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# CoNet Demo

# About CoNet

- Cytoscape plugin and command line tool to do ensemble-based relevance (similarity, dissimilarity, correlation) network inference

- web pages:

  http://systemsbiology.vub.ac.be/conet

  http://apps.cytoscape.org/apps/conet

- well documented (help pages, manual, tutorials, FAQ)

- support for row groups, presence/absence data, lagged similarities, minet integration, settings loading/saving and more

Demo data

- 52 arctic tundra soil samples collected in 2007 and 2008 by Chu and co-workers

- Roche FLX 454 sequencing using V1V2 region

- Processed with the QIIME pipeline

Soil bacterial diversity in the Arctic is not fundamentally different from that found in other biomes

Download demo data from QIIME

QIIME database needs registration, which is for free

ID: Chu_arctic_soils

http://www.microbio.me/qiime/

- convert biom file into classical OTU table using converter from http://biom-format.org/

- Command:

```
biom convert -i study_104_closed_reference_otu_table.biom -o arctic_soils.txt -b --header-key taxonomy
```

Extract features from mapping file

- mapping file (study_104_mapping_file.txt) contained in zip file downloaded from the QIIME database

- open mapping file in Excel

- select SampleID (remove #) and PH column

- save selection as tab-delimited file

Processed Demo Data

- Processed demo data are available from the CoNet web page, tutorial 5
- demo data contain:
  - OTU table (arctic_soils.txt)
  - feature matrix (arctic_soils_features.txt)
  - precomputed permutations (arctic_soils_permutations.txt)
  - precomputed bootstraps (arctic_soils_bootstraps.txt)

Configure OTU table loading

input file location

standard QIIME OTU table (lineages, if present, are parsed directly from this table)
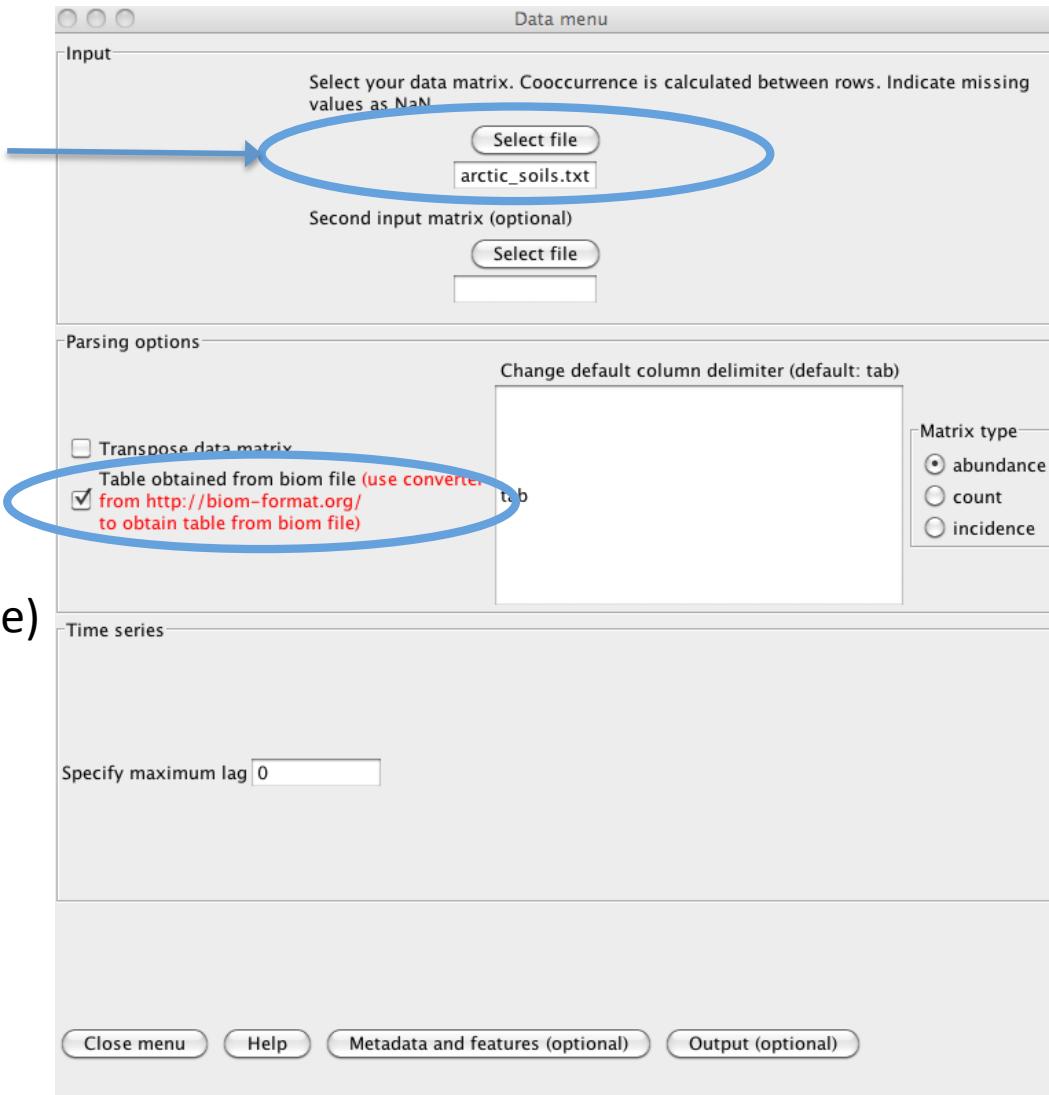
Higher-level taxa assignment

