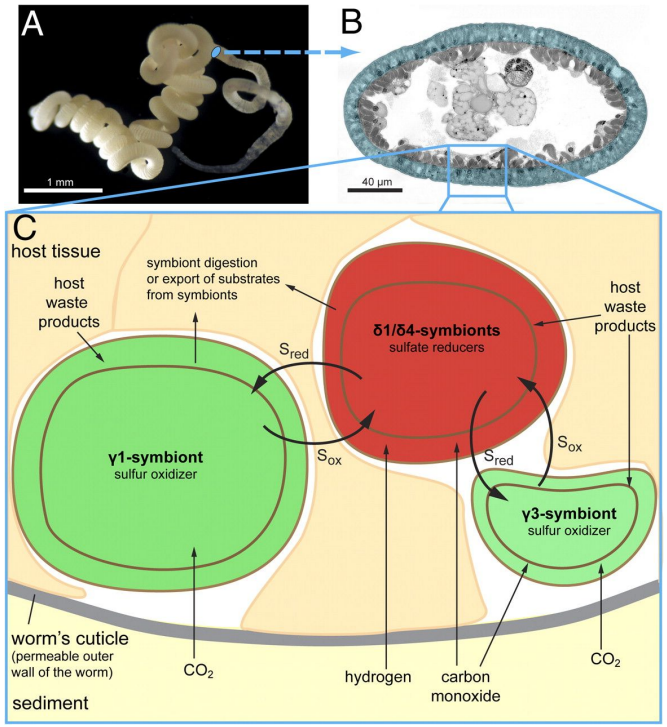
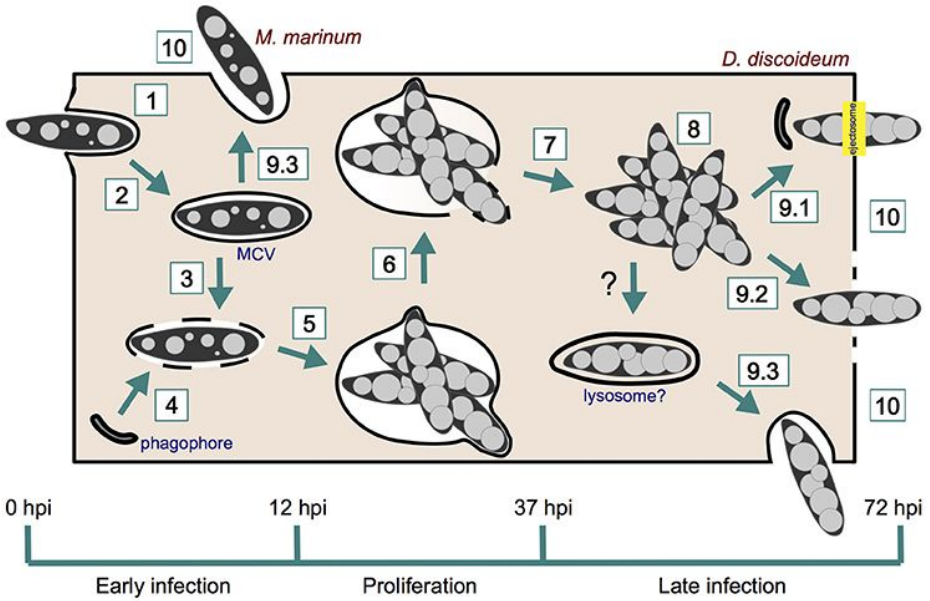
Network Analyses

network analysis represents an approach for exploring and identifying patterns in **large**, **complex** datasets, patterns that may be more difficult to detect using the standard alpha/beta diversity metrics widely used in microbial ecology.

