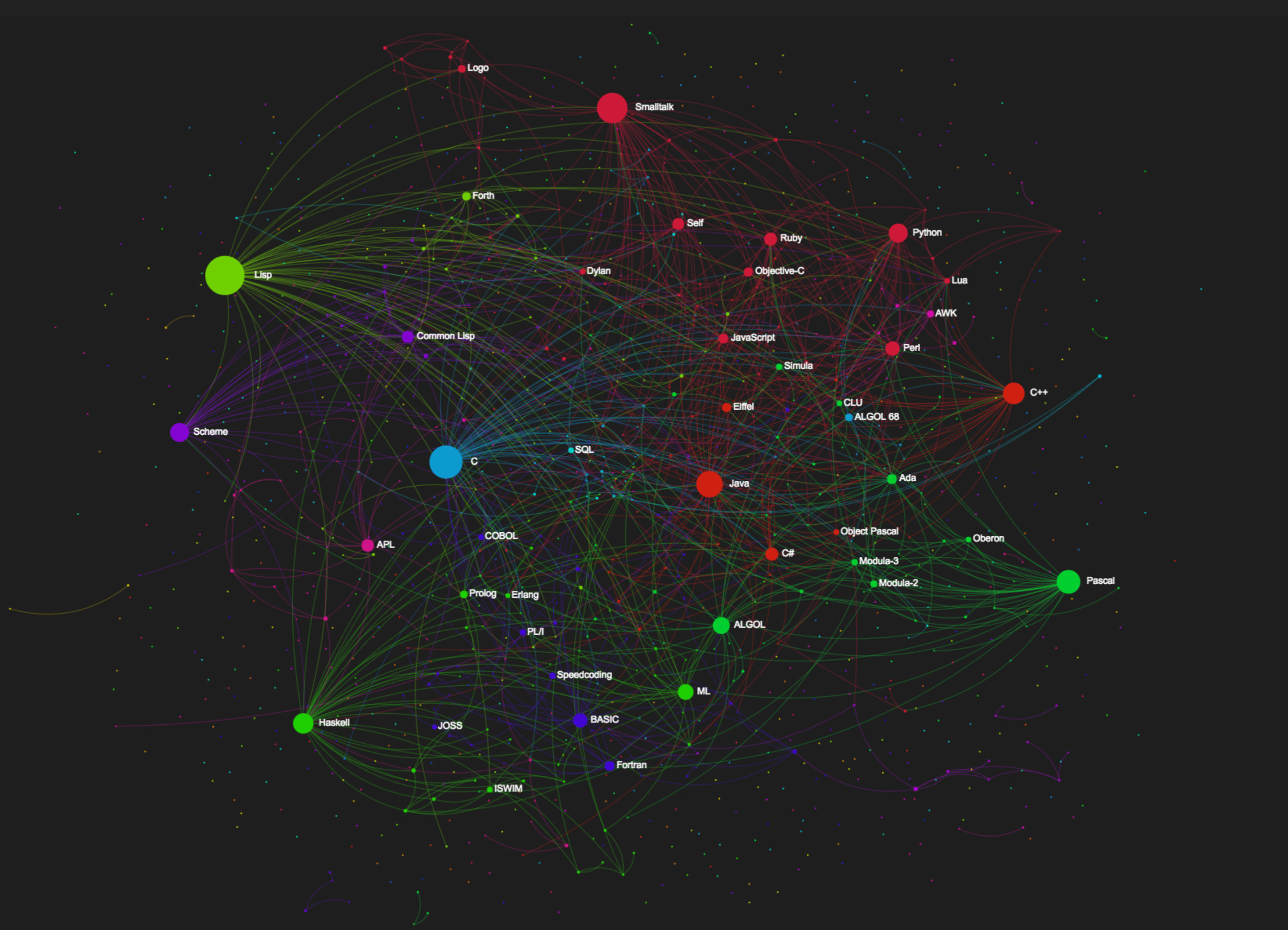
WHY NETWORKS?

- Networks are perfect for exploring relational data
  - Facebook friends
  - Kevin Bacon game
  - Erdöz number
- Visualise and analyse high-dimensional datasets with complex distribution
- Exploration of network topology can give insight into associations and interactions between the parts (nodes) in the network



http://blog.hackerearth.com/six-degrees-separation-theory-meaning


200.33.210.250
207.205.230.105
207.205.230.110
207.205.230.123
207.205.230.128
207.205.249.112
207.205.230.117
207.205.230.174
207.205.230.134
207.205.230.118
207.205.249.117
207.205.230.126
207.205.230.155
207.205.230.120


Logo
Smalltalk
Forth
Self
Ruby
Python
Lisp
Dylan
Objective-C
Lua
AWK
Common Lisp
JavaScript
Perl
Simula
C++
Eiffel
CLU
ALGOL 68
Scheme
C
SQL
Java
Ada
Object Pascal
Oberon
C#
Modula-3
Modula-2
Pascal
APL
COBOL
Prolog
Erlang
ALGOL
PL/I
Speedcoding
ML
Haskell
JOSS
BASIC
Fortran
ISWIM

BACKGROUND

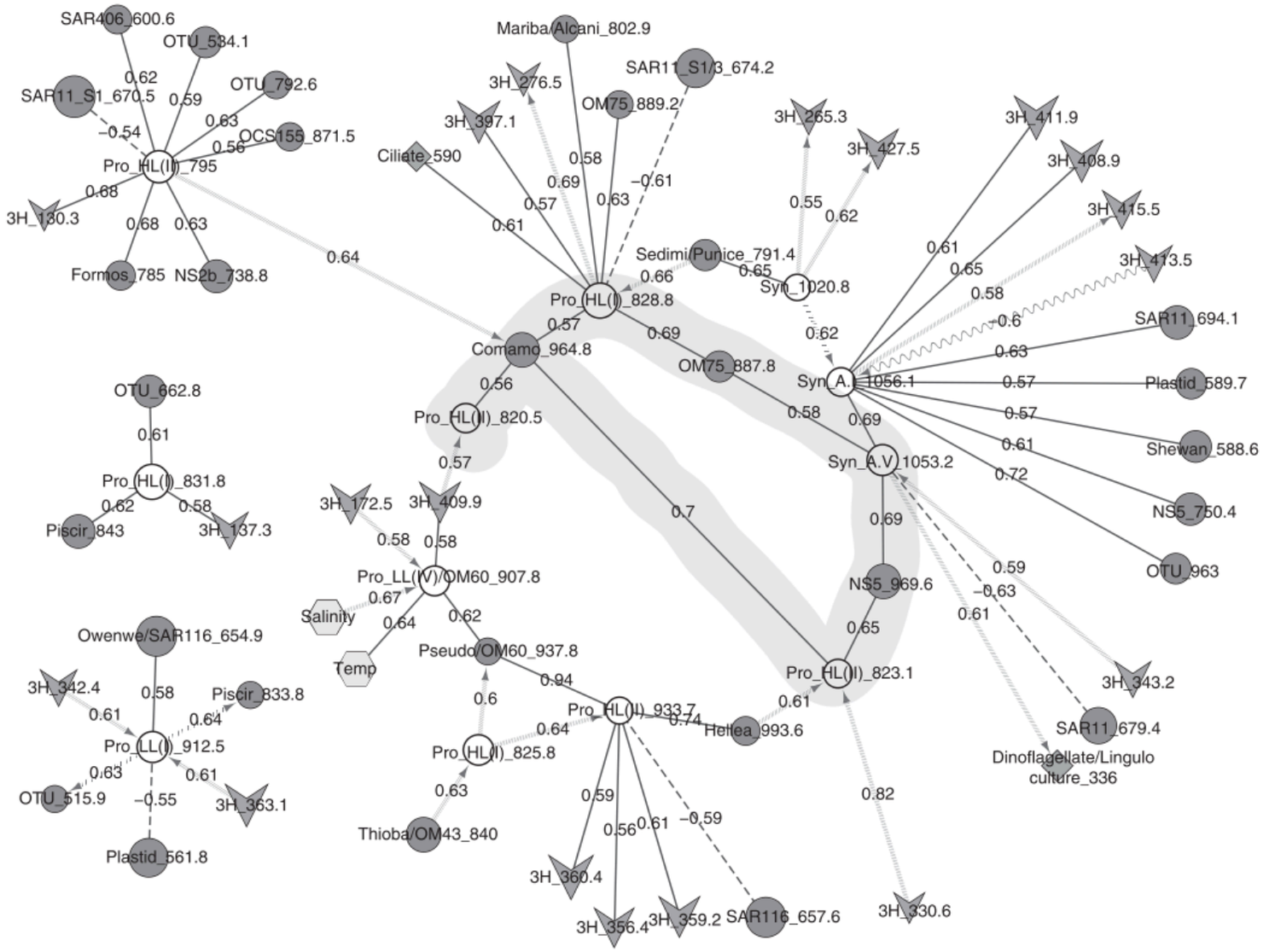


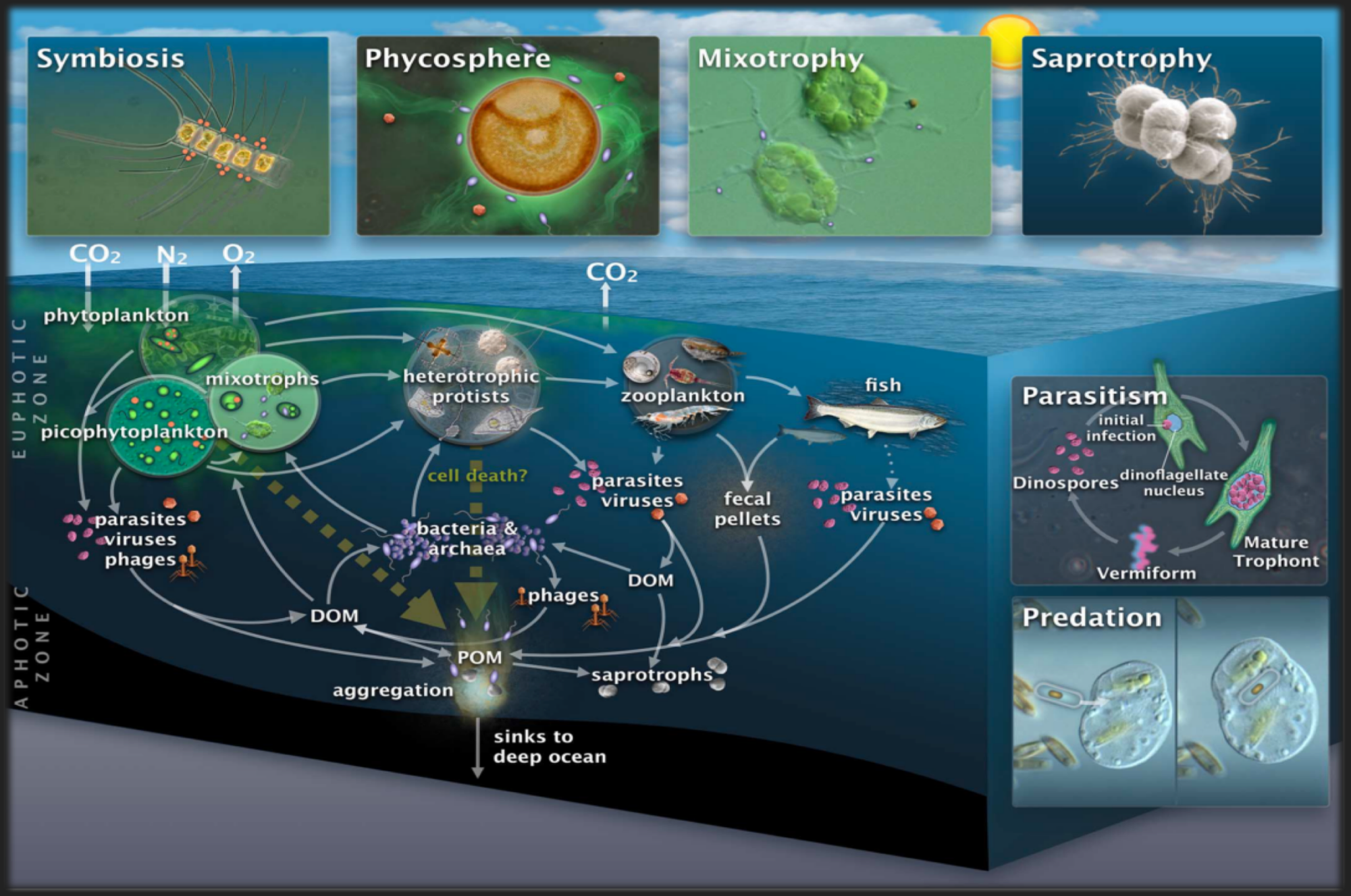
Figure 5 Cyanobacterial OTU correlations to other microbial OTUs reveal potential lytic virus–host relationships, grazing and temporal trends. *Cyanobacteria* OTUs are noted as white circles and labeled as *Prochlorococcus* (Pro) or *Synechococcus* (Syn), followed by ecotype designation (HL: high light; LL: low light; A/B: *Synechococcus* group). All other nodes are bacteria, circles; protists, diamonds; viruses, v-shapes; abiotic, hexagons. Node labels indicate an abbreviated identity (where available) and fragment length. Solid lines are positive correlations with no delay; dashed lines, negative correlations with no delay; sine-wave lines, negative-delayed correlations; and forward-slashed lines, positive-delayed correlations. Arrows point toward the lagging OTU.

Chow et al (2014)

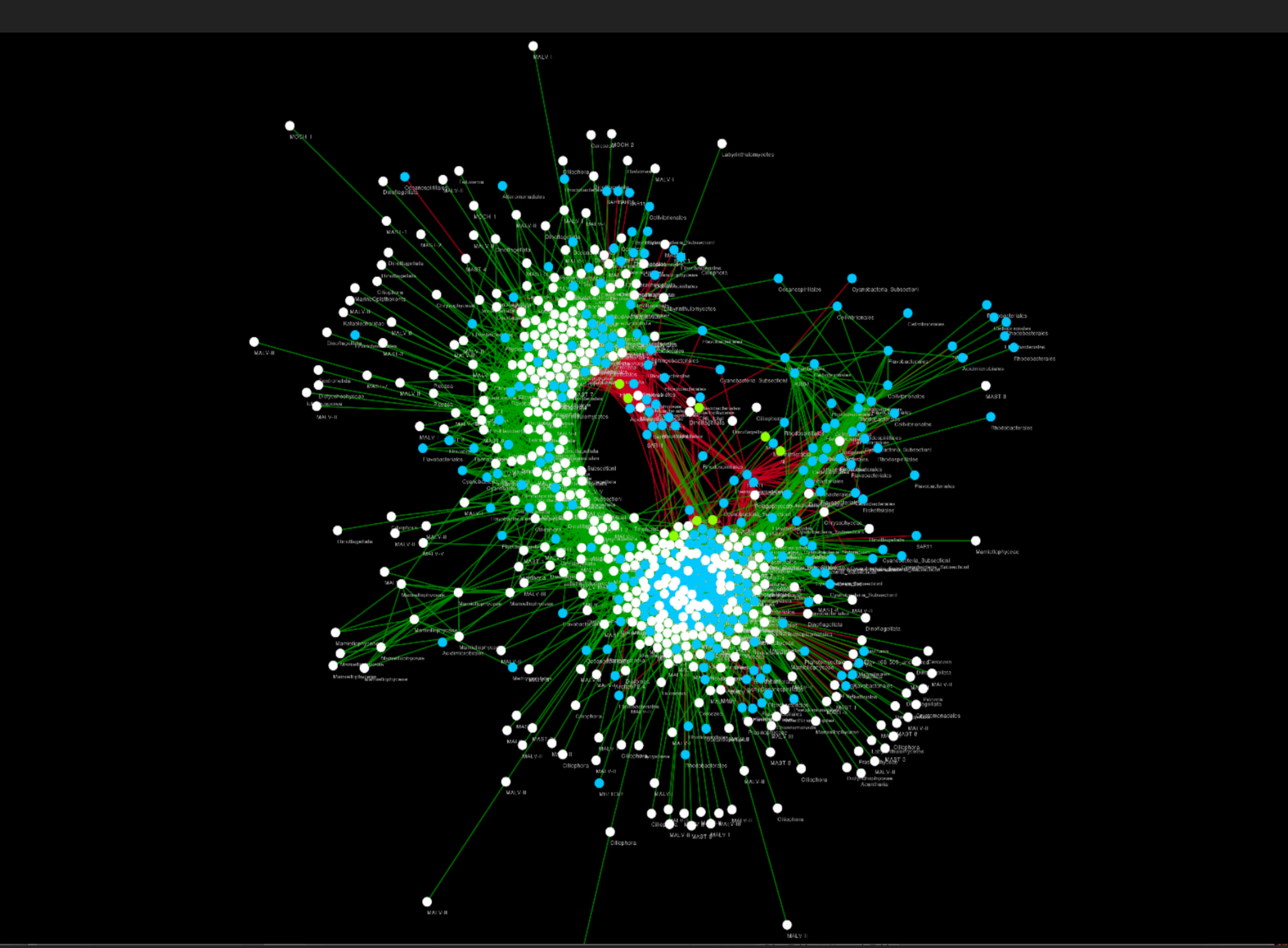
WHY NETWORKS?

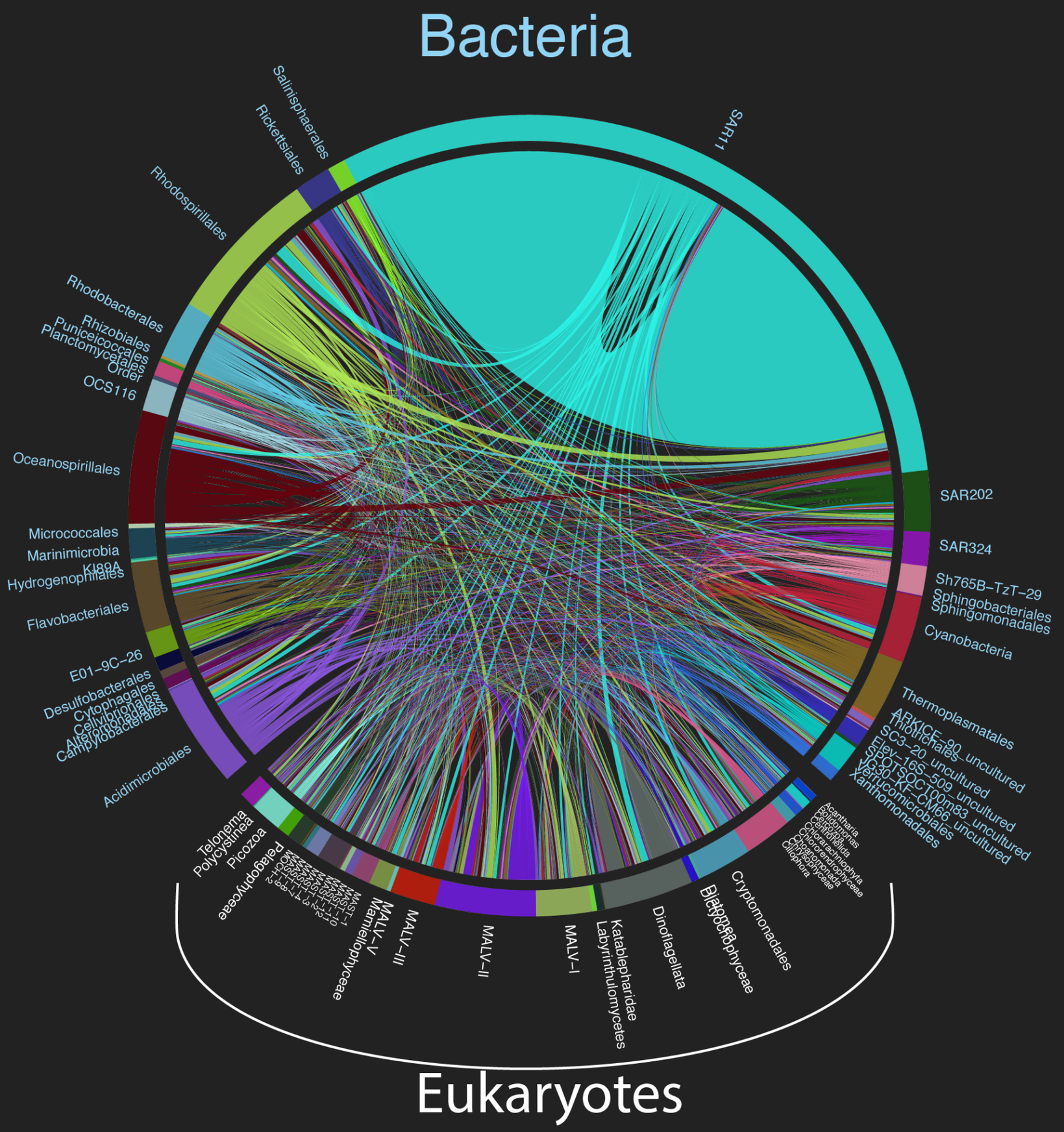
- For microbial data
  - Networks can help us find patterns behind small- and large-scale ecological and evolutionary processes
- Moving from from identification of parts (species classification, diversity, community composition, geographical distribution etc.) to connections of parts.