enable higher-level taxon assignment
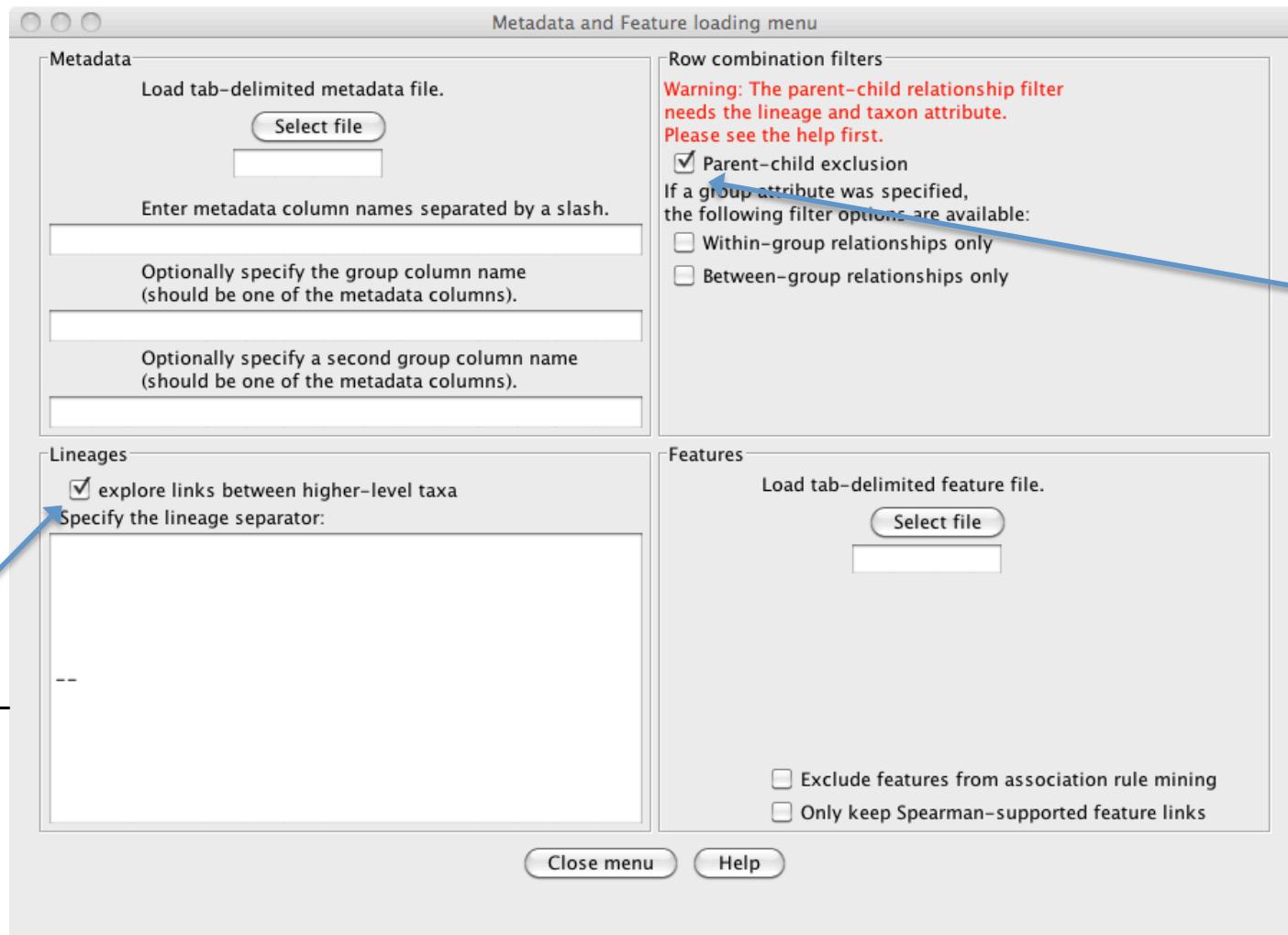
exclusion of parent-child relation-ships