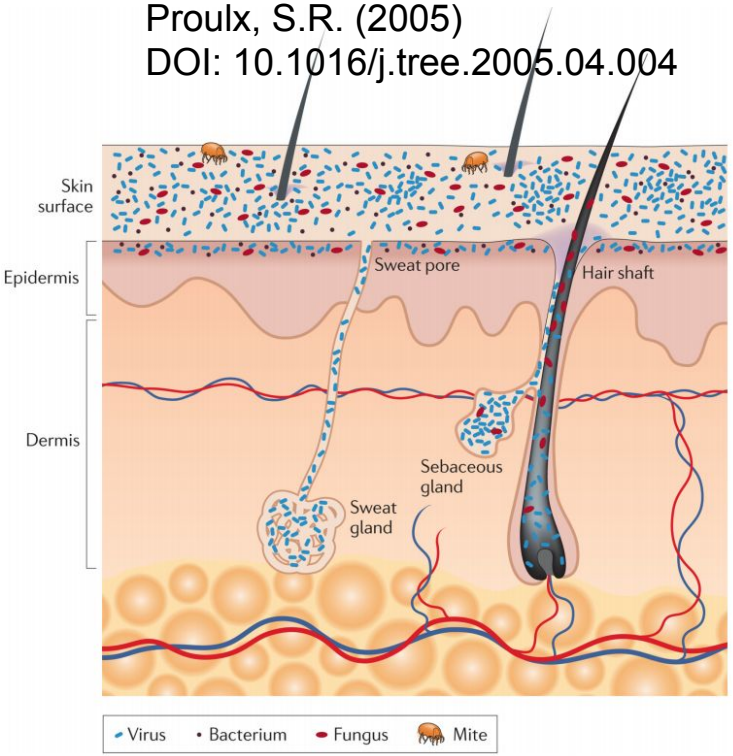


Kleiner, M. (2012)
DOI: 10.1073/pnas.1121198109



Cardenal-Muñoz, E. (2018)
DOI: 10.3389/fcimb.2017.00529

Proulx, S.R. (2005)
DOI: 10.1016/j.tree.2005.04.004



Grice, E.A. & Segre, J. A. (2011)
DOI: 10.1038/nrmicro2537

What are networks?

Essentially, **graphs.**

What are networks?

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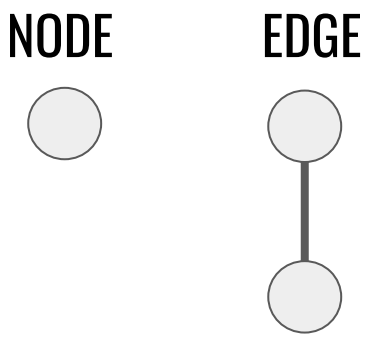
Entities

- nodes
- edges



What are networks?