FOODWEBS



Worden et al (2015)


MALV I
MOCH 1
MOCH 2
Labyrinthulomycetes
Ciliophora
Oceanospirillales
Cyanobacteria_Subsection I
Cellvibrionales
Flavobacteriales
Rhodobacterales
MAST-1
MAST-2
MAST-4
MALV-II
MALV-III
MALV-V
Dinoflagellata
Rhodospirillales
Sphingobacteriales
Acidimicrobiales
Mamiellophyceae
Chrysophyceae
SAR11
MAST 2
MAST 8
Cryptomonadales
Thalassiosirales
Prasinophyceae
Acantharea

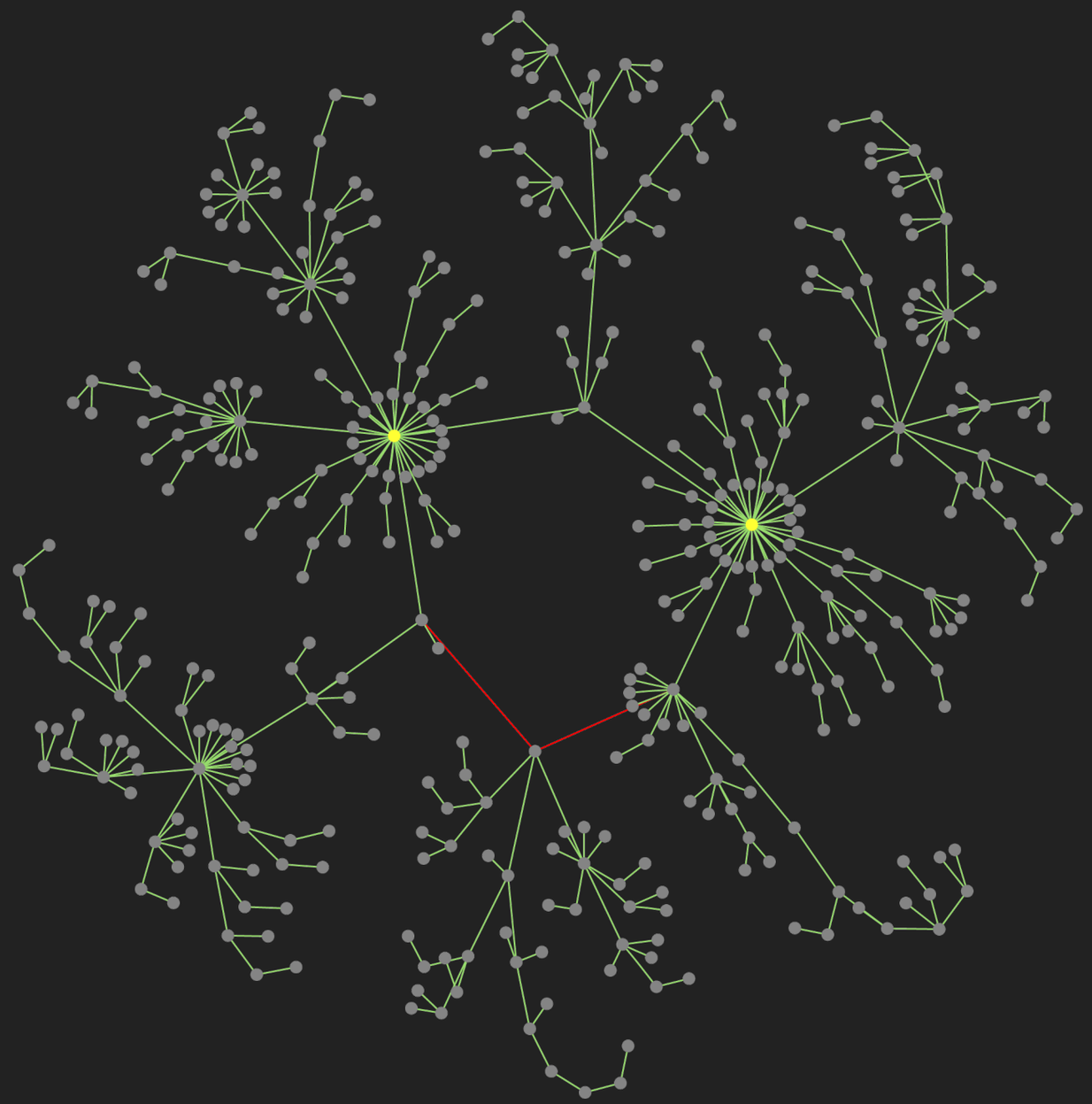

Bacteria
Salinisphaerales
Rickettsiales
Rhodospirillales
Rhodobacterales
Rhizobiales
Puniceicoccales
Planctomycetales
Order
OCS116
Oceanospirillales
Micrococcales
Marinimicrobia
Kiloo
Hydrogenophilales
Flavobacteriales
E01–9C–26
Desulfobacterales
Cytophagales
Cellvibrionales
Alteromonadales
Campylobacterales
Acidimicrobiales
SAR11
SAR202
SAR324
Sh765B–TzT–29
Sphingobacteriales
Sphingomonadales
Cyanobacteria
Thermoplasmatales
ARKICE–90_uncultured
Thiotrichales
SC3–20_uncultured
Elev–16S–509_uncultured
SPOTSOCT00m83_uncultured
JG30–KF–CM66_uncultured
Verrucomicrobiales
Xanthomonadales
Acantharia
Centrohelida
Chlorarachniophyta
Chlorarachniophyceae
Chlorophyceae
Chlorophyta
Cryptomonadales
Bicosoecophyceae
Dinoflagellata
Katablepharidae
Labyrinthulomycetes
MALV–I
MALV–II
MALV–III
MALV–V
Mamiellophyceae
Pelagophyceae
Picozoa
Polycystinea
Telonema
Eukaryotes

MICROBIAL NETWORKS

- Associations/co-occurrence between taxa can reveal:
  - similar response to environmental variation
  - similar niche preference
  - direct interactions between organisms, e.g. host/symbiont, prey/predator
  - important relationships in the community
    - key species (hubs) and assemebalges of interacting species (modules)

NETWORK FEATURES – SOME TERMINOLOGY

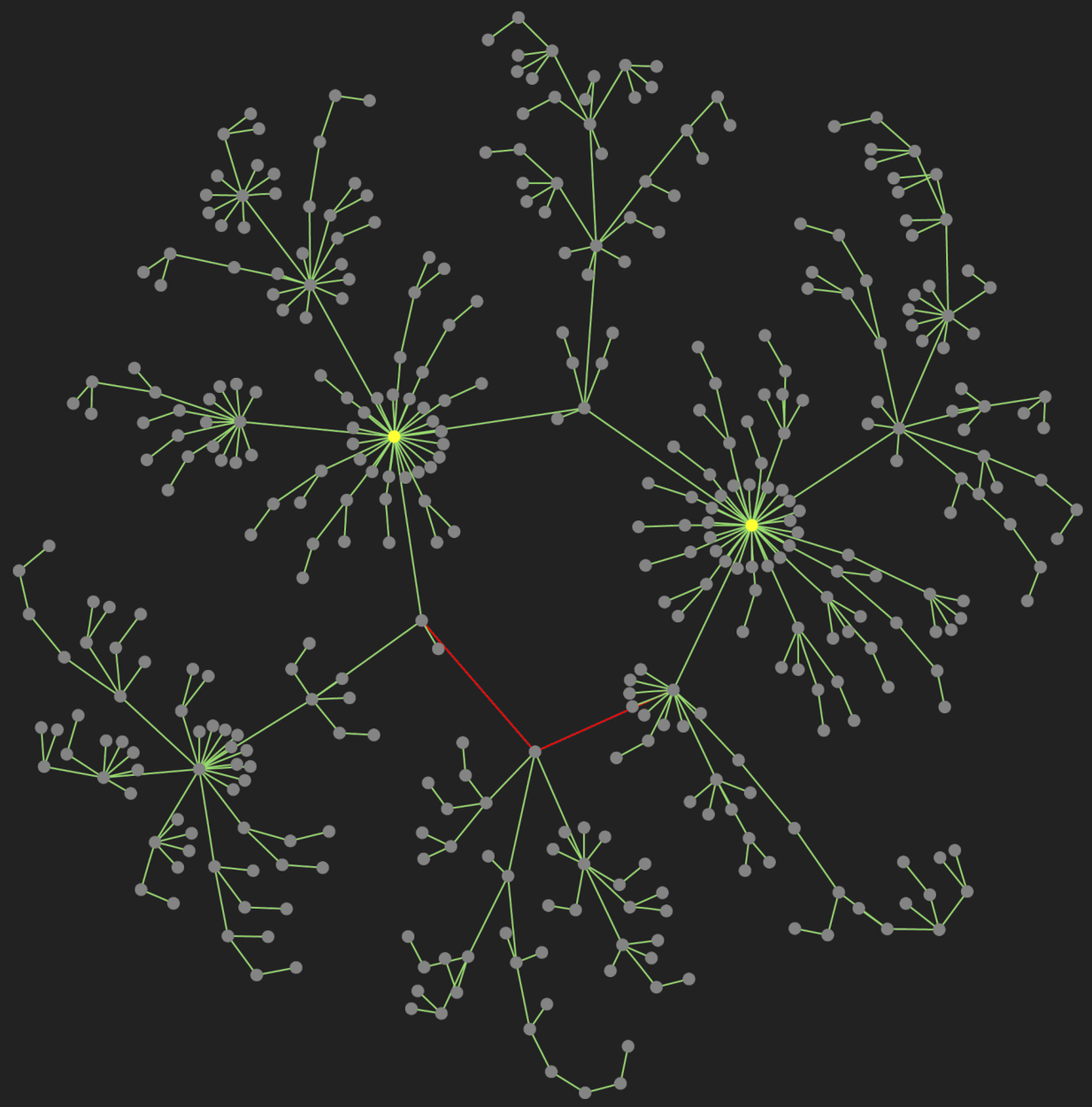
- Nodes (dots) represents OTUs and environmental varaibles
- Edges (lines) connects the OTUs, signifying co-occurrence (or interaction)
- By analysing the distribution of the nodes, the edges and the topology of the network we can hopefully say something about the co-occurrence or interactions between species in the network.



Krabberød et al. (2017)

NETWORK FEATURES – SOME TERMINOLOGY

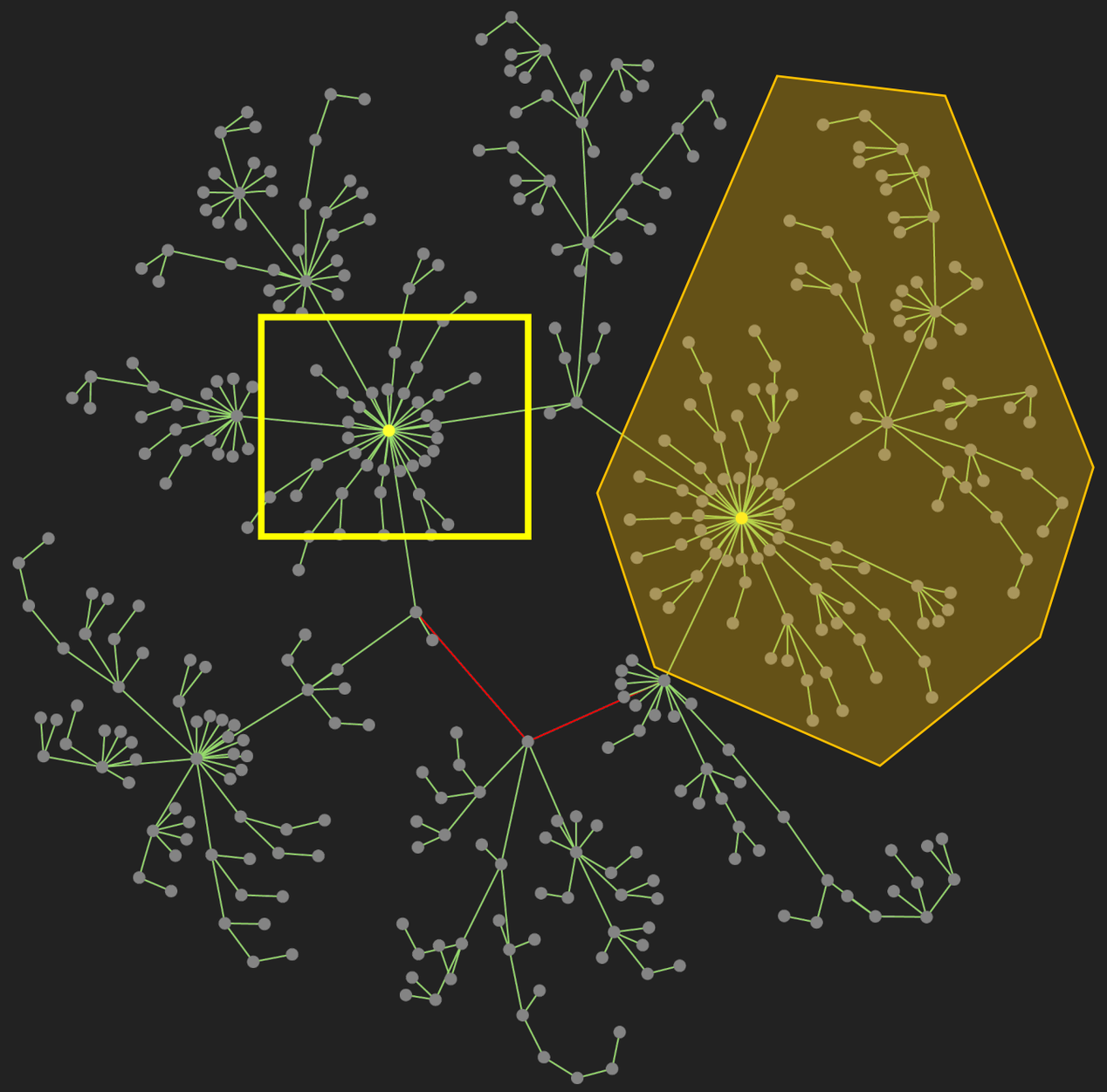
- Association network: network built using positive or negative correlation between taxa
- Degree: number of edges connected to a node
- Degree distribution: cumulative distribution of node's degrees
- Distance: shortest path between two nodes
- Characteristic path length: mean number of steps along the shortest paths for all node-pair in a network (distance average)
- Clustering coefficient: a measure of the clustering of nodes in a network.



Krabberød et al. (2017)

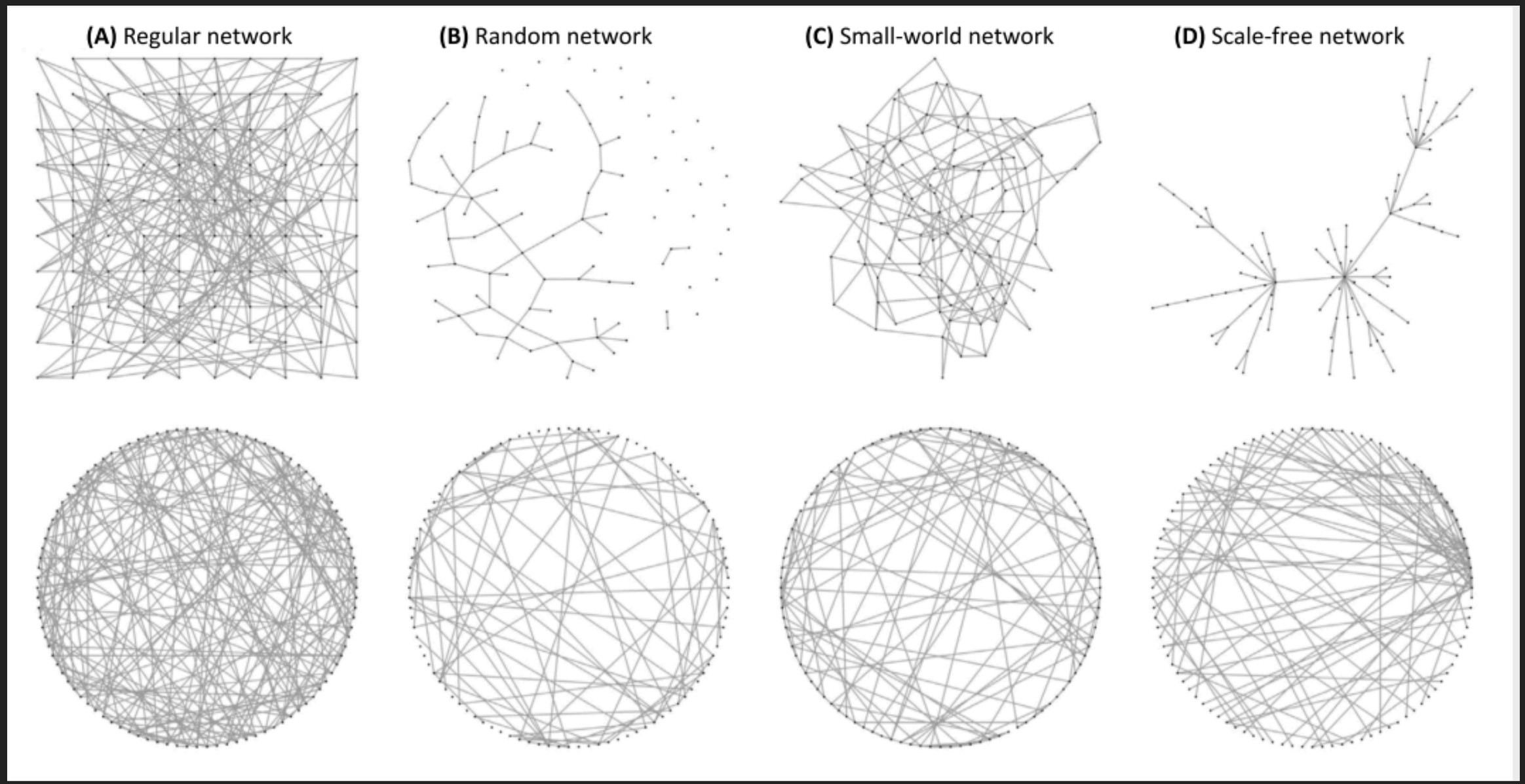
NETWORK FEATURES – SOME TERMINOLOGY

- Hubs are highly connected nodes, often key species in the network.
- Modules: sets of nodes that are more linked to each other than the rest of the network.



Krabberød et al. (2017)

NETWORK TOPOLOGY



Layeghifard et al (2017)

NETWORKS CONSTRUCTION

- Methods for network construction are many and varies in speed, accuracy and application,
  - for more see Faust et al (2012), Layeghifard et al. (2017)
- Dissimilarity based, for instance Bray-Curtis
- Correlation-based; Pearson, Spearman
- Regression-based
- Probabilistic Graphical Models

SOFTWARE

- Software for inferring networks
  - SparCC (Friedman and Alm, 2012) - For compositional data
  - CoNet (Faust et al. 2012)
  - WGCNA - Weighted correlation network analysis, often used to find clusters of co-expressed genes. (Langfelder and Horvath, 2008)
  - eLSA - Extended local similarity analysis (Ruan et al. 2006, Xia et a.l 2015)
    - For time series

  - etc.
  - etc.