Configure feature loading

select feature file

transpose feature matrix

match feature samples to OTU table samples
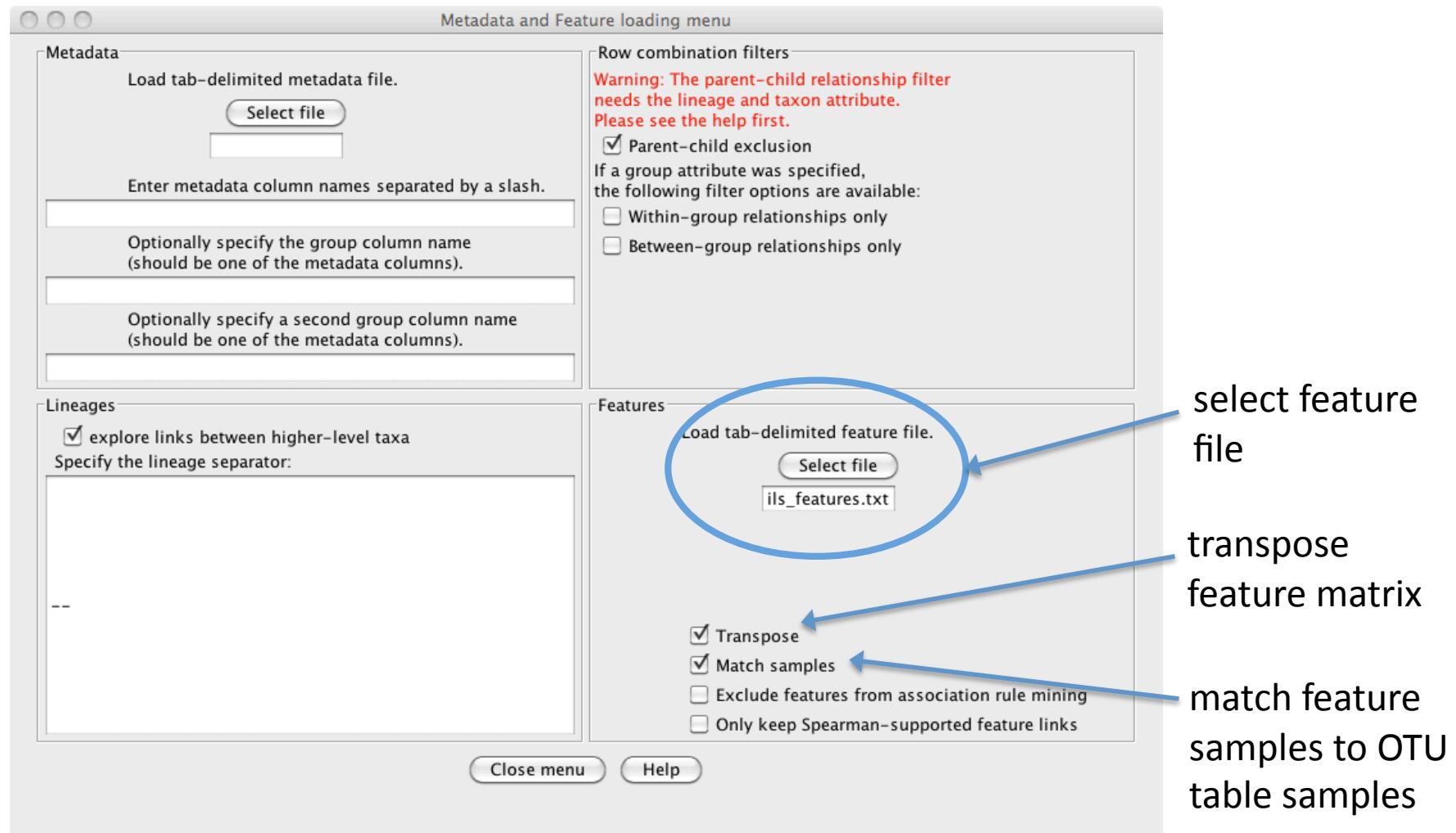
Configure preprocessing