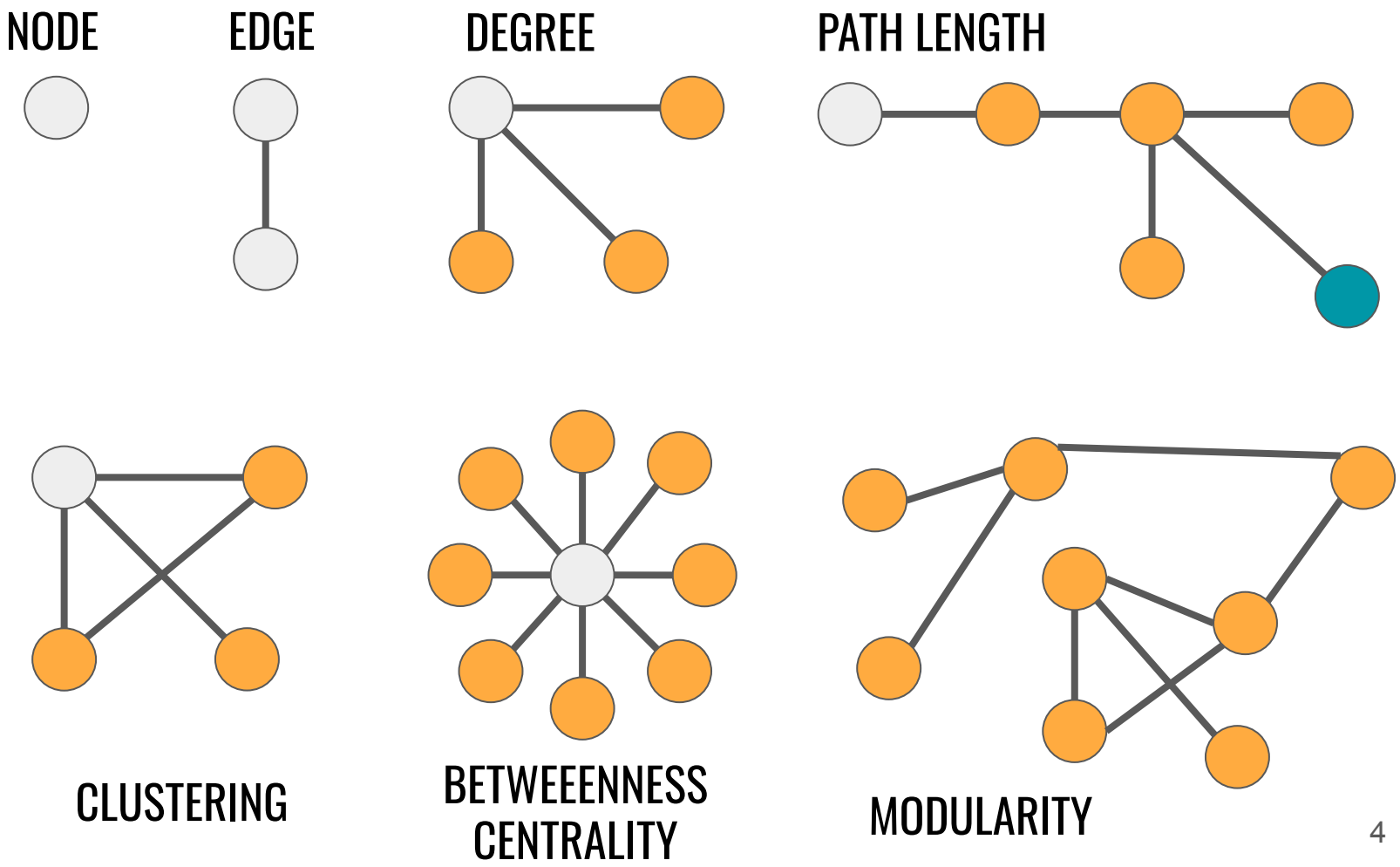
Essentially, **graphs.**

Entities

- nodes
- edges

Topology

- connectivity
- path length
- diameter
- clustering coefficient
- modularity



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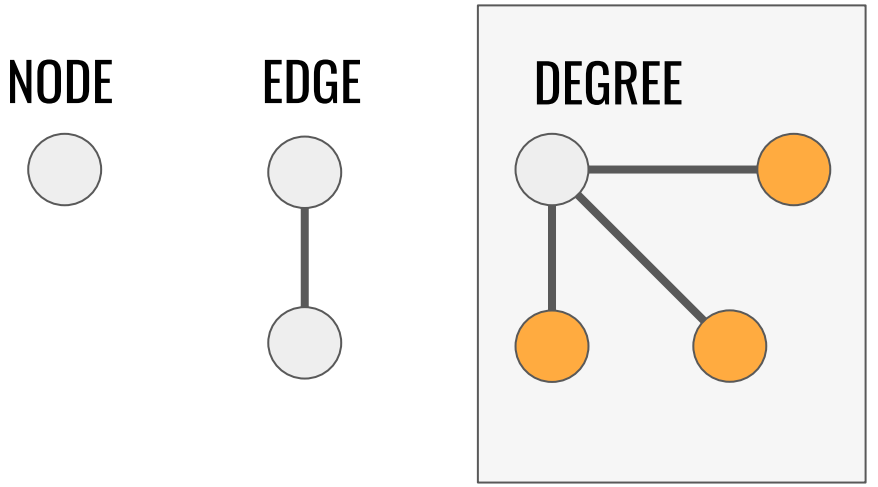
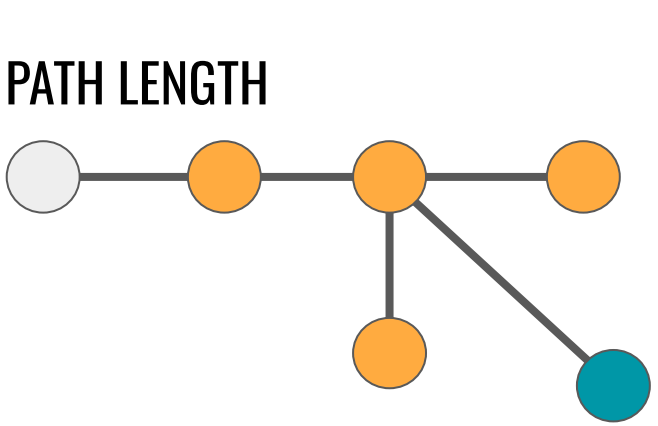
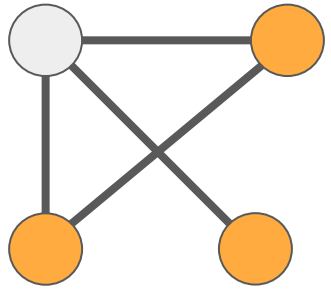
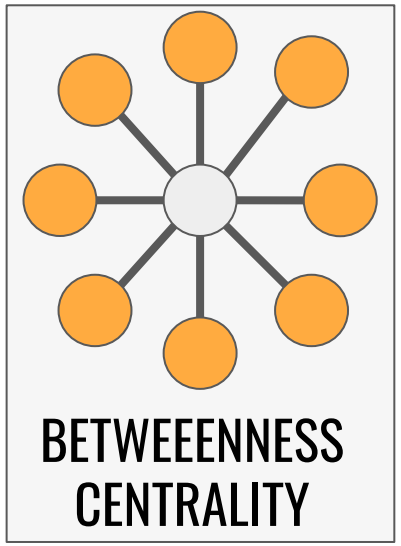
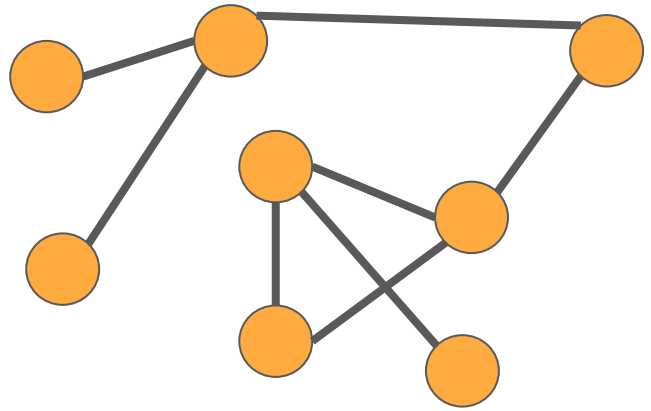