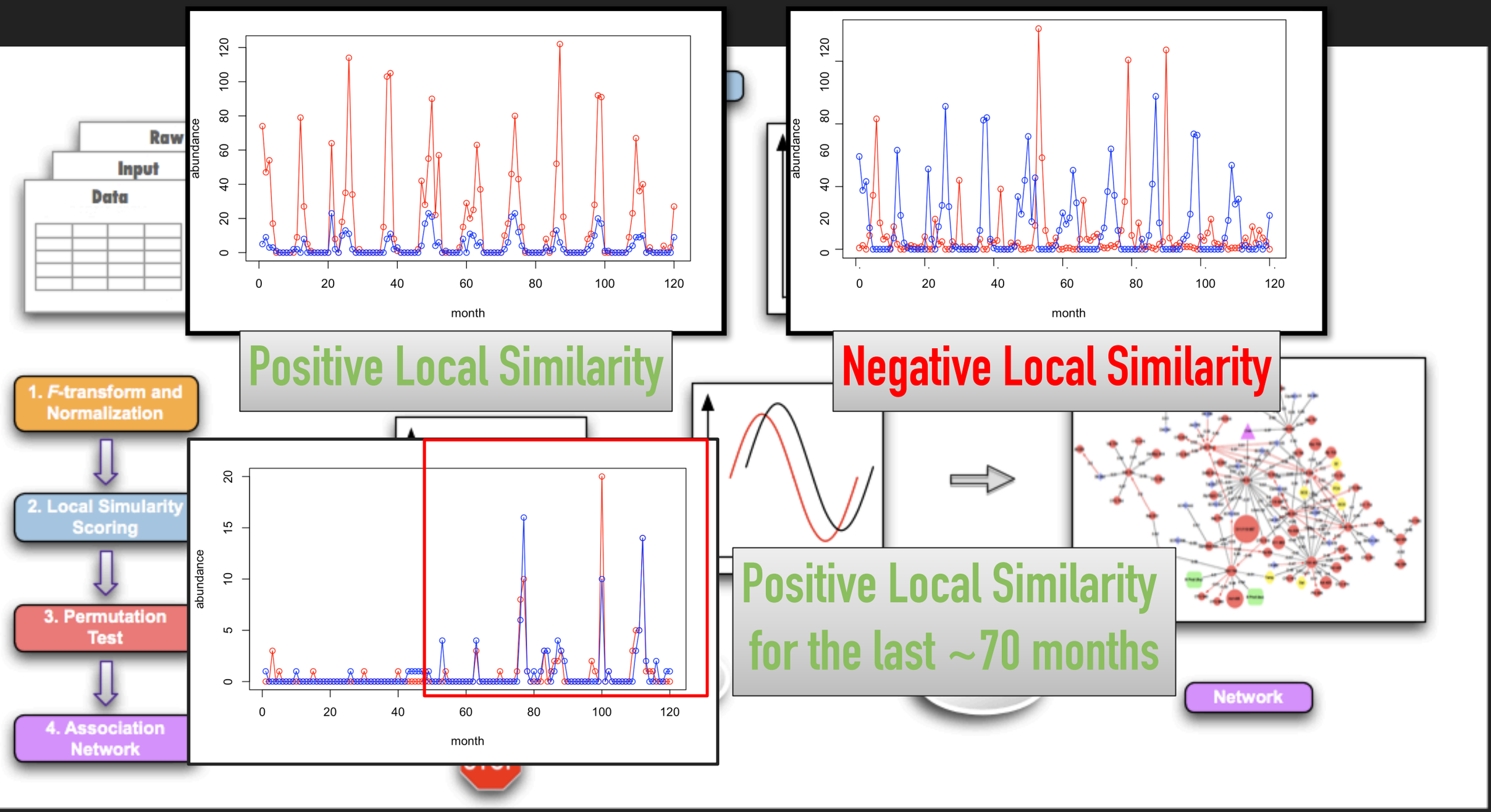
TYPES OF NETWORKS

- Spatial sampling:
  - larger geographic coverage but unless samples are taken at the same time, each sample is a snapshot.
- Temporal
  - Smaller geographic coverage, but multiple data points for the same location. Allows following microbial communities, and their changes, in time.

ELSA – EXTENDED LOCAL SIMILARITY ANALYSIS

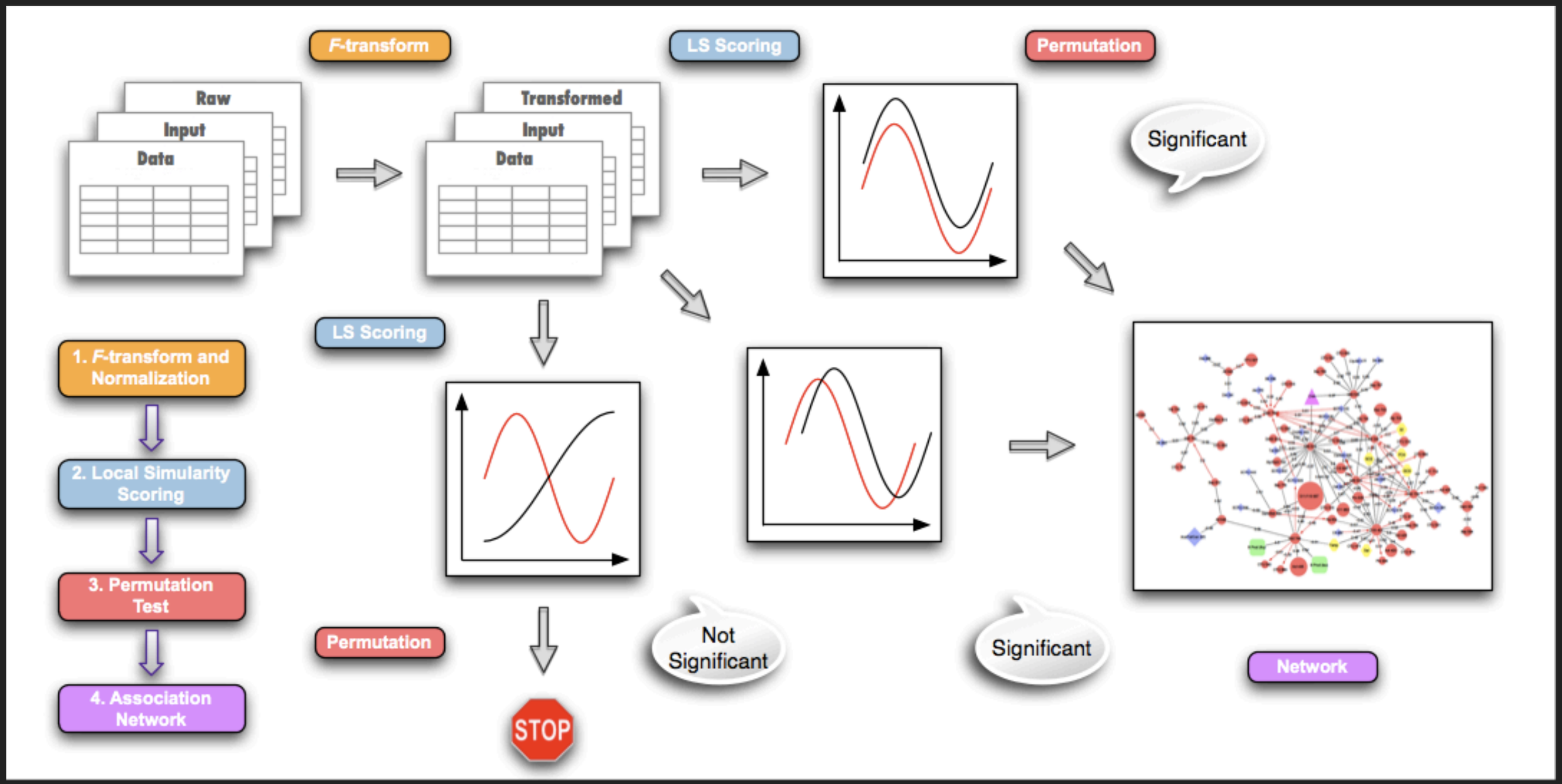
- Designed for time series
- Pairwise comparison between OTUs (and OTUs and environmental variables; n)
  a total of n(n-1)/2 comparisons (edges)
- Multiple co-occurrences and co-exclusions in the same community
- Can incorporate time delays (the maximum allowed time delay has to be specified)
- https://bitbucket.org/charade/elsa/wiki/FAQ.wiki

WORKFLOW



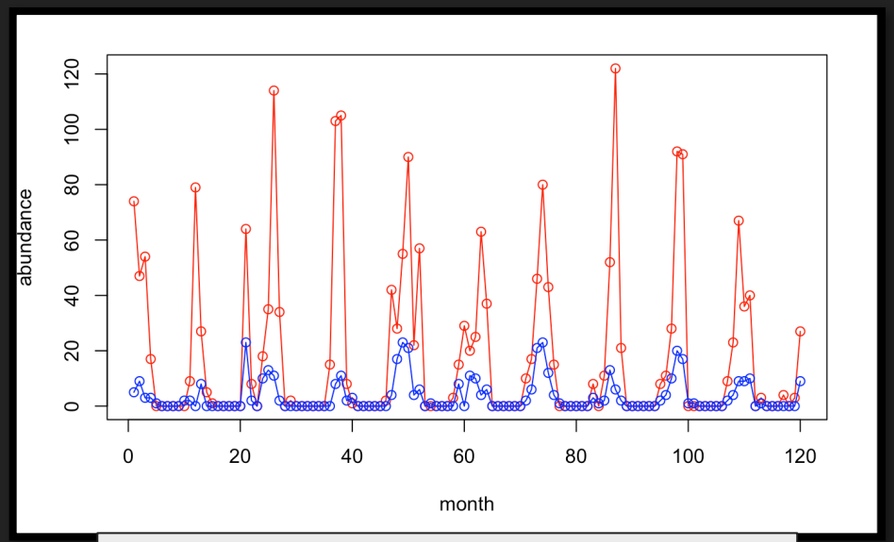
Ruan et al. (2006), Xia et al. (2013, 2015)

WORKFLOW

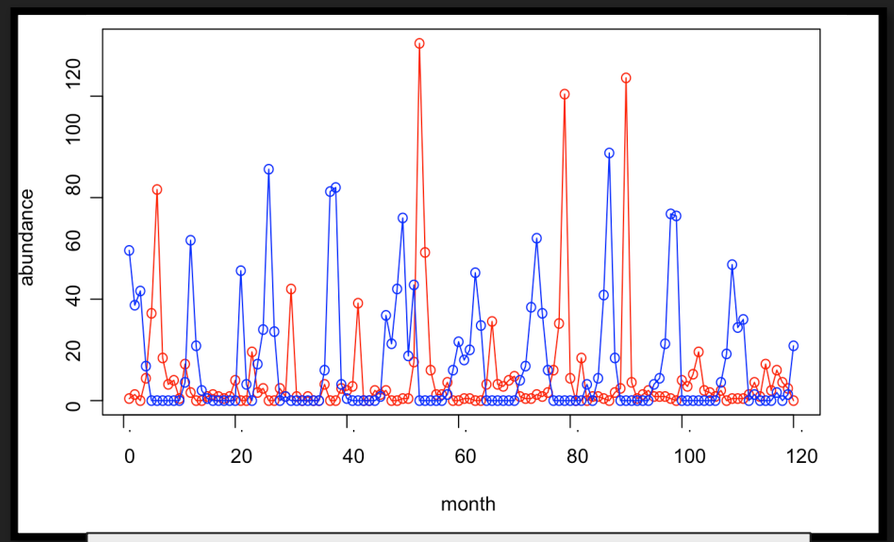


Ruan et al. (2006), Xia et al. (2013, 2015)

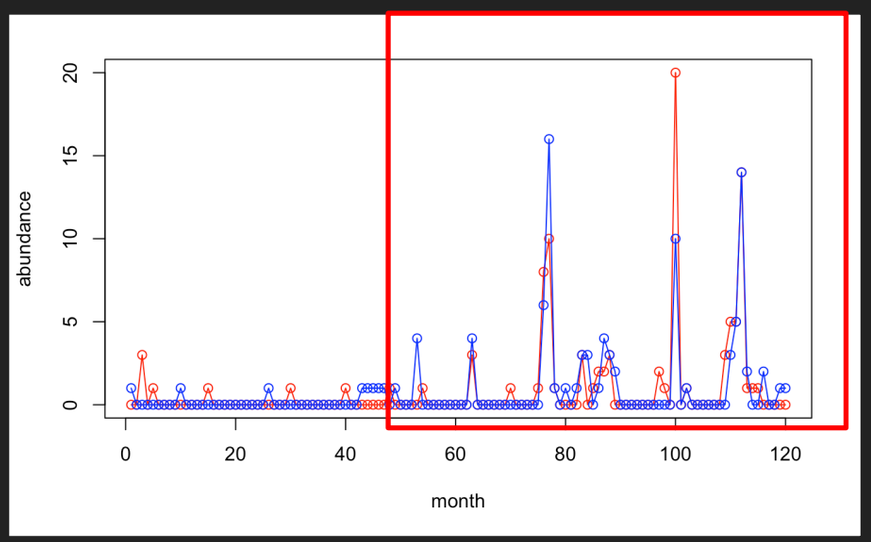
WORKFLOW



Positive Local Similarity



Negative Local Similarity



Positive Local Similarity for the last ~70 months

Ruan et al. (2006), Xia et al. (2013, 2015)

ELSA – THE PARAMETERS

- Specify the number of time spots (***s***) and if you have replicates (***r***)
- Normalization method (*n*; default robustZ)
- Delay-limit (*d;* default 3)
- P-value calculation (*p*; perm, theo or mix)
- Permutation /precision (x; the number of permutations)
- Missing values (*f*; none, zero, linear, quadratic...)
- If you have replicates you can set the number of bootstraps for 95% confidence interval estimation (b; default 100)
- Example command for 24 months
- lsa_compute <in> <out> -r 1 -s 24 -d 0 -p perm-x 1000 -f linear -n robustZ

ELSA – THE OUTPUT

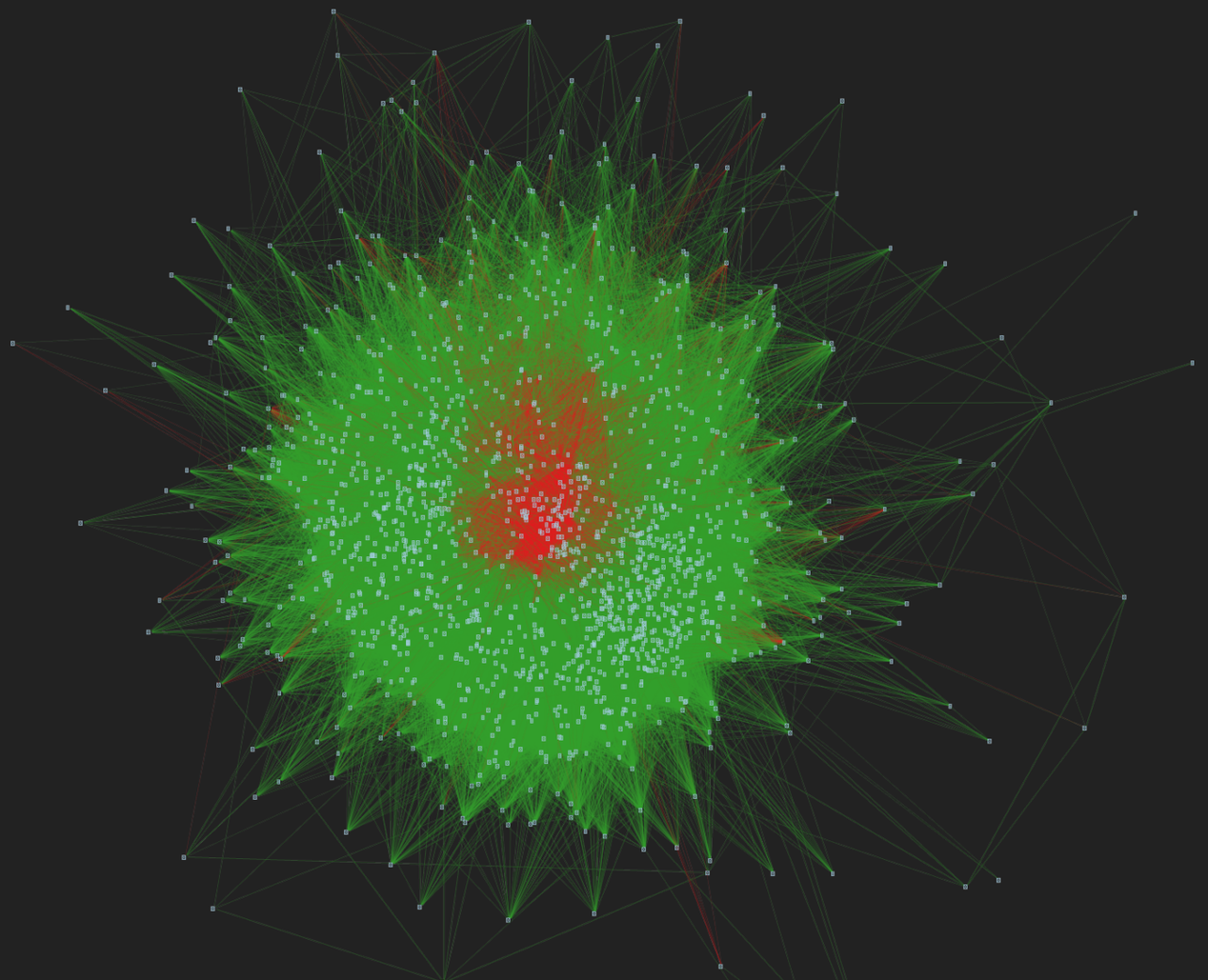
- X: The name of the first OTU/variable in the pairwise comparison
- Y: The name of the first OTU/variable in the pairwise comparison
- LS: Local similarity score. It is defined as "For two normal transformed sequences of the same length, the local similarity score is defined as the maximal sum of the product of the corresponding entries of all their subsequences within some predefined time delay D." Ruan et al 2006.
- P and Q values, Spearman
- etc.
- An explanation of the output is on Github.

BLANES BAY DATA – 10YEARS MONTHLY

- Results from pico fraction (<3 um)
  - Illumina amplicons from 18S (V4) and 16S (V3)
- 16 Millions sequences
- Clustered at 99%
  - Bacteria: 16 196 OTUs
  - Eukaryotes: 36 020 OTUs
- Rarified
- Removed OTUs that were not present in at least 10% of the samples
- 515 bacteria OTUs, 1065 eukaryote OTUs, and 18 Environmental var.

RESULTS - EXAMPLE

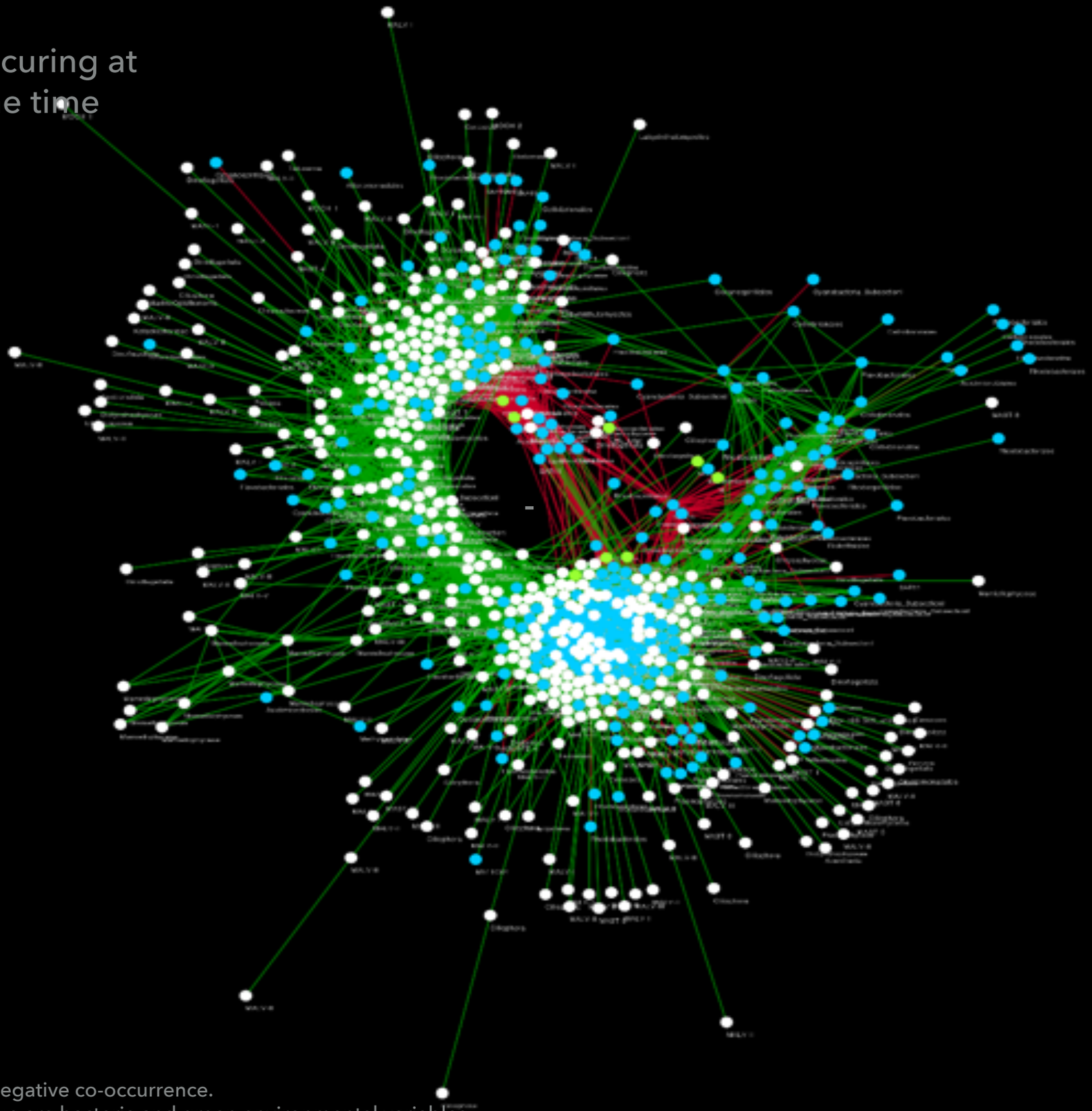
- With 1598 OTUs and ENVs for pairwise comparisons there are more than 1.2 million possible edges in the network.
- After removing non-significant edges (P & Q < 0.05)
  - 222199 edges (17,4 %)
  - 197541 positive (88%) and 24658 negative (12%)



Green edges are positive, red negative co-occurrence.
White nodes are eukaryotes, blue are bacteria and green environmental variables

- Which are the most important species, the core community?
- Some of the edges are due to organisms reacting to the environment.
- What about interactions between organisms (symbiosis, parasitism, predation) ?