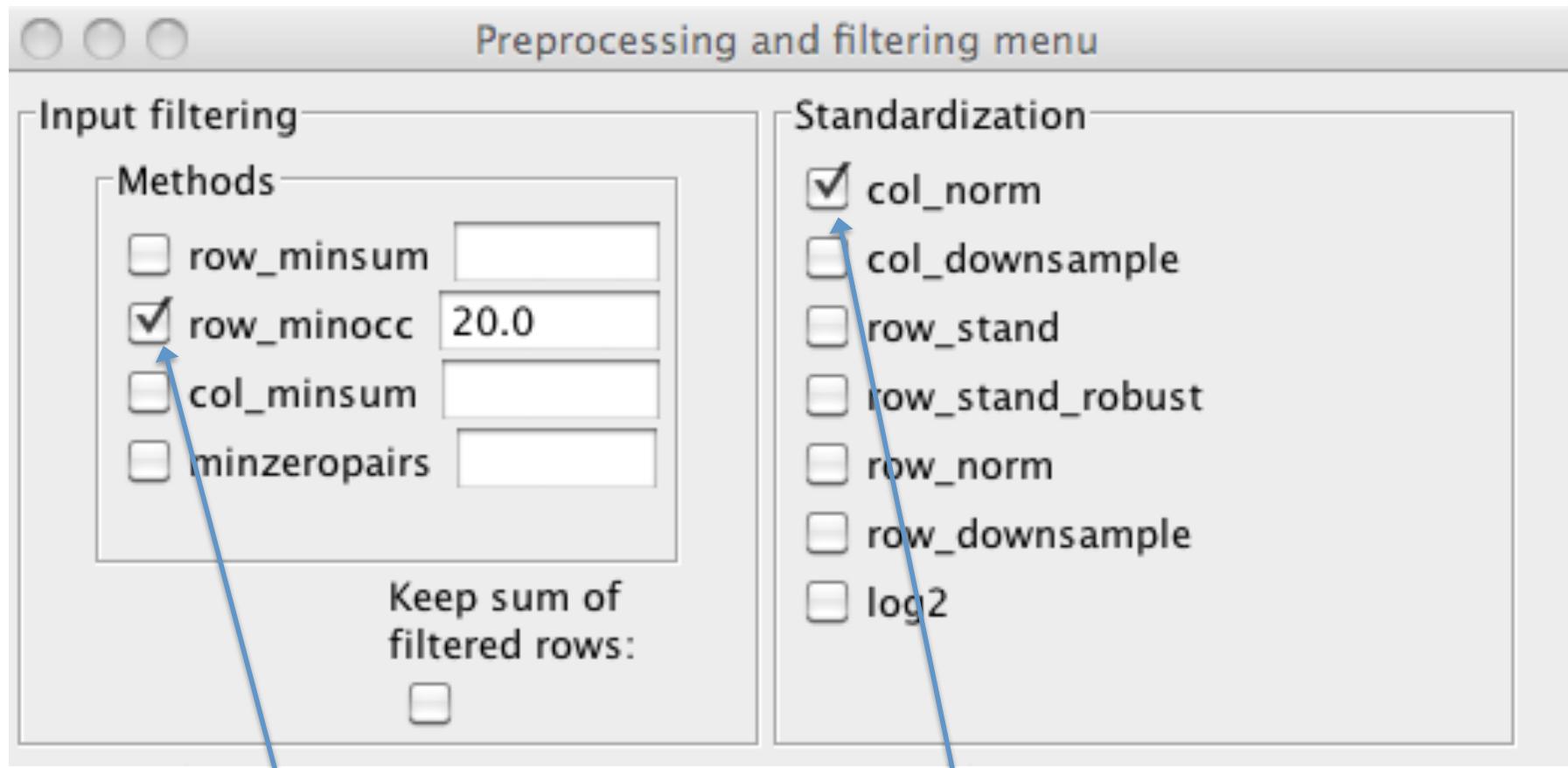
filter rows with too many zeros
(zeros bias correlation measures)

divide entries by the total count of their
corresponding column (takes out effects of
varying sequencing depth)