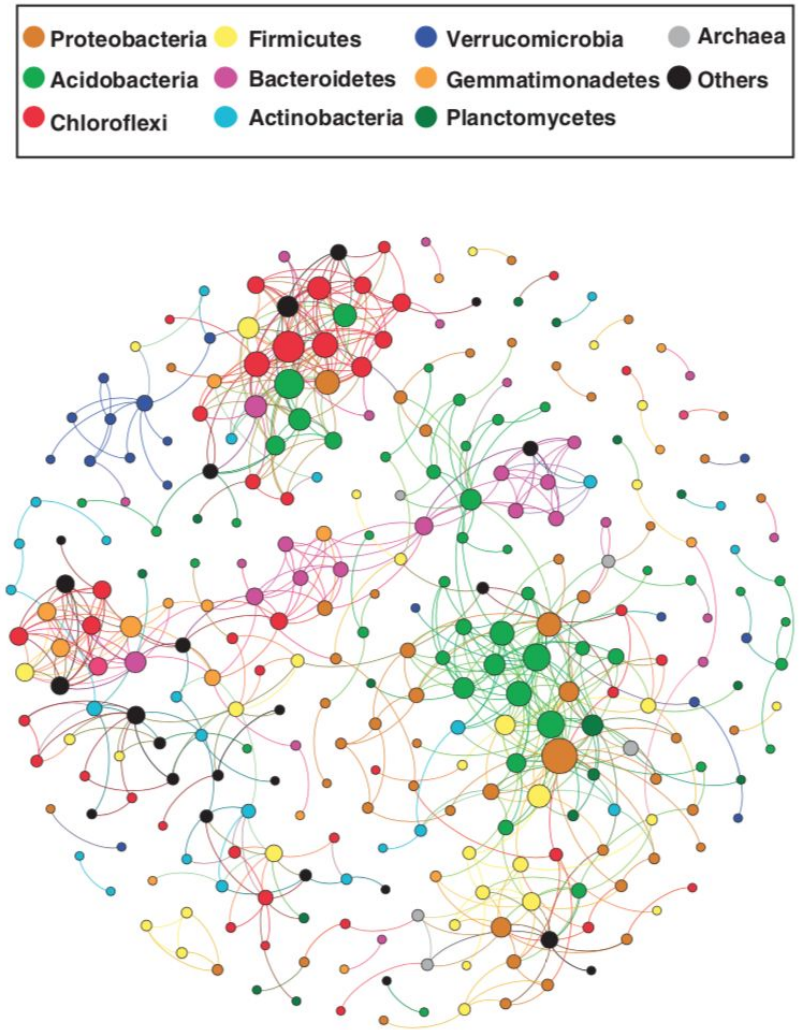




What are networks?

Using network analysis to explore co-occurrence patterns in soil microbial communities

Barberan, A. (2012)
DOI: 10.1038/ismej.2011.119



What are networks?