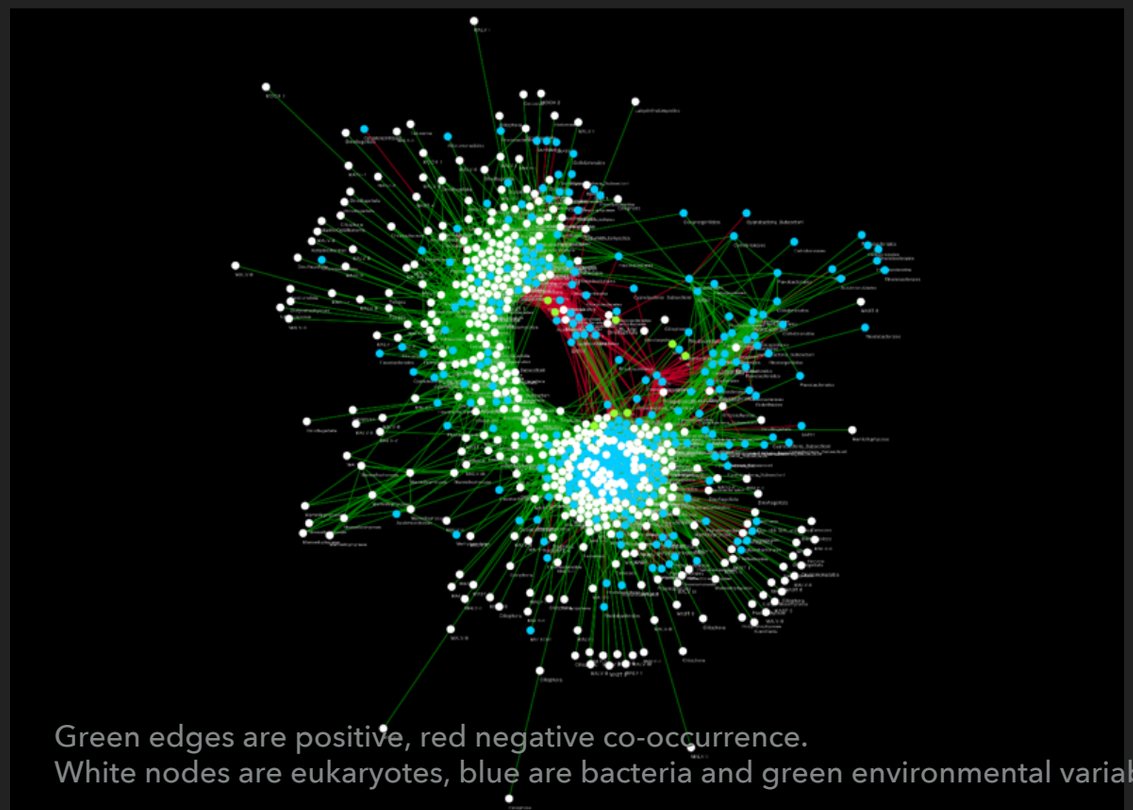
- Interactions occuring at least 60% of the time
- P&Q<0.0001



Green edges are positive, red negative co-occurrence.
White nodes are eukaryotes, blue are bacteria and green environmental variables

PRUNING INDIRECT EDGES

- Remove environment-driven co-occurrence
- Identification of triplets were the environmental factor is stronger than OTU-OTU interactions



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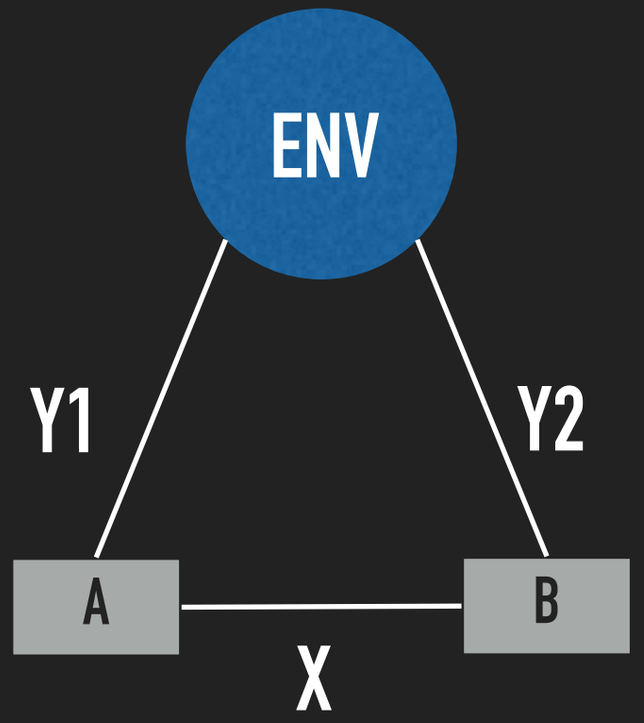

Ina Deutschmann

PRUNING INDIRECT EDGES

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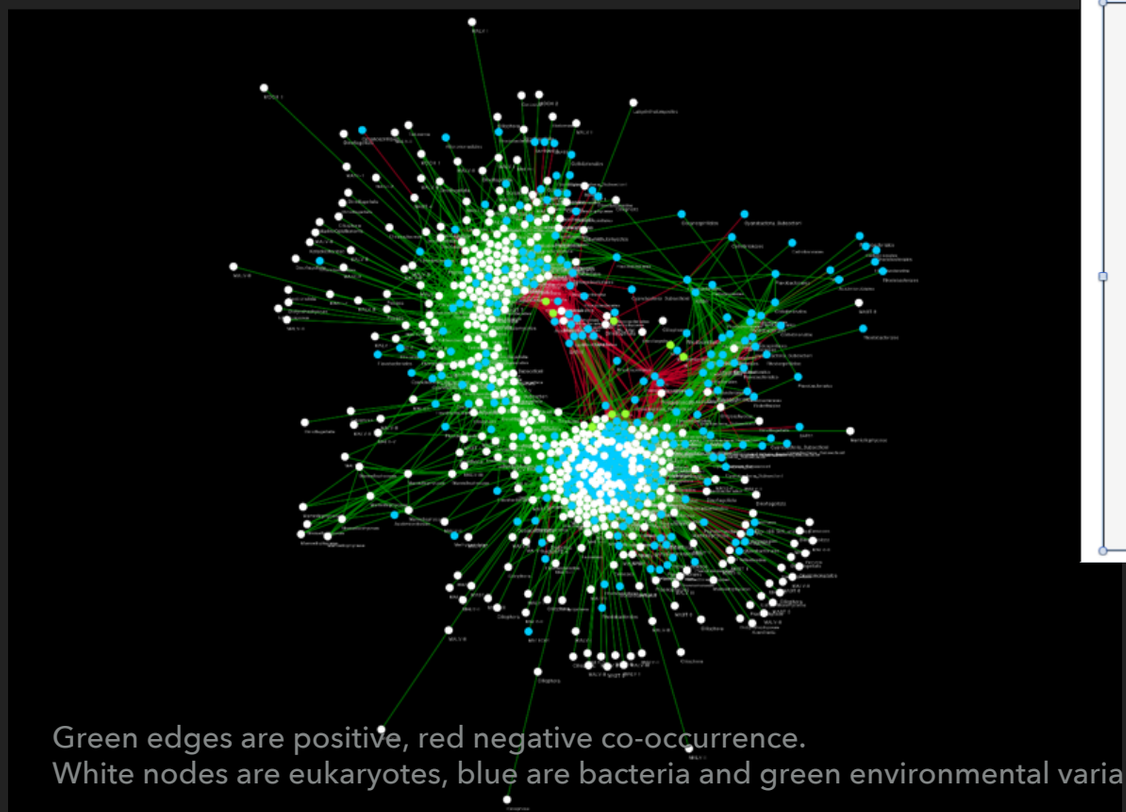
- Identification of triplets were the environmental factor is stronger than OTU-OTU interactions



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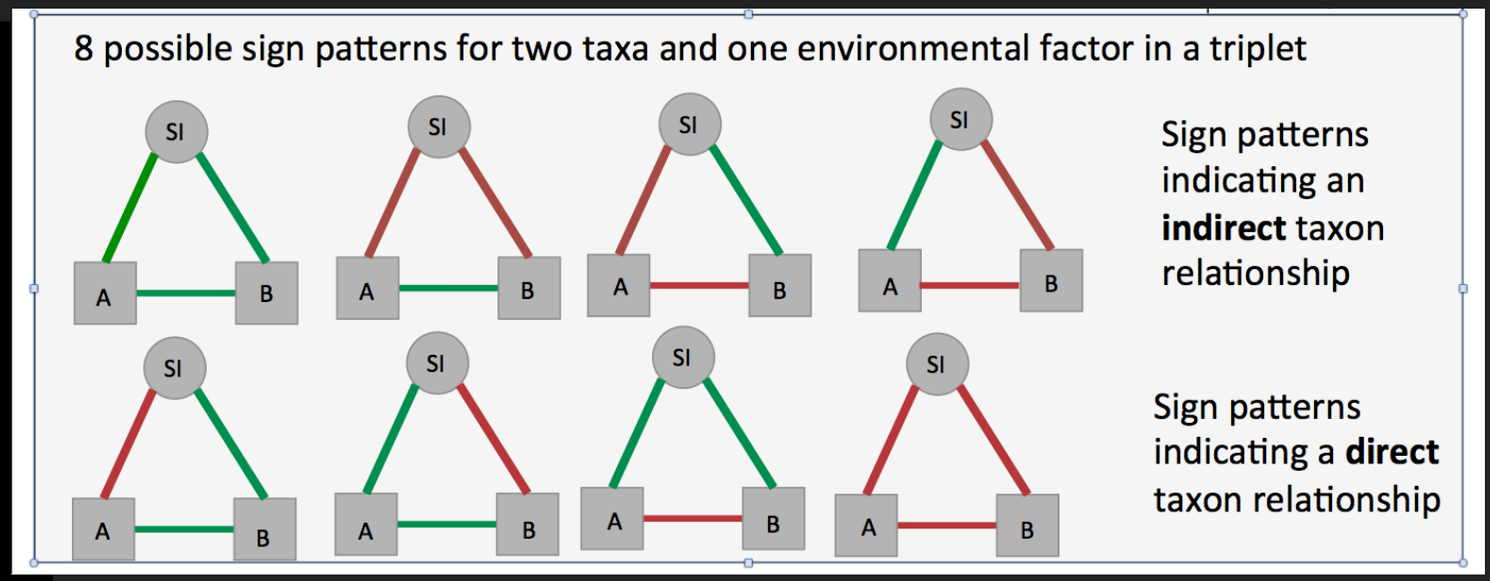
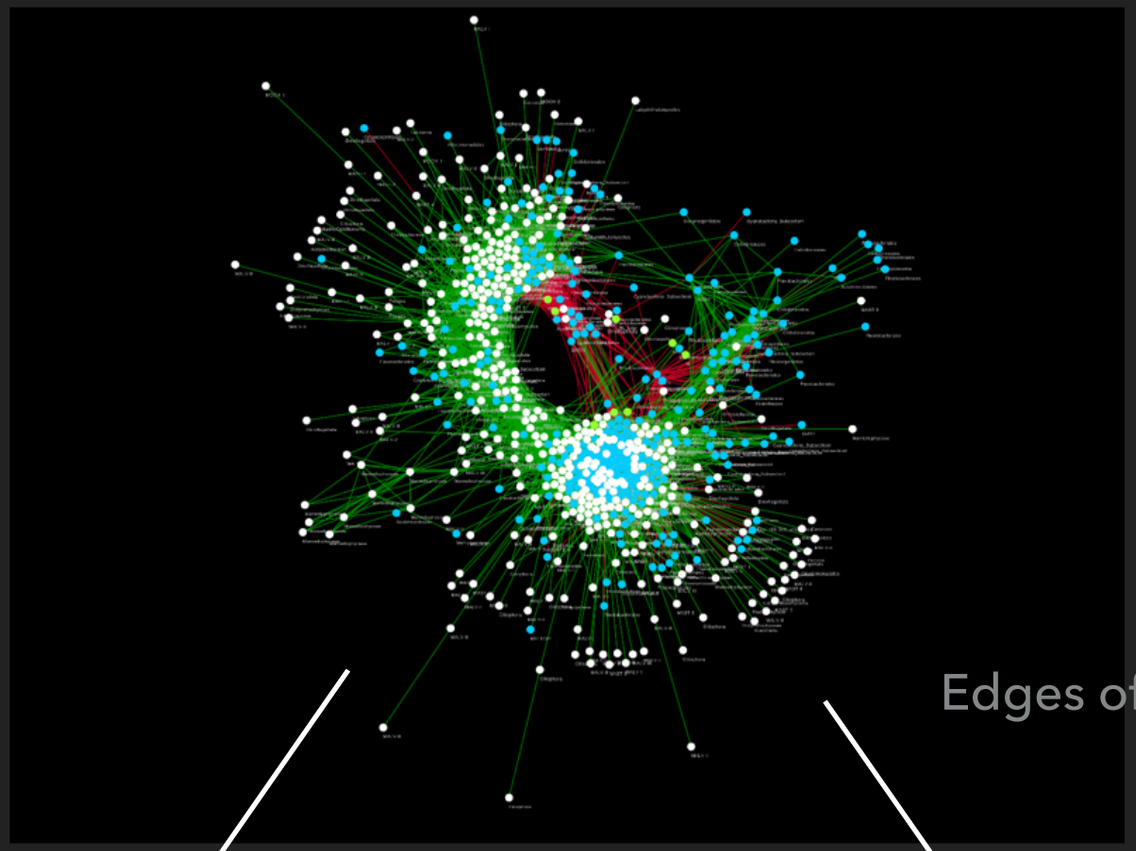
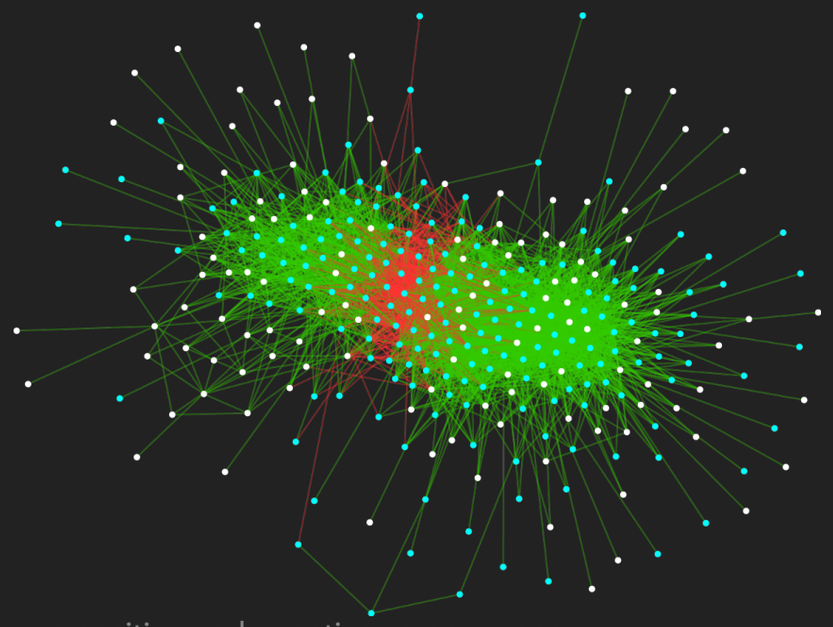


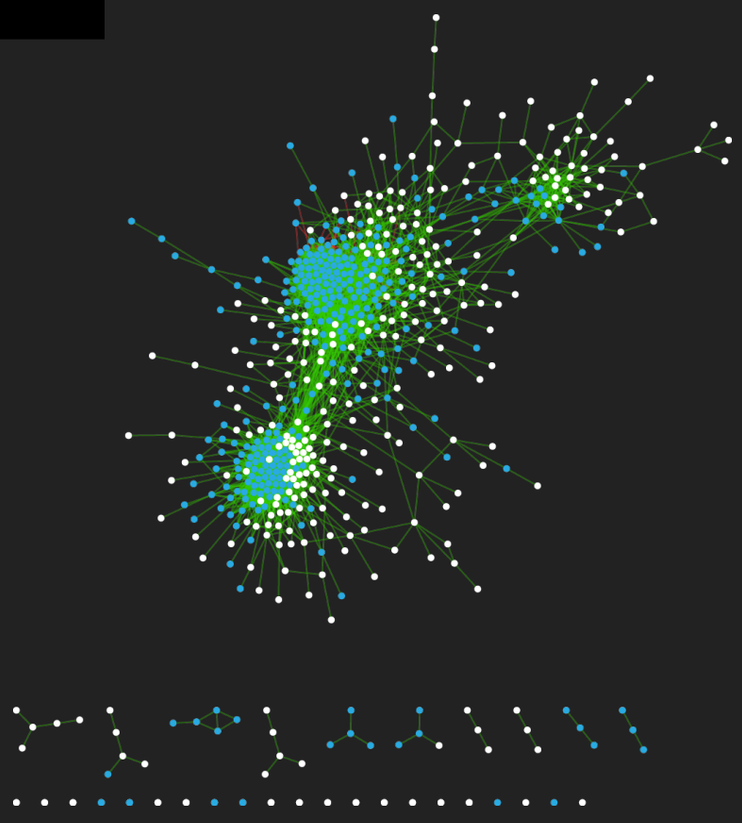
Lima-Mendez et al. 2015, Karoline Faust



Edges that depend on the environment

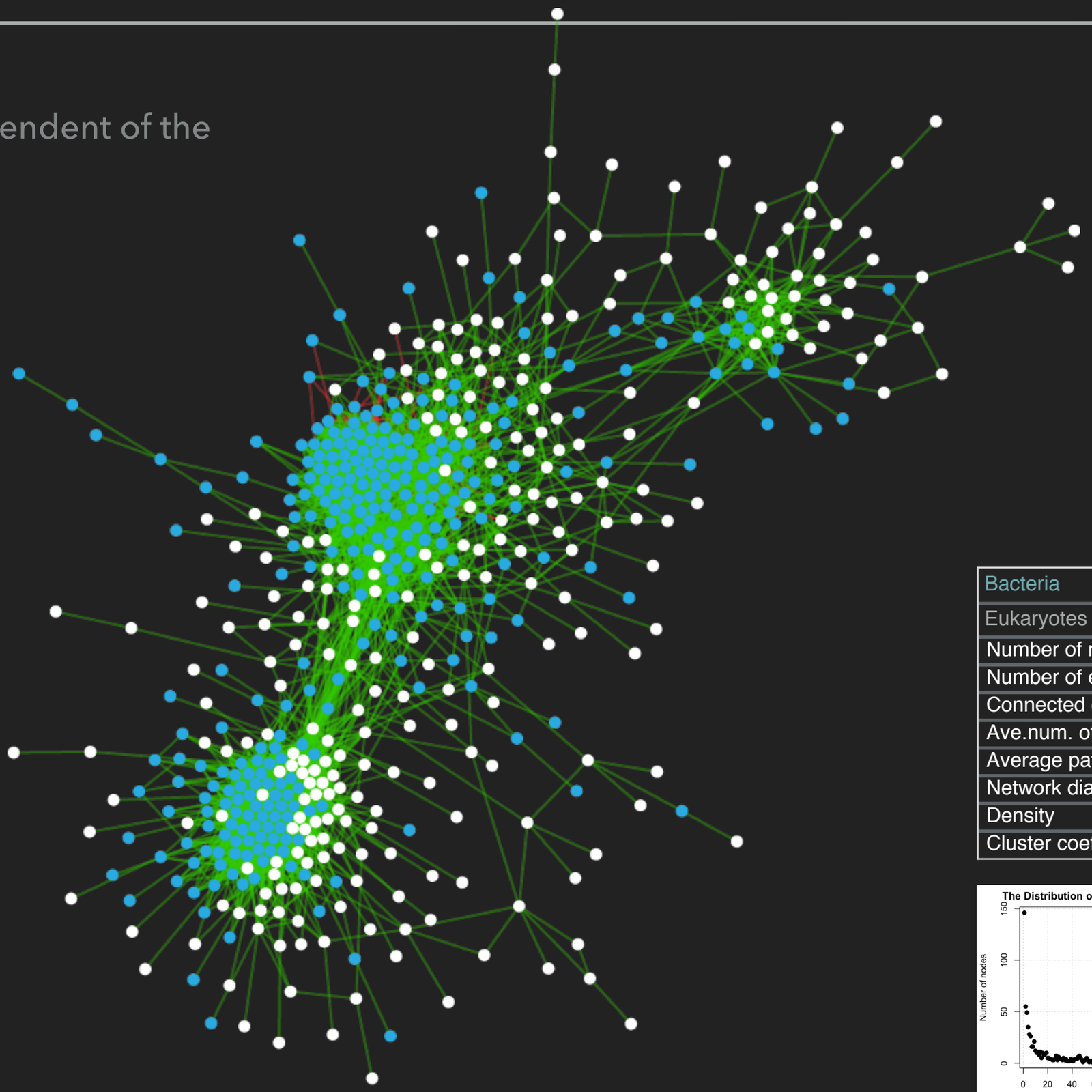
Edges of potential interactions



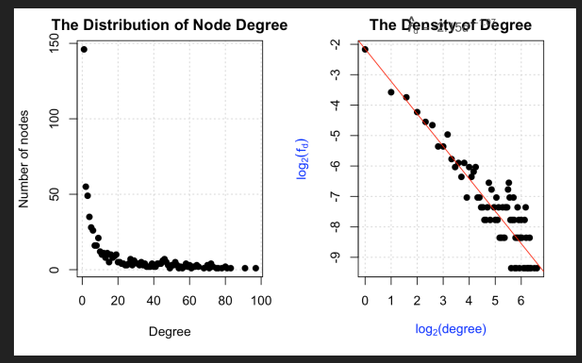


Green edges are positive, red negative co-occurrence.
White nodes are eukaryotes, blue are bacteria and green environmental variables