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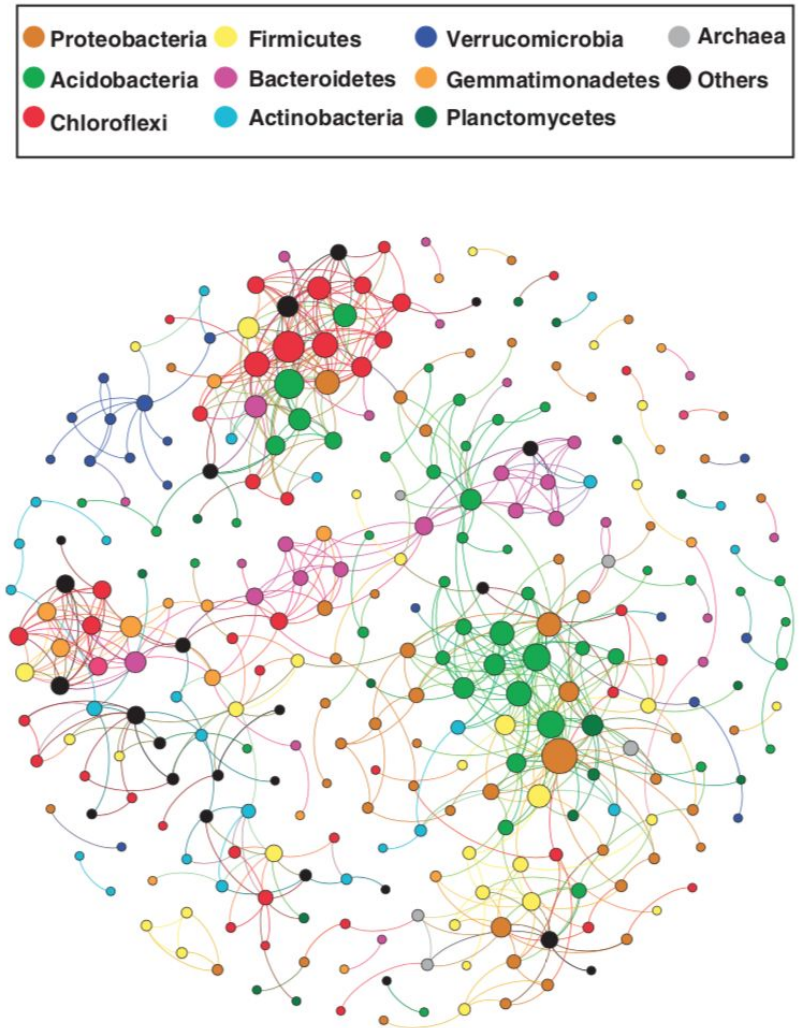
Essentially, **graphs.**

Entities

- nodes: OTUs ; 296
- edges: ρ > 0.6 & p<0.01 ; 679

Topology

- connectivity: 4.59
- path length: 5.53
- diameter: 18
- clustering coefficient: 0.33
- modularity: 0.77



What are networks?

Essentially, **graphs.**

Entities

- nodes
- edges

Topology

- connectivity
- path length
- diameter
- degree distribution
- clustering coefficient
- modularity

Using network analysis to explore co-occurrence patterns in soil microbial communities

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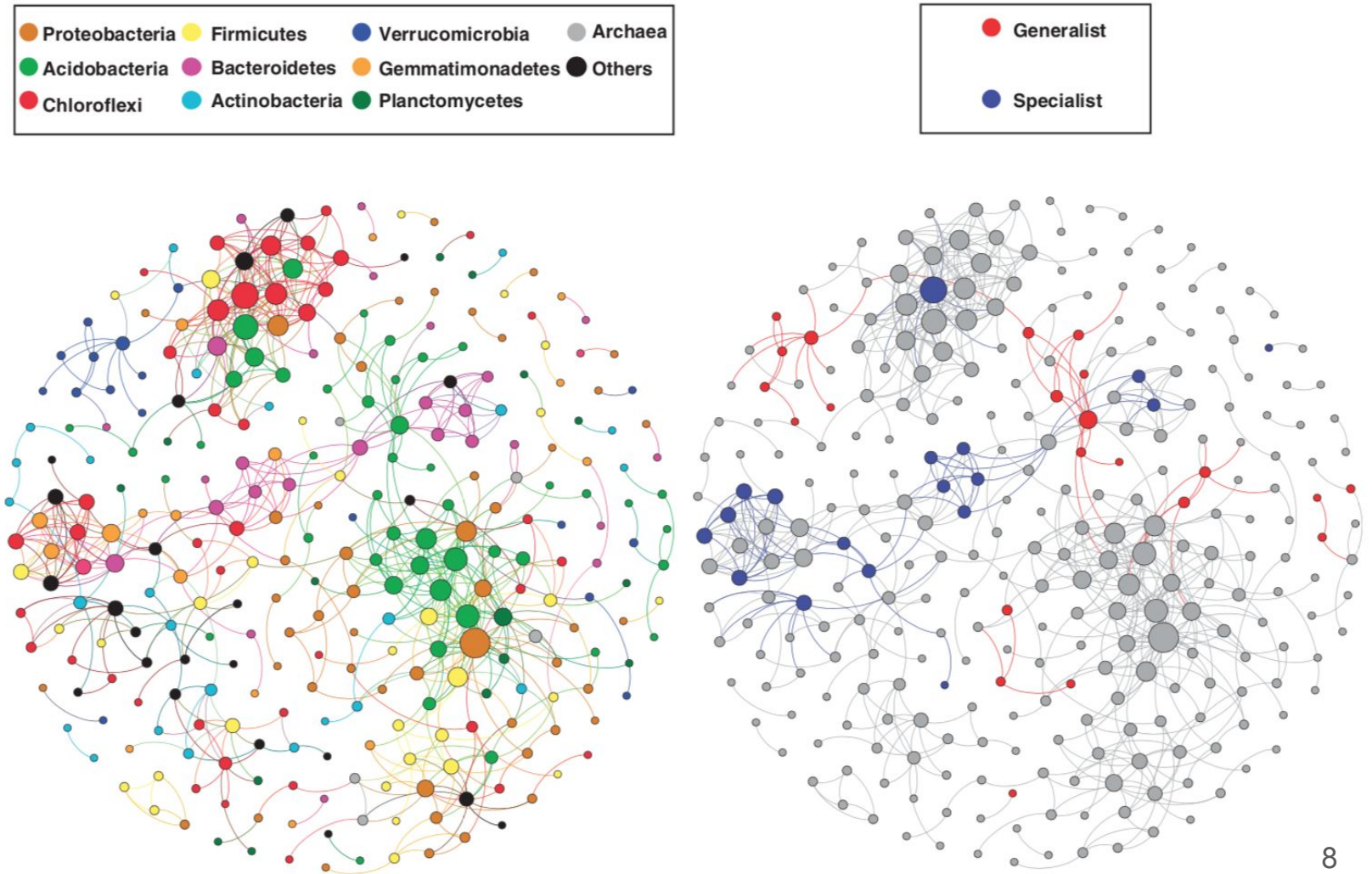
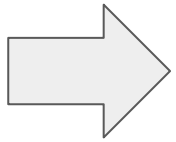