Edges independent of the environment



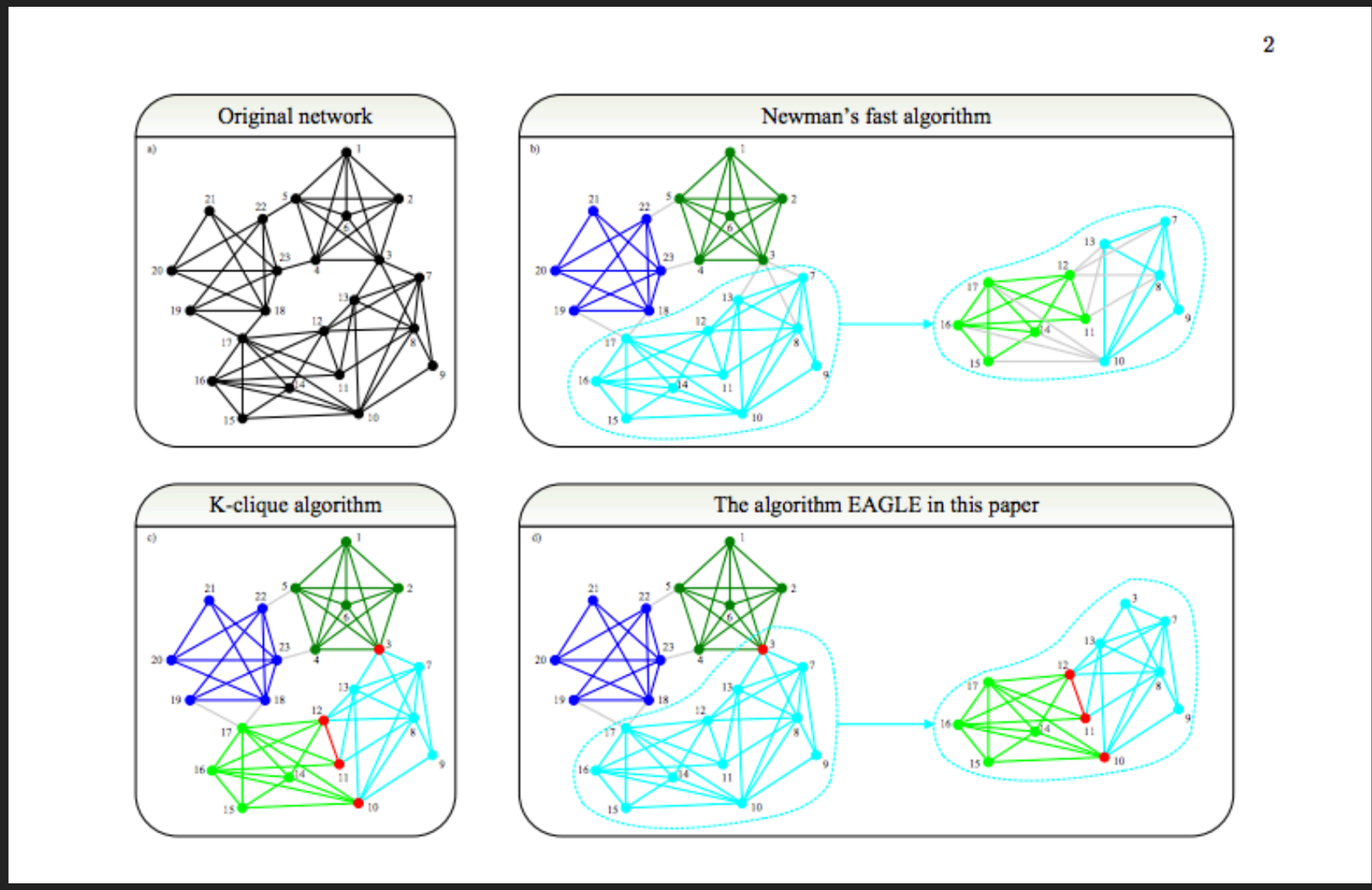
Bacteria	335
Eukaryotes	325
Number of nodes	656
Number of edges	5070
Connected components	28
Ave.num. of neighbors	15.45732
Average path length	4.135381
Network diameter	12
Density	0.02359896
Cluster coefficient	0.5271591



Green edges are positive, red negative co-occurrence.
White nodes are eukaryotes, blue are bacteria and green environmental variables

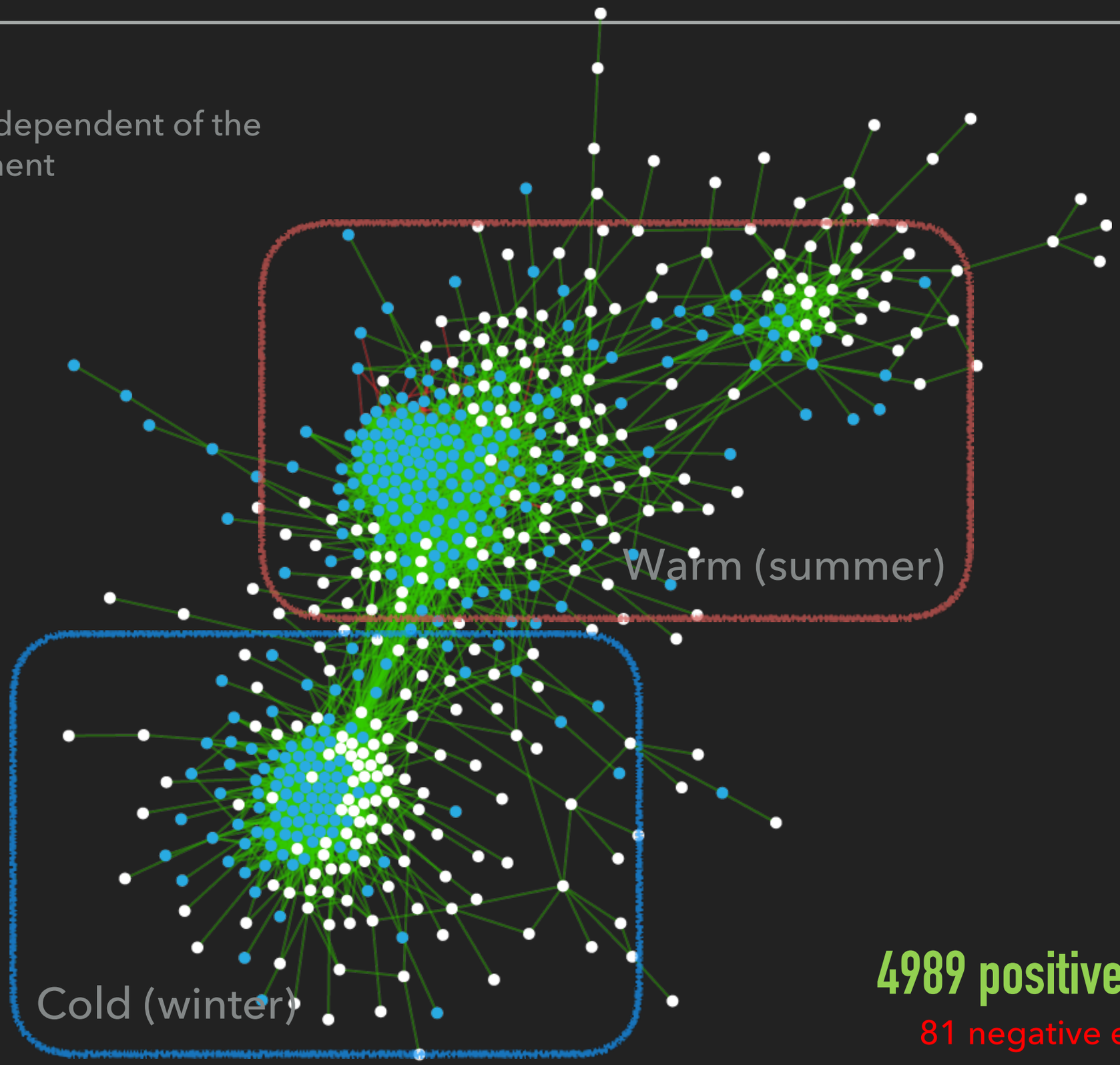
FINDING MODULES

- MCODE (Bader et al 2002), Eagle, K-clique...



Shen et al. (2008)

Edges independent of the environment



4989 positive edges

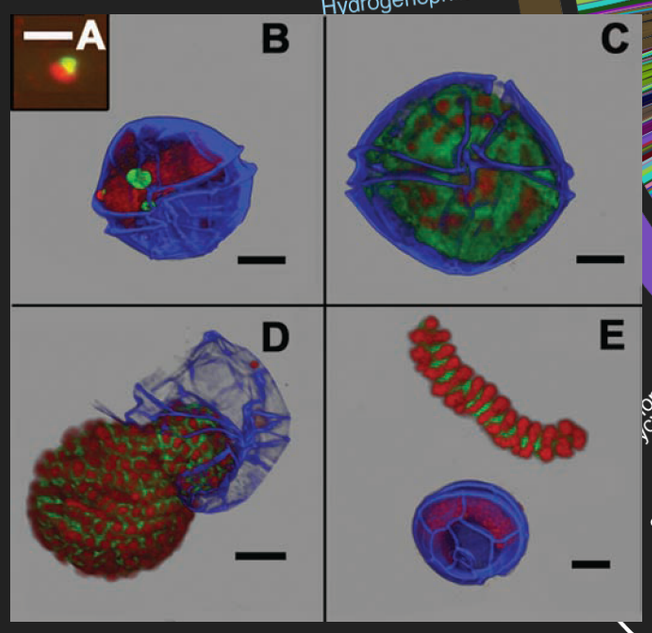
81 negative edges

Green edges are positive, red negative co-occurrence.
White nodes are eukaryotes, blue are bacteria and green environmental variables

Bacteria

SAR11

SAR11
Salinisphaerales
Rickettsiales
Rhodospirillales
Rhodobacterales
Rhizobiales
Puniceicoccales
Planctomycetales
Order
OCS116
Oceanospirillales
Micrococcales
Marinimicrobia
Kiloo4
Hydrogenophilales
SAR202
SAR324
Sh765B-TzT-29
Sphingobacteriales
Sphingomonadales
Cyanobacteria
Thermoplasmatales
ARKICE-90
Thiotrichales_uncultured
SC3-20_uncultured
Elev-16S-509_uncultured
SPOTSOC-T00m83_uncultured
JG30-KF-CM66_uncultured
Verrucomicrobiales
Xanthomonadales
Acantharia
Bolidomonas
Centrohelida
Chlorarachniophyta
Chlorarachniophyceae
Chlorokybomonadida
Chlorokybomonadaceae
Chlorophyceae
Cryptomonadales
Bacillariophyceae
Dinoflagellata
Katablepharidae
Labyrinthulomycetes
MALV-I
MALV-II
MALV-III
MALV-V
Mamiellophyceae
Pelagophyceae
Picozoa
onema
ycystinea



Chambouvet et al. 2008

MALV I,II and III

Eukaryotes

PROGRAMS FOR VISUALIZATIONS

- Cytoscape (http://www.cytoscape.org/)
- Gephi
- Several packages for R
  - iGraph
  - ProNet
  - circlize

SOME RESOURCE

- The code repository for Schmidt et. al 2017 “A Family of Interaction-Adjusted Indices of Community Similarity” doi:10.1038/ismej.2016.139
  - https://github.com/defleury/Schmidt_et_al_2016_community_similarity/
- Tutorial for WGCNA: https://labs.genetics.ucla.edu/horvath/CoexpressionNetwork/Rpackages/WGCNA/Tutorials/index.html
- eLSA: https://bitbucket.org/charade/elsa/wiki/Home
- fast eLSA: http://www.cmde.science.ubc.ca/hallam/fastLSA/
- SparCC: a python module for computing correlations in compositional data (16S, metagenomics, etc'). https://bitbucket.org/yonatanf/sparcc
- iGraph package for R:
  - https://www.r-bloggers.com/an-example-of-social-network-analysis-with-r-using-package-igraph/

CYTOSCAPE – SHORT TUTORIAL

THE NETWORK FILES

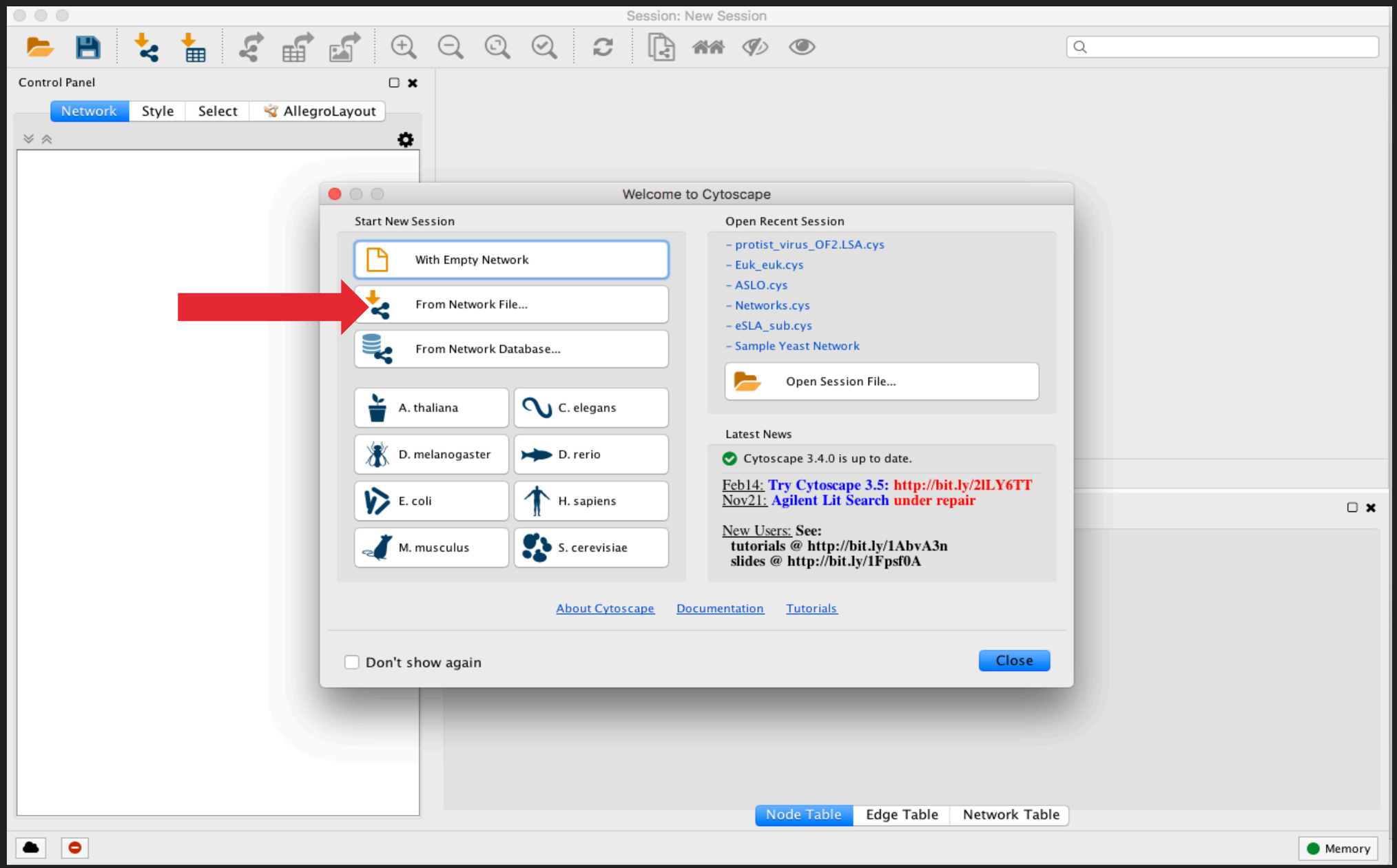
- *https://github.com/bio9905/course-material*
- *eLSA_installation_guide_for_abel.sh*
  - If you want to install on abel for yourself
- *eLSA_starting_script.sh*
  - The commands for a typical run
- *eLSA_otu_table.tsv* -> input data
  eLSA_top100_otus.tsv -> input data

THE NETWORK FILES

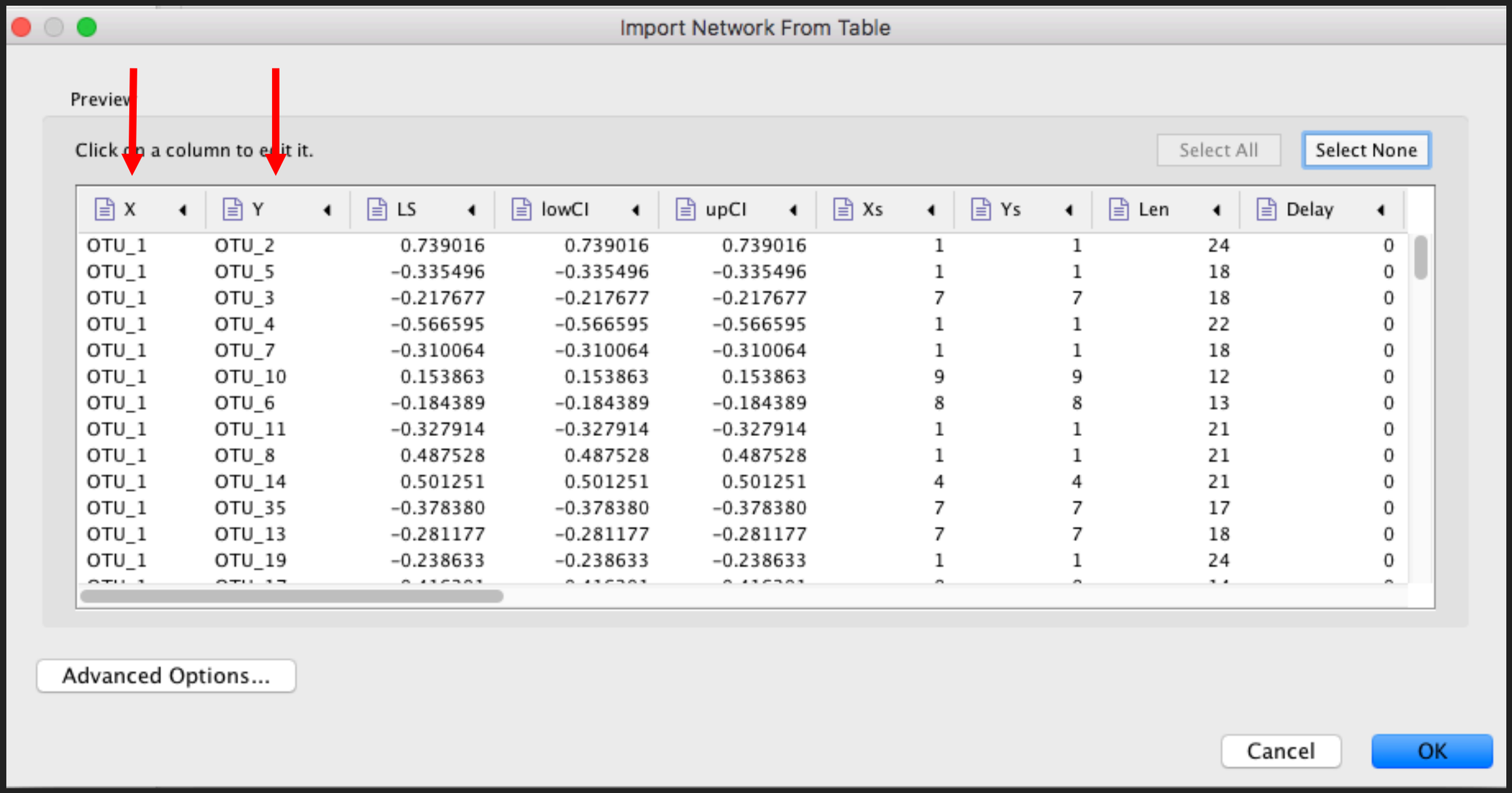
- *https://github.com/bio9905/course-material*
- *Output from eLSA*
  - ***eLSA_network_top100.perm.d0.tsv***
    eLSA_network_top100.perm.d1.tsv
    eLSA_network.d0.tsv
    eLSA_network.d1.tsv
- *eLSA_node_annotation_relabund.tsv*
- *eLSA_node_annotation_tax.tsv*
- *eLSA_for_cytoscape.cys*