Network inference workflow

INPUT



Abundance Matrix

OTU ID	Sample 1	Sample 2	Sa
1	0	3	0
2	43	0	2
3	153	23	8
4	0	0	0

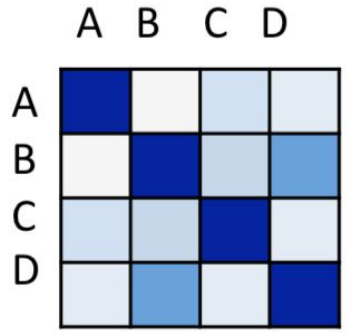
Sample data table

Sample ID	Treatment	Host
Sample 1	treated	A
Sample 2	treated	B
Sample 3	control	A
Sample 4	control	B

Network inference workflow

INPUT

SCORING



similarity based
taxon pairs

Faust, K (2012)
DOI: 10.1038/nrmicro2832

sparsity

compositionality

Network inference workflow

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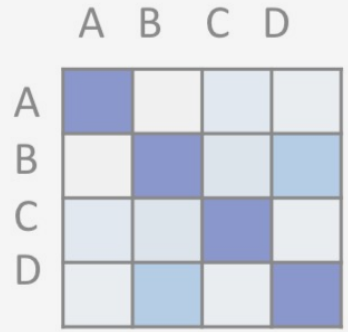

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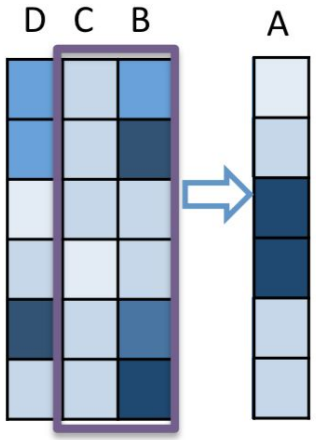


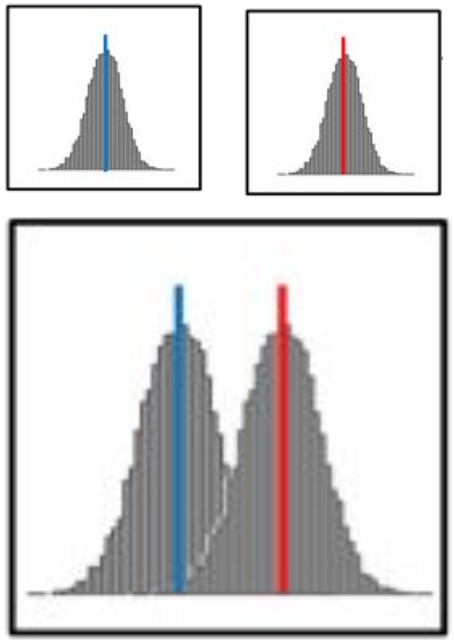
regression based
source taxa and target taxon

overfitting

hyperedges

Network inference workflow

INPUT → SCORING → ASSESSMENT OF SIGNIFICANCE



Randomize data multiple times and score

Compute p-values

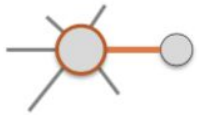
Discard below p-val threshold

Faust, K (2012)
DOI: 10.1038/nrmicro2832

Network inference workflow

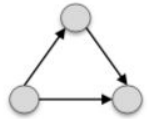
INPUT → SCORING → ASSESSMENT OF SIGNIFICANCE → VISUALIZATION & DESCRIPTION

Key actors and links

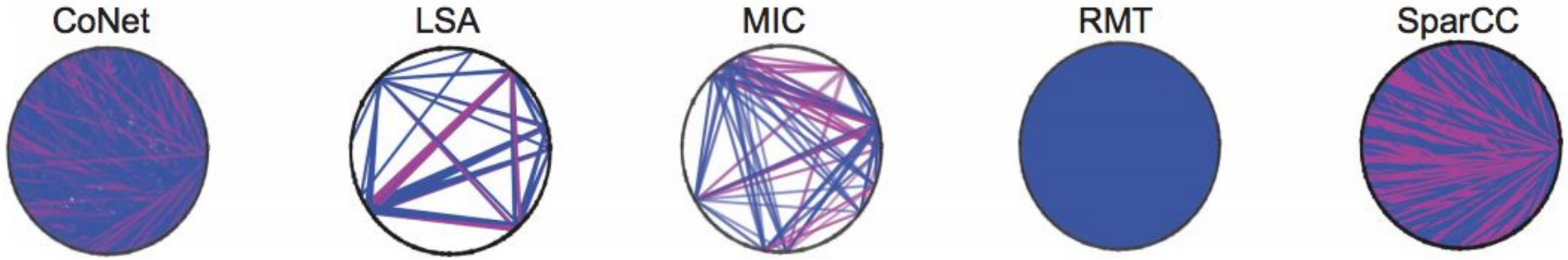


Relationship strength

Structural properties



Adapted from:
www.kateto.net



Weiss, S (2016)
DOI: 10.1038/ismej.2015.235

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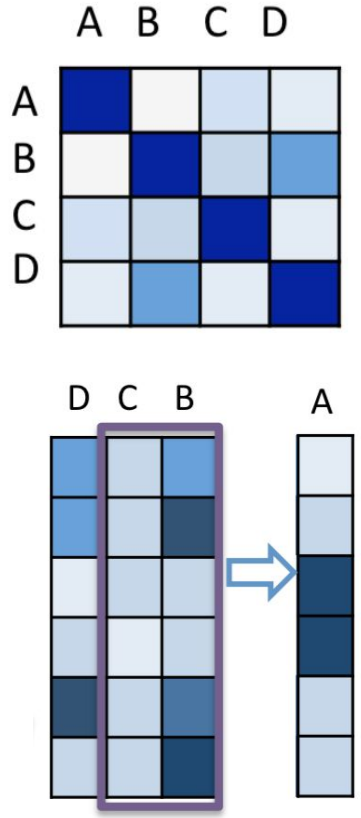