USING CYTOSCAPE

- open Cytsocape, import *eLSA_network_top100.perm.d0.tsv*

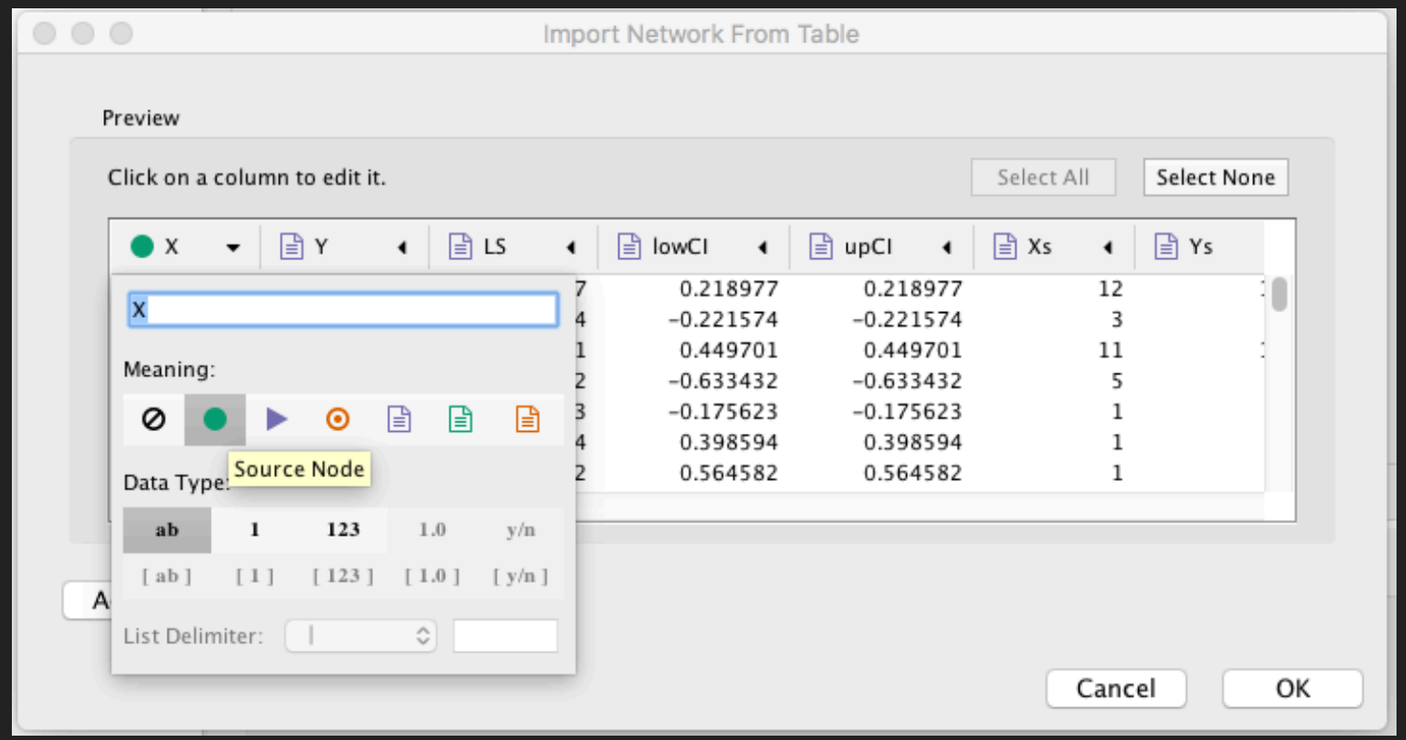


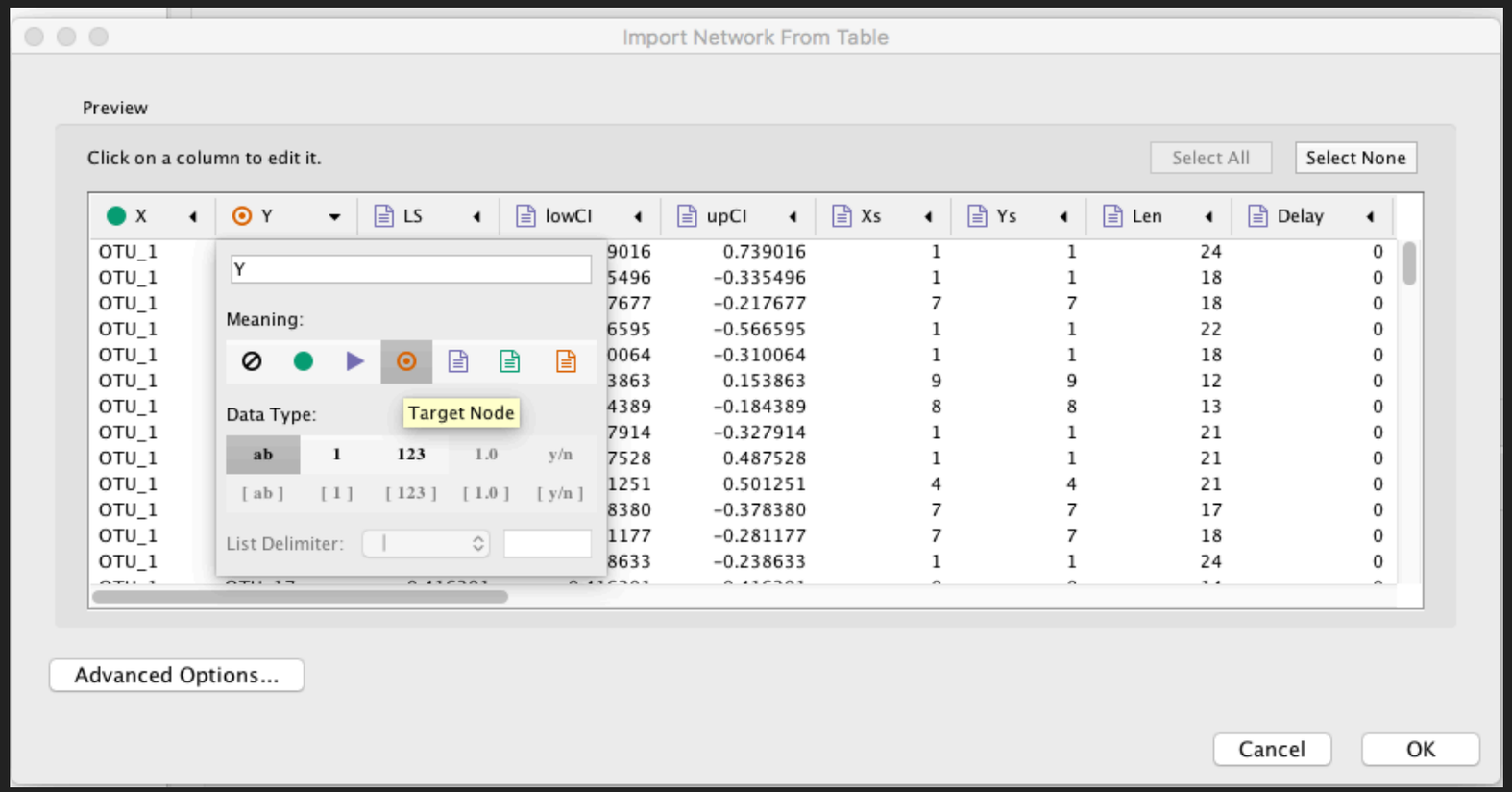
- Define target and source node (this is an undirected networks so the order of the nodes doesn't matter)

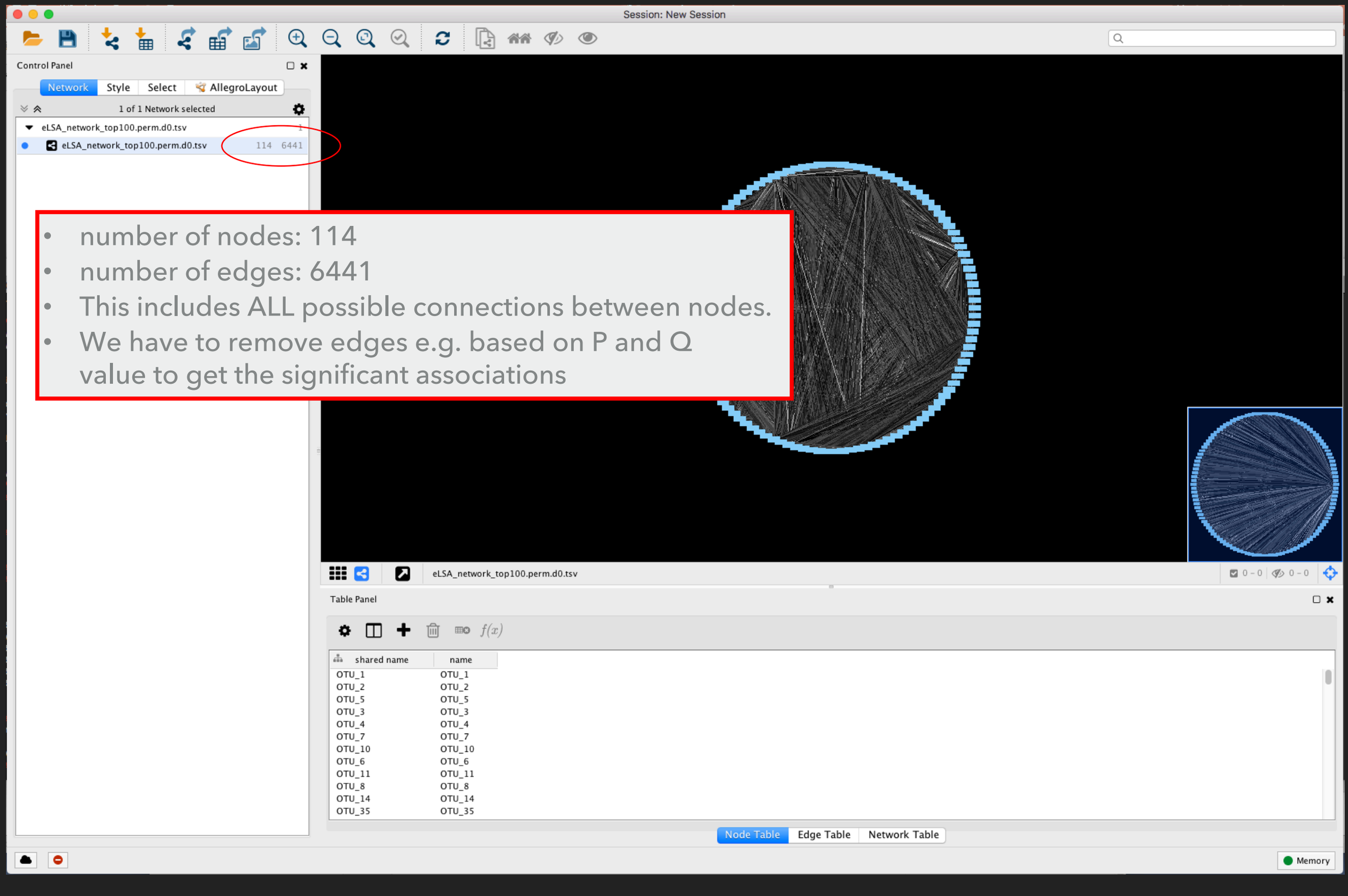


X	Y	LS	lowCI	upCI	Xs	Ys	Len	Delay
OTU_1	OTU_2	0.739016	0.739016	0.739016	1	1	24	0
OTU_1	OTU_5	-0.335496	-0.335496	-0.335496	1	1	18	0
OTU_1	OTU_3	-0.217677	-0.217677	-0.217677	7	7	18	0
OTU_1	OTU_4	-0.566595	-0.566595	-0.566595	1	1	22	0
OTU_1	OTU_7	-0.310064	-0.310064	-0.310064	1	1	18	0
OTU_1	OTU_10	0.153863	0.153863	0.153863	9	9	12	0
OTU_1	OTU_6	-0.184389	-0.184389	-0.184389	8	8	13	0
OTU_1	OTU_11	-0.327914	-0.327914	-0.327914	1	1	21	0
OTU_1	OTU_8	0.487528	0.487528	0.487528	1	1	21	0
OTU_1	OTU_14	0.501251	0.501251	0.501251	4	4	21	0
OTU_1	OTU_35	-0.378380	-0.378380	-0.378380	7	7	17	0
OTU_1	OTU_13	-0.281177	-0.281177	-0.281177	7	7	18	0
OTU_1	OTU_19	-0.238633	-0.238633	-0.238633	1	1	24	0

USING CYTOSCAPE







- number of nodes: 114
- number of edges: 6441
- This includes ALL possible connections between nodes.
- We have to remove edges e.g. based on P and Q value to get the significant associations

Session: New Session

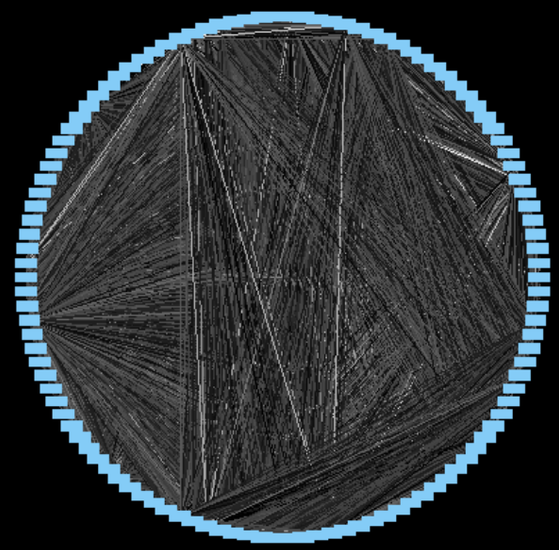
Control Panel

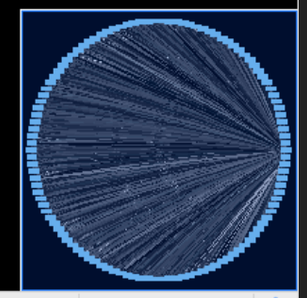
Network | Style | Select | AllegroLayout

1 of 1 Network selected

eLSA_network_top100.perm.d0.tsv 1

eLSA_network_top100.perm.d0.tsv 114 6441





eLSA_network_top100.perm.d0.tsv

0 - 0 0 - 0

Table Panel

$f(x)$

shared name	shared interaction	name	interaction	LS	lowCI	upCI	Xs	Ys	Len	Delay	P	PCC	F
OTU_1 (interacts wi...	interacts with	OTU_1 (in...	interacts with	0.153863	0.153863	0.153863	9	9	12	0	0.785	-0.106066	0
OTU_1 (interacts wi...	interacts with	OTU_1 (in...	interacts with	-0.184389	-0.184389	-0.184389	8	8	13	0	0.994	-0.168376	0
OTU_1 (interacts wi...	interacts with	OTU_1 (in...	interacts with	-0.327914	-0.327914	-0.327914	1	1	21	0	0.597	-0.162993	0
OTU_1 (interacts wi...	interacts with	OTU_1 (in...	interacts with	0.487528	0.487528	0.487528	1	1	21	0	0.003	0.212294	0
OTU_1 (interacts wi...	interacts with	OTU_1 (in...	interacts with	0.501251	0.501251	0.501251	4	4	21	0	0.068	-0.098955	0
OTU_1 (interacts wi...	interacts with	OTU_1 (in...	interacts with	-0.37838	-0.37838	-0.37838	7	7	17	0	0.027	-0.22254	0
OTU_1 (interacts wi...	interacts with	OTU_1 (in...	interacts with	-0.281177	-0.281177	-0.281177	7	7	18	0	0.063	-0.187045	0
OTU_1 (interacts wi...	interacts with	OTU_1 (in...	interacts with	-0.238633	-0.238633	-0.238633	1	1	24	0	0.155	-0.252386	0
OTU_1 (interacts wi...	interacts with	OTU_1 (in...	interacts with	-0.416301	-0.416301	-0.416301	8	8	14	0	0.346	-0.112801	0
OTU_1 (interacts wi...	interacts with	OTU_1 (in...	interacts with	0.801767	0.801767	0.801767	1	1	24	0	0.004	0.57226	0
OTU_1 (interacts wi...	interacts with	OTU_1 (in...	interacts with	-0.121821	-0.121821	-0.121821	7	7	10	0	0.764	-0.2283	

Node Table | Edge Table | Network Table

Memory

Session: New Session

Control Panel

Network | Style | Select | AllegroLayout

Default filter

Edge: P | is

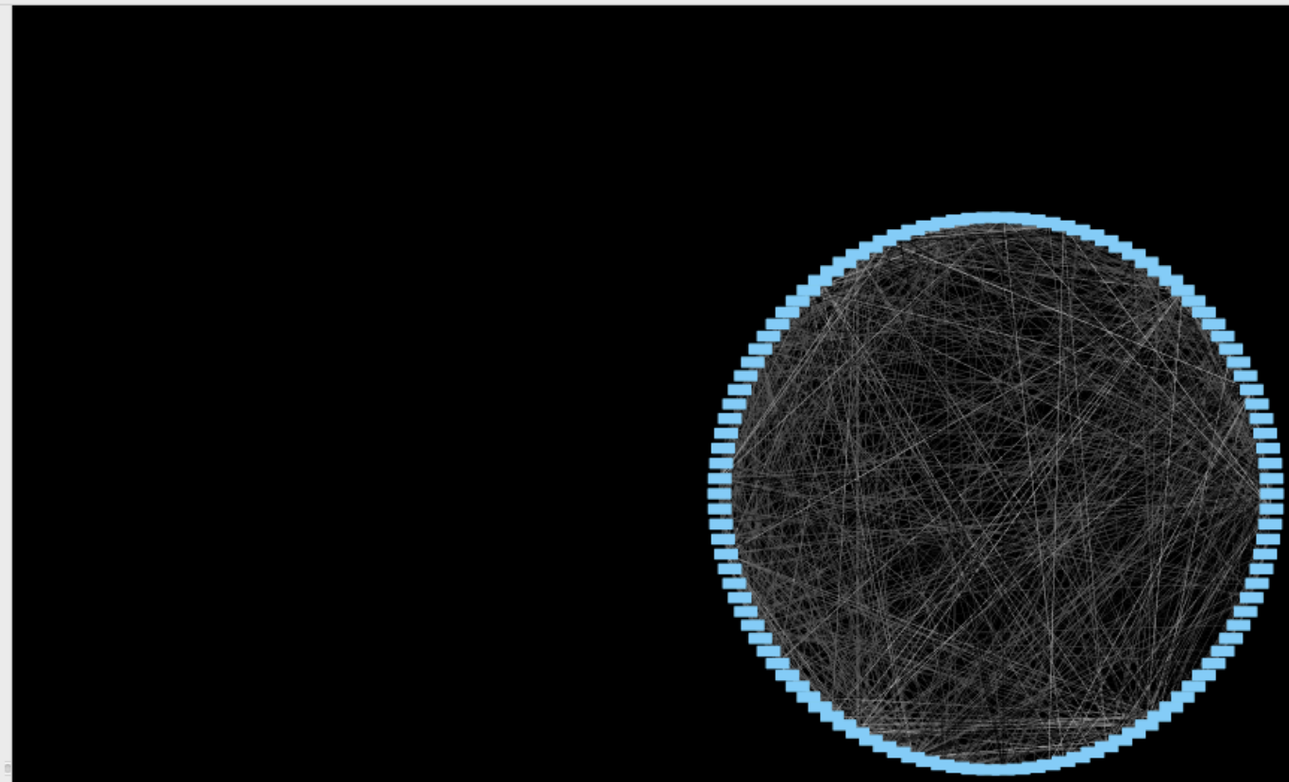
Select '*select*' make a filter (see next slide)

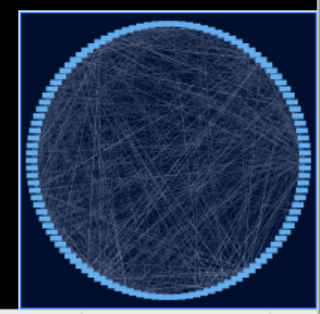
Apply when filter changes

Apply

Selected 0 nodes and 5413 edges in 60ms

Filter | Chain





eLSA_network_top100.perm.d0.tsv

0 - 0 | 0 - 0

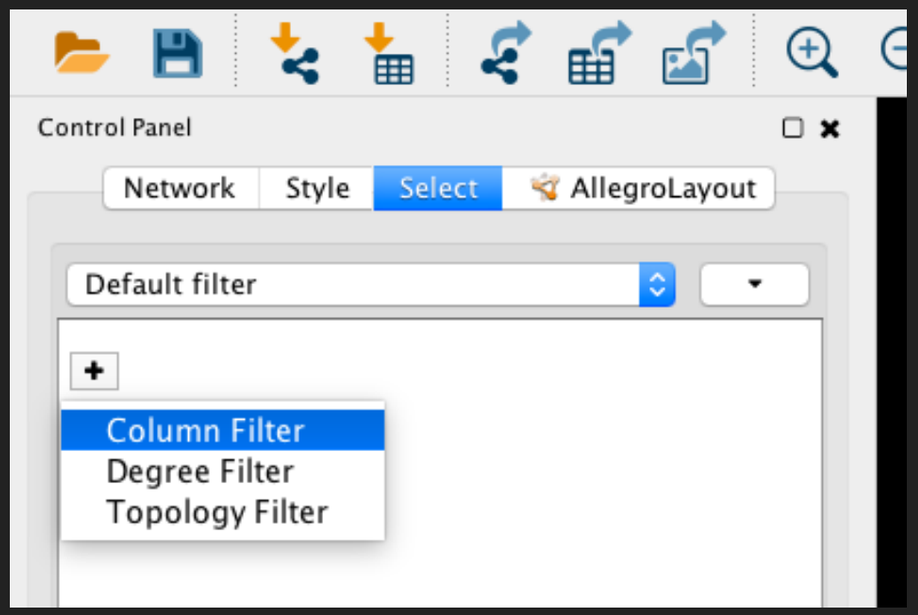
Table Panel

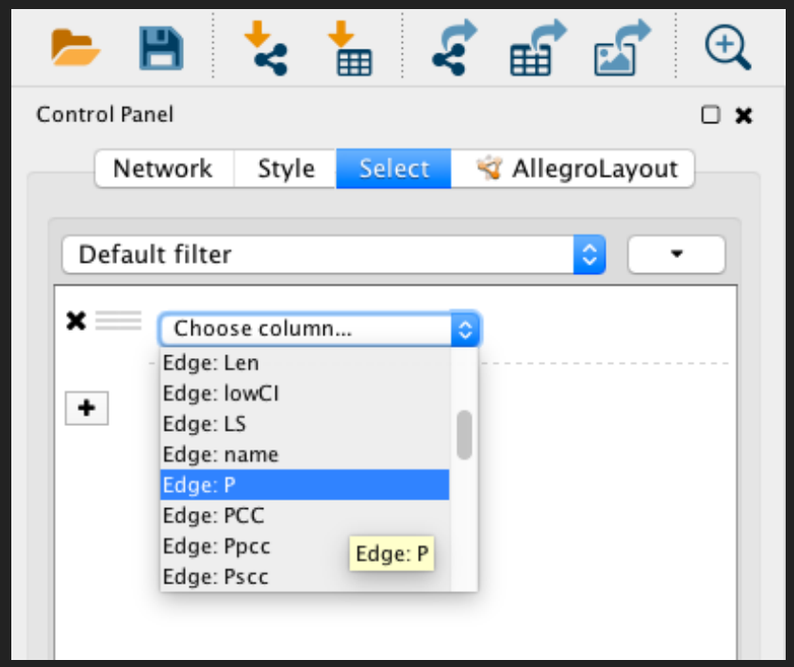
shared name	shared interaction	name	interaction	LS	lowCI	upCI	Xs	Ys	Len	Delay	P	PCC	F
OTU_1 (interacts wi...	interacts with	OTU_1 (in...	interacts with	0.595614	0.595614	0.595614	1	1	24	0	0.0	0.627636	0
OTU_1 (interacts wi...	interacts with	OTU_1 (in...	interacts with	0.493818	0.493818	0.493818	1	1	23	0	0.001	0.269963	0
OTU_1 (interacts wi...	interacts with	OTU_1 (in...	interacts with	-0.675737	-0.675737	-0.675737	6	6	15	0	0.015	-0.231905	0
OTU_1 (interacts wi...	interacts with	OTU_1 (in...	interacts with	0.458132	0.458132	0.458132	1	1	23	0	0.0	0.115034	0
OTU_1 (interacts wi...	interacts with	OTU_1 (in...	interacts with	0.453943	0.453943	0.453943	1	1	24	0	0.0	0.355021	0
OTU_1 (interacts wi...	interacts with	OTU_1 (in...	interacts with	-0.609257	-0.609257	-0.609257	6	6	17	0	0.033	-0.161748	0
OTU_1 (interacts wi...	interacts with	OTU_1 (in...	interacts with	0.464045	0.464045	0.464045	1	1	22	0	0.0	0.447127	0
OTU_1 (interacts wi...	interacts with	OTU_1 (in...	interacts with	0.915955	0.915955	0.915955	1	1	24	0	0.0	0.519998	0
OTU_1 (interacts wi...	interacts with	OTU_1 (in...	interacts with	-0.346843	-0.346843	-0.346843	6	6	16	0	0.019	-0.274883	0
OTU_1 (interacts wi...	interacts with	OTU_1 (in...	interacts with	-0.579472	-0.579472	-0.579472	5	5	20	0	0.036	-0.146915	0
OTU_1 (interacts wi...	interacts with	OTU_1 (in...	interacts with	-0.342188	-0.342188	-0.342188	1	1	18	0	0.04	-0.27767	0

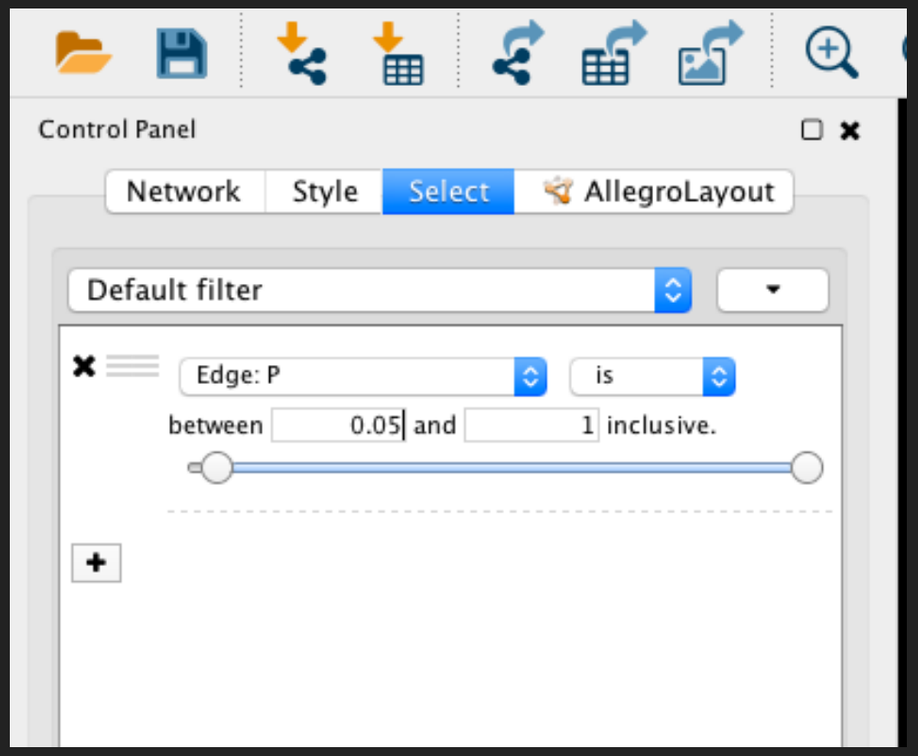
Node Table | Edge Table | Network Table

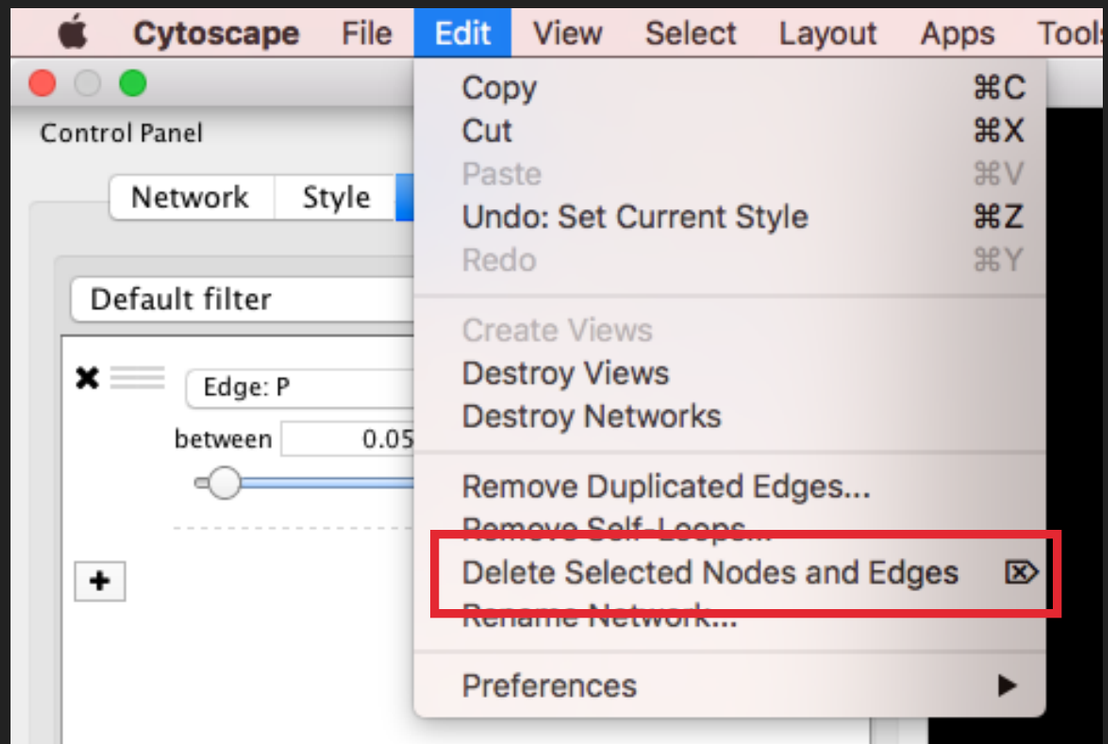
Memory

- Setting up a filter for P value (repeat for Q value)
  How many edges are left?

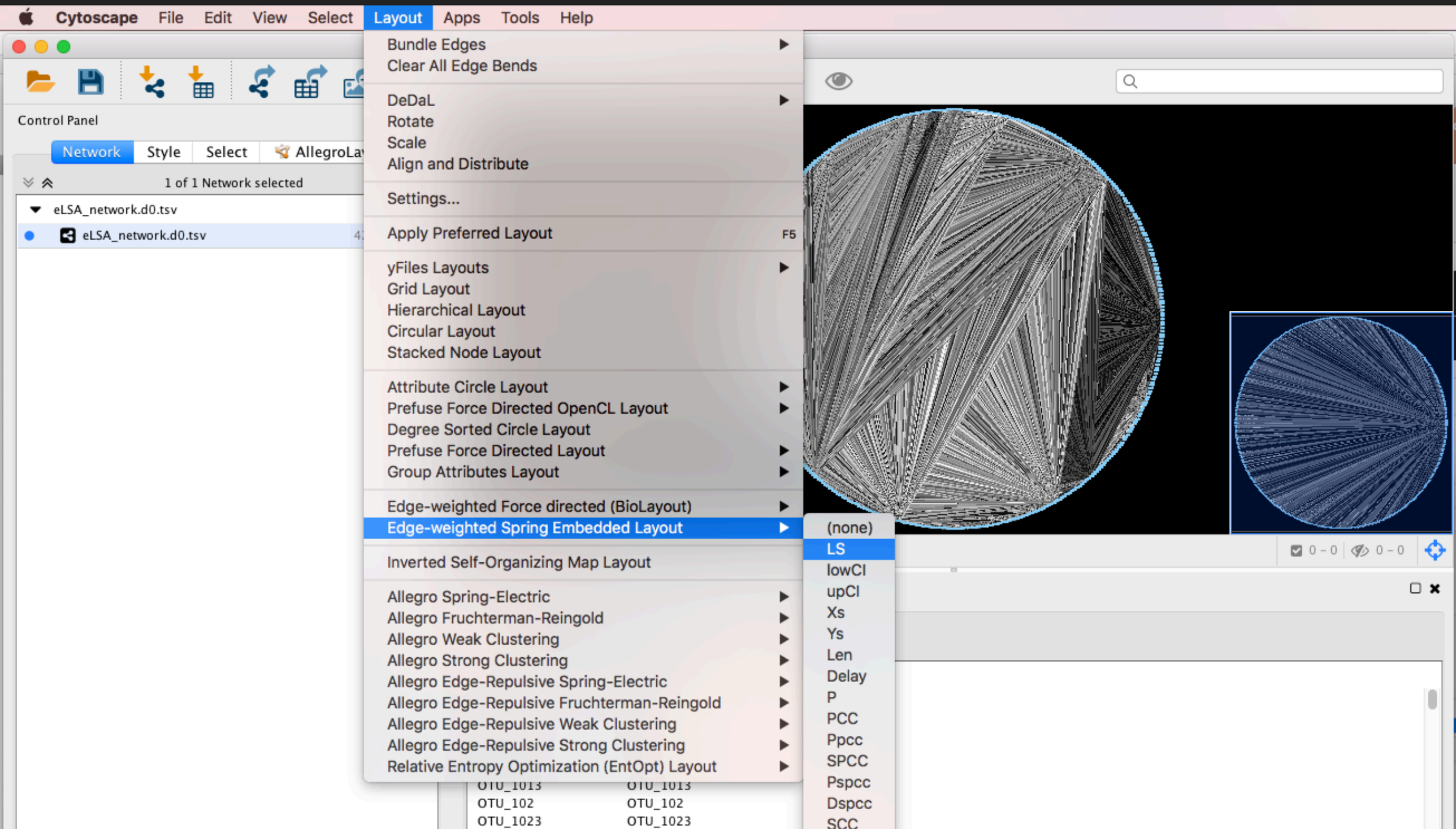




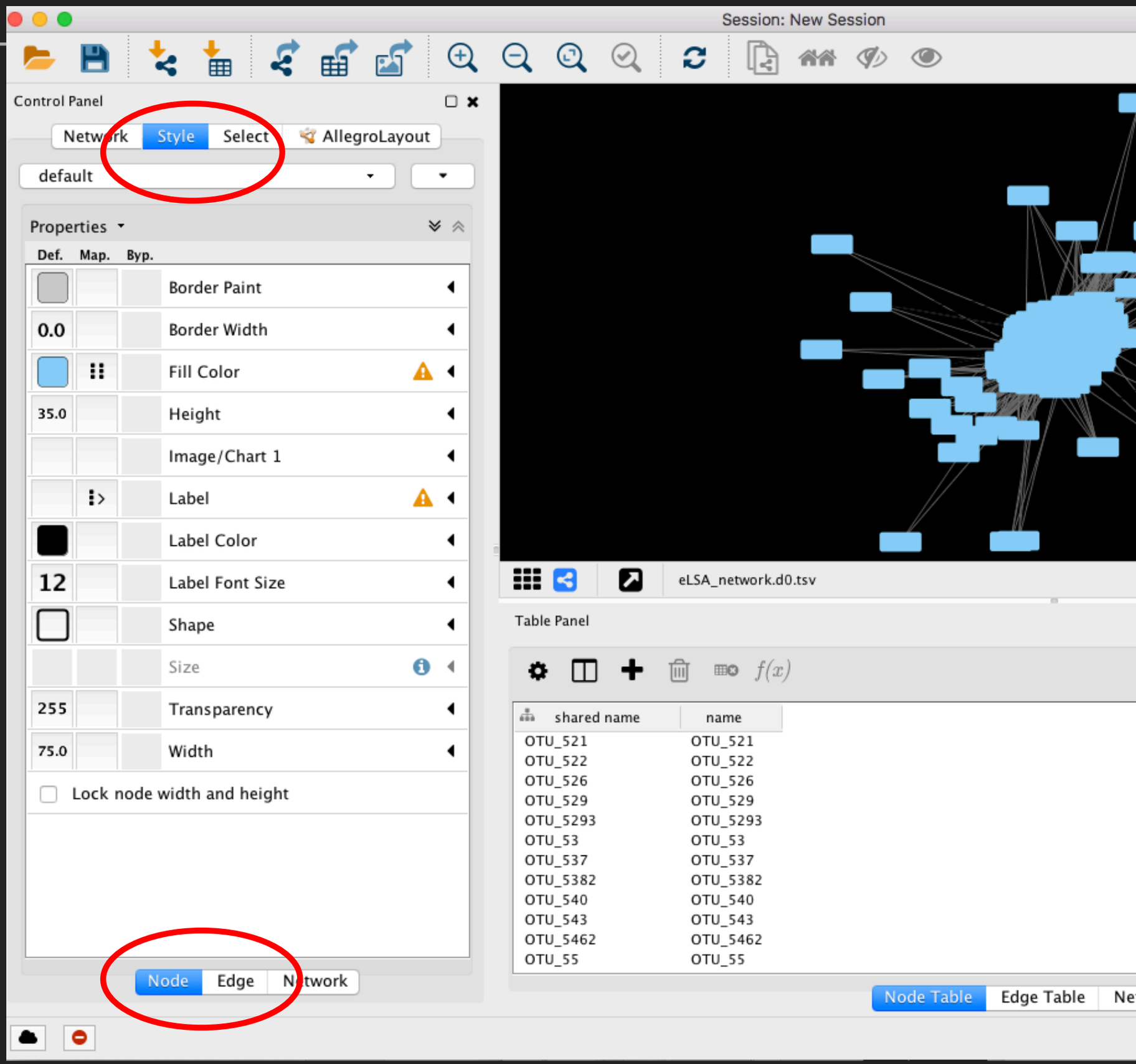




Choose a layout – Circular is fastest
Edge-weighted Spring Embedded Layout (LS) looks better☺



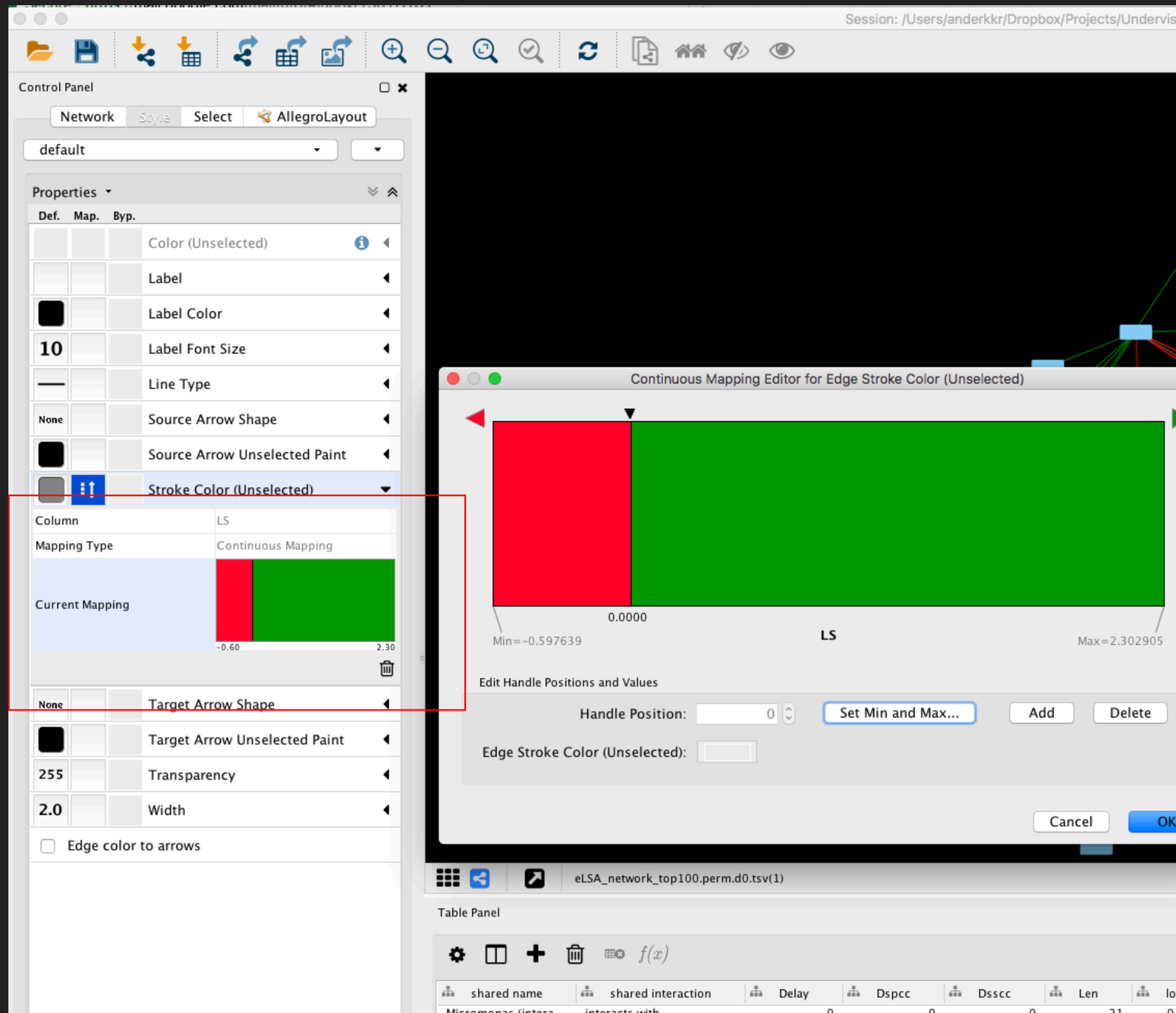
Now choose '*Style*' and then '*Edge*' to change the color of the edges