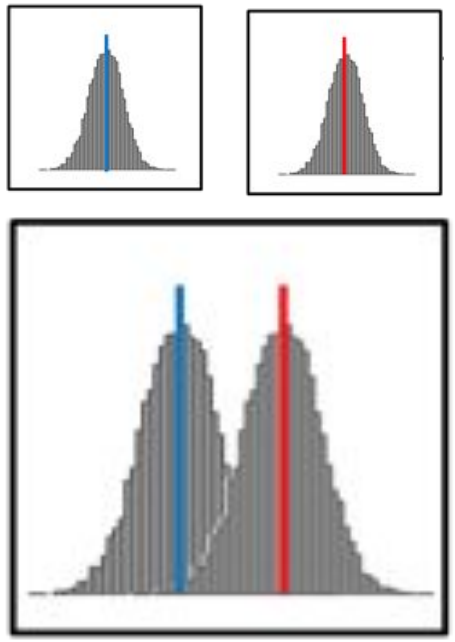

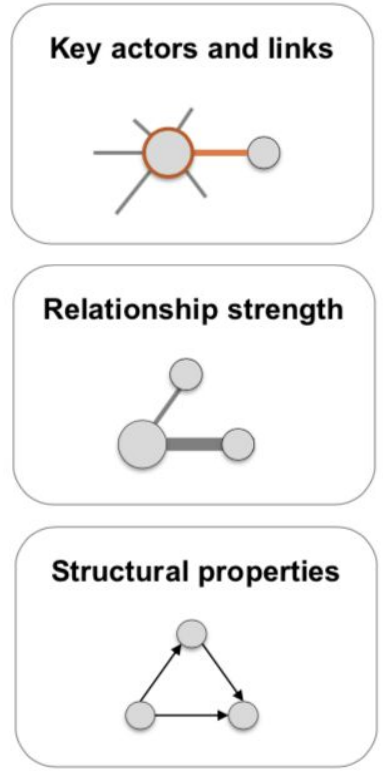

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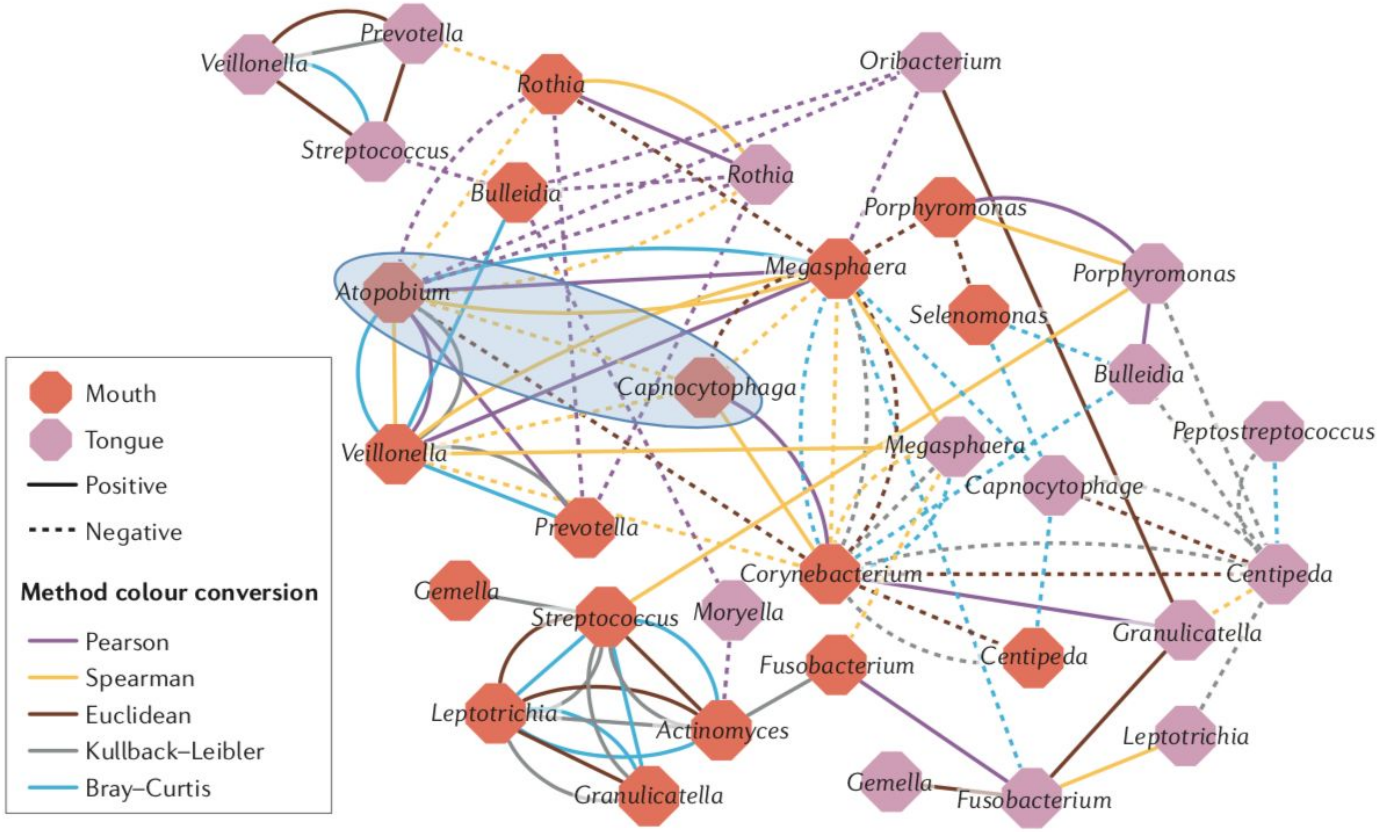
Network example: CoNet



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