Use *Stroke Color* to make the positive edges green and the negative edges red

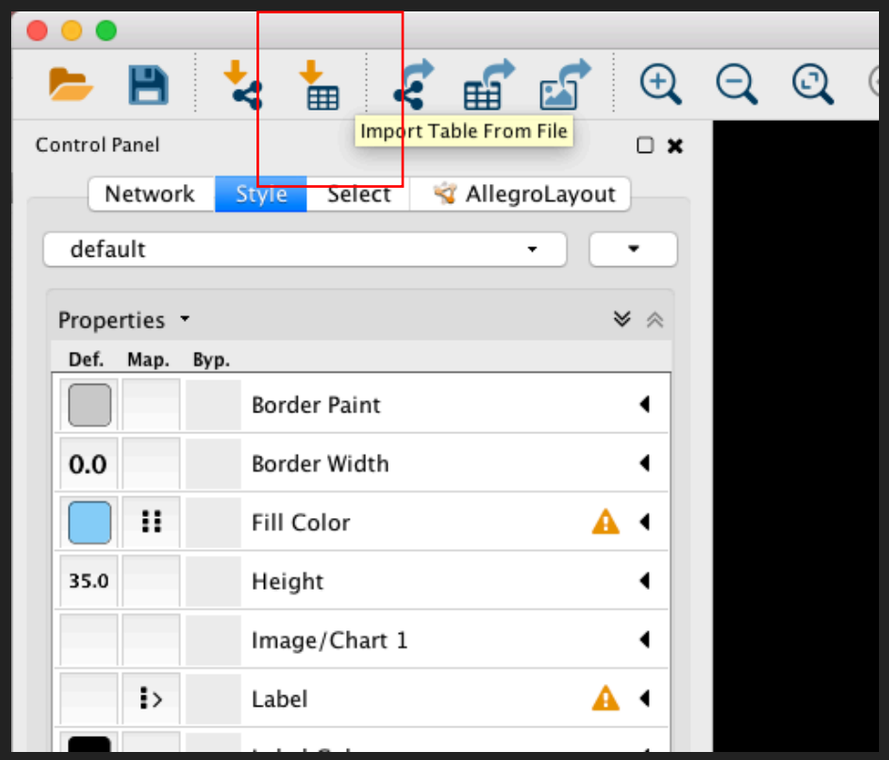
Column: LS

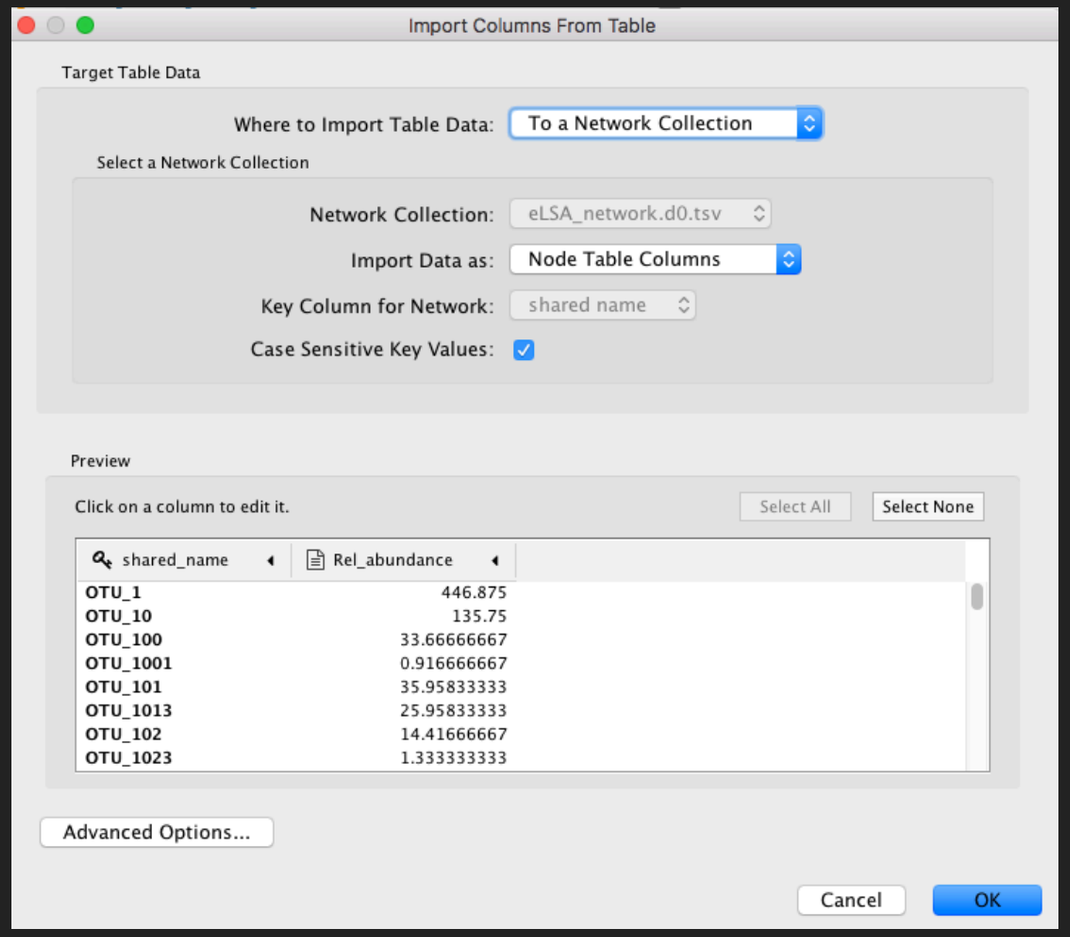
Mapping type: Continuous



ADD ANNOTATIONS TO THE NODES– IMPORT TABLE

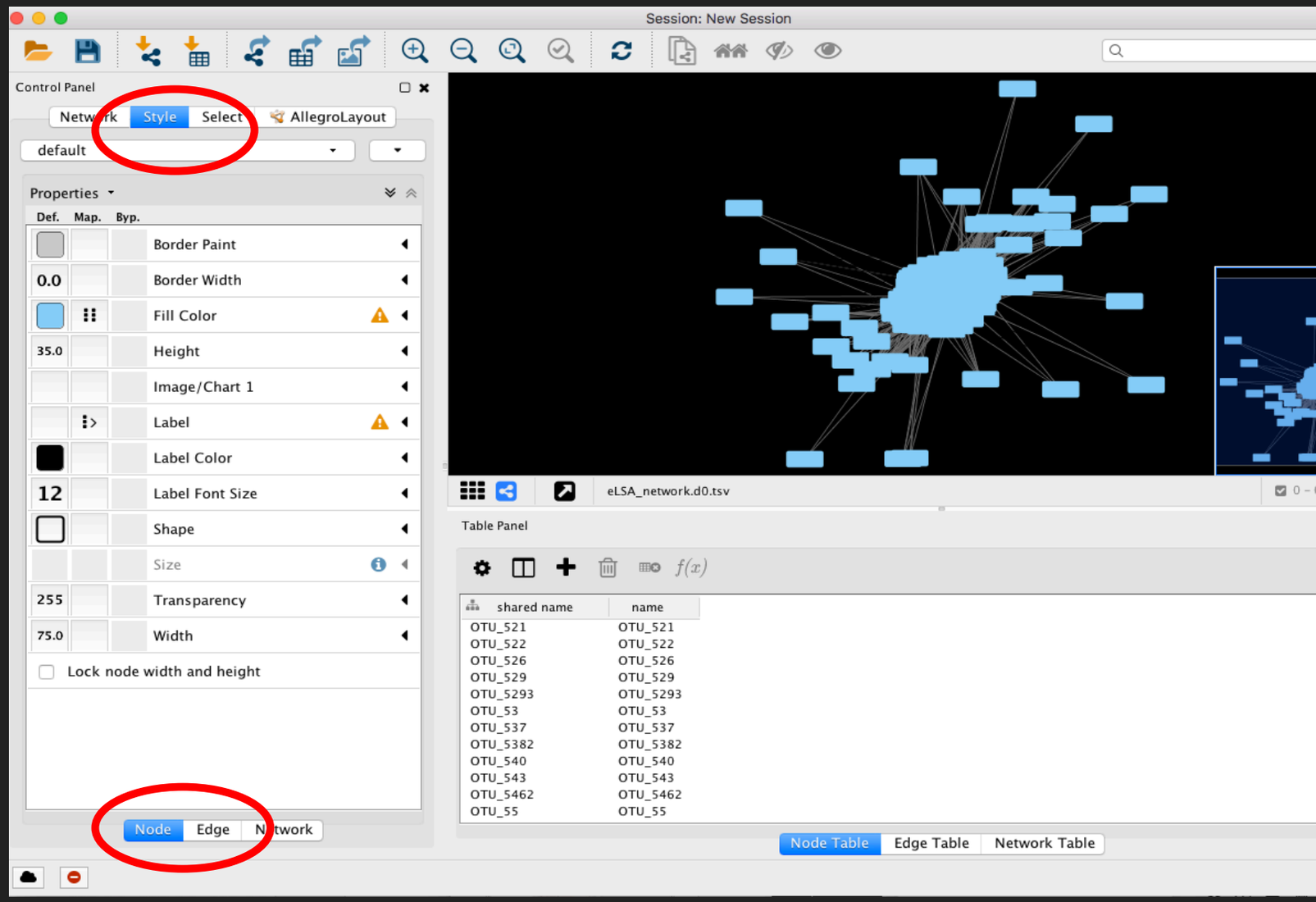
- Two annotation files:
  1) Relative abundance (eLSA_annotation_relabund.tsv)
  2) Taxonomic assignment (blastn vs MAS from UParse pipeline)



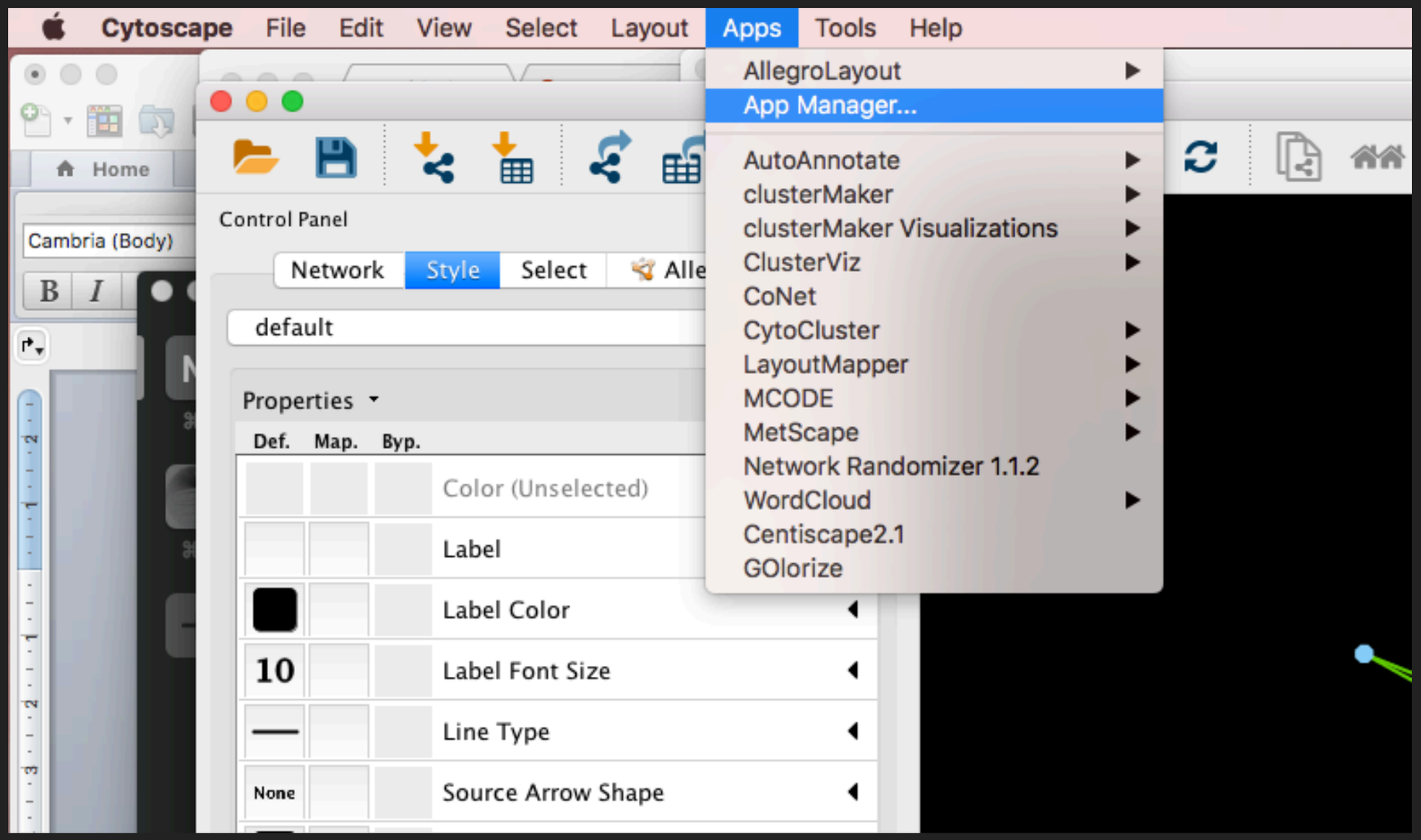


- Change the name, shape, color and/or size of the nodes based on the relative abundance and the taxonomic assignment of the OTUs

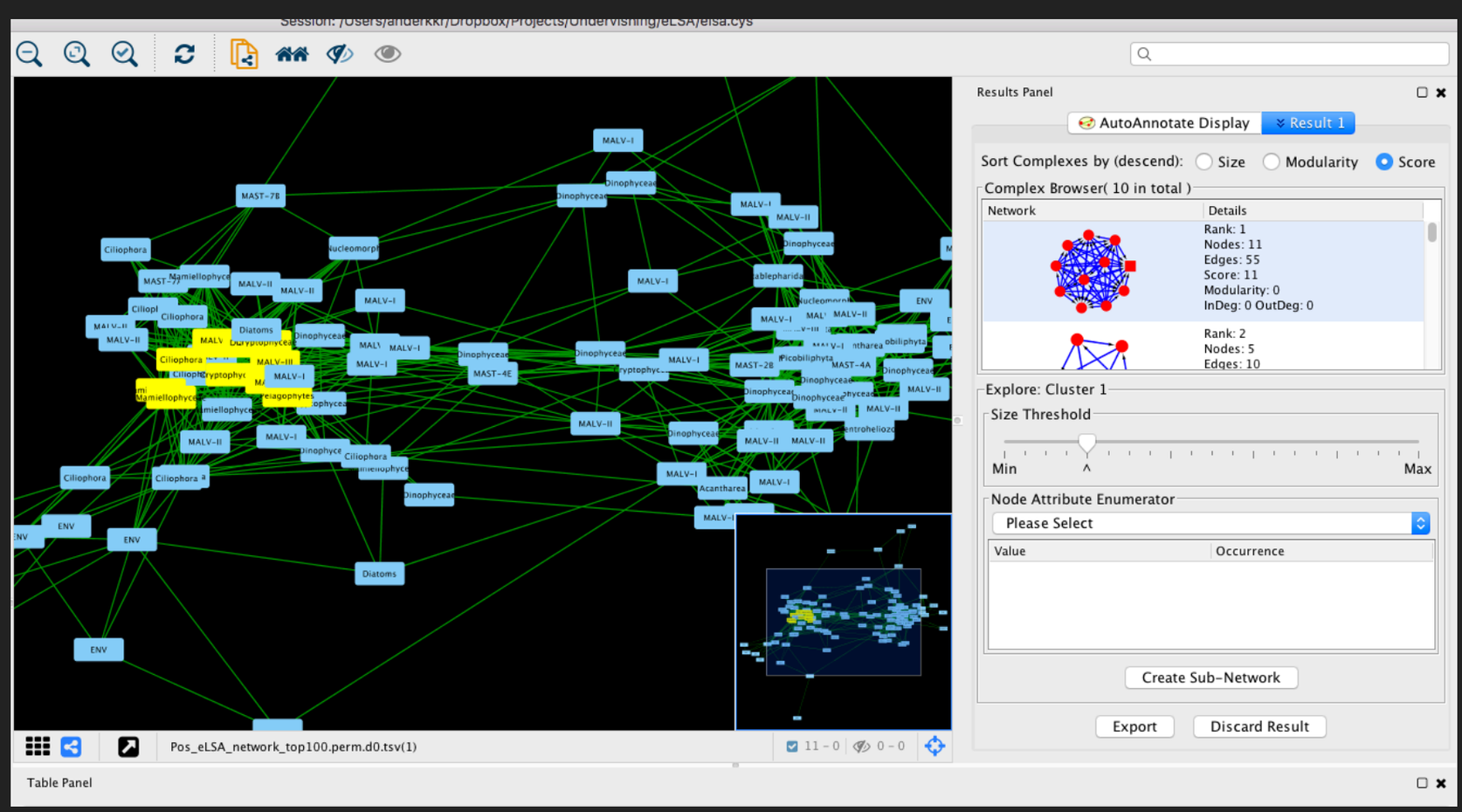
Choose '*select*'
and then '*node*' to change
the color, shape etc of the nodes



- Searching for **Modules**:
- Install **ClusterViz** from the App Manager



- Searching for Modules:
- (Save your project before moving on, just in case)
- Remove the negative edges, then search for Modules using MCODE in the ClusterViz App.



- Searching for Hubs (species that are highly connected, or have a high Degree). MCODE added the Degree for each node to the Node table.

Table Panel

shared name	name	AverageShortestPathLength	BetweennessCentrality	ClosenessCentrality	ClusteringCoefficient	Degree	Eccentricity
OTU_1	OTU_1	1.65486726	0.03309071	0.60427807	0.37439024	41	3
OTU_2	OTU_2	1.68141593	0.02127558	0.59473684	0.4048583	39	3
OTU_8	OTU_8	1.84955752	0.02086659	0.54066986	0.41269841	28	3
OTU_15	OTU_15	1.92035398	0.00404103	0.52073733	0.63333333	25	3
OTU_16	OTU_16	1.73451327	0.01822451	0.57653061	0.44507576	33	3
OTU_28	OTU_28	1.78761062	0.01807856	0.55940594	0.4516129	32	3
OTU_23	OTU_23	1.83185841	0.00877496	0.54589372	0.54232804	28	3
OTU_30	OTU_30	1.79646018	0.00946158	0.55665025	0.52643678	30	3
OTU_64	OTU_64	1.86725664	0.0054171	0.53554502	0.58465608	28	3
OTU_69	OTU_69	1.78761062	0.01844582	0.55940594	0.48790323	32	3
OTU_62	OTU_62	1.85840708	0.01512415	0.53809524	0.48029557	29	3

Degree (Integer)

Node Table | Edge Table | Network Table

- If there is time you can repeat these steps with the network with allowed delay to see if there are any differences. And see which if any species have a higher LS value when delay is allowed in the LS scoring.
- eLSA_network_top100.perm.d1.tsv