Select methods
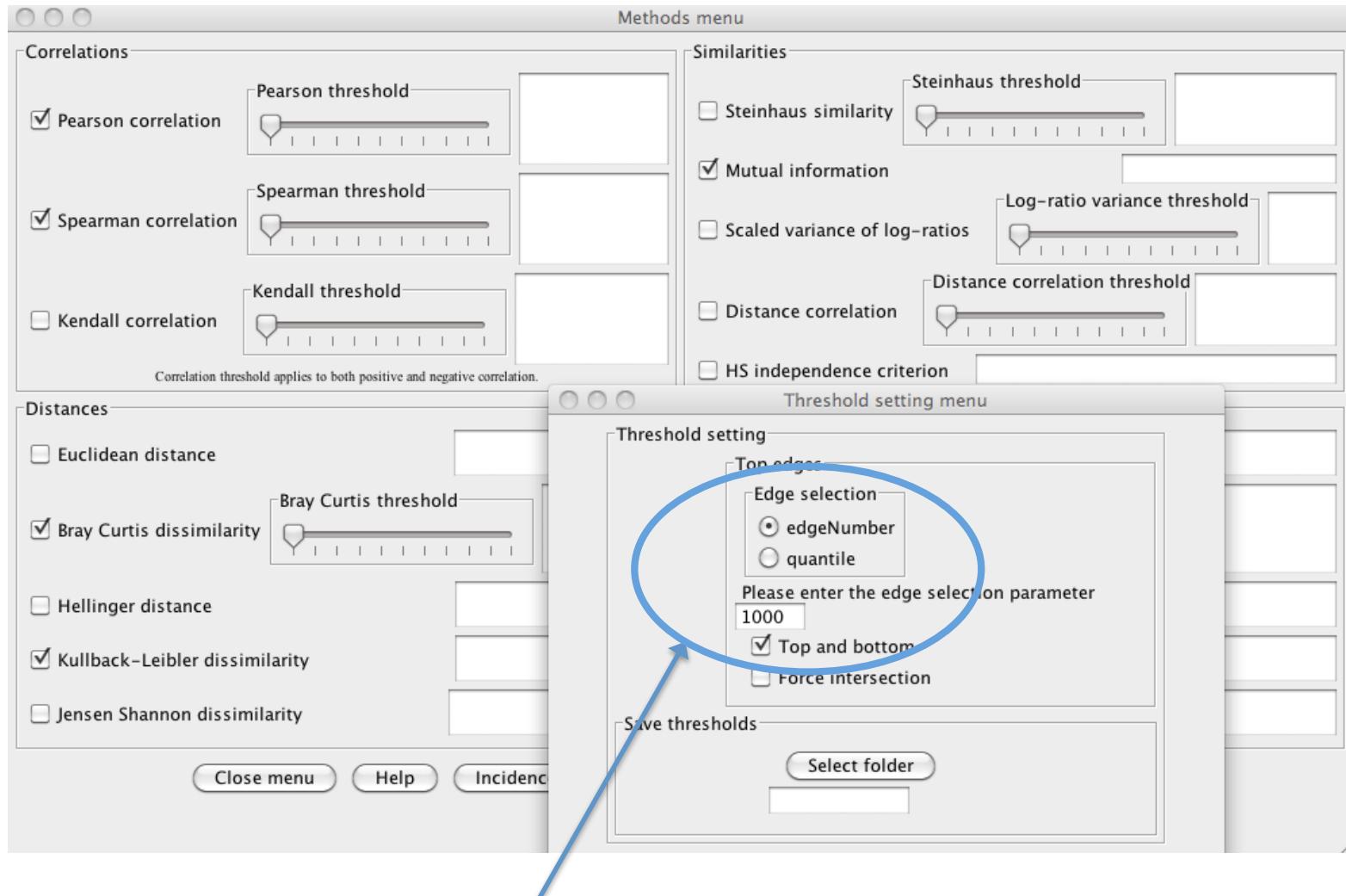
set thresholds such that the 1,000 highest and lowest scoring edges for each method are included in the initial network

Optional: Run CoNet on command line

Control Panel

Network VizMapper™ Editor Filters **CoNet**

CoNet command line

# Note that you need to point to the CoNet jar file using –cp and that a number of options have to be set via a con figuration file. You can open the command line help page to learn more about CoNet on command line. The followi ng options have to be set via a configuration file (check t he help or command line option –Z for configuration file parameter names): PseudoCounts, LineageSeparator, MiI mplementation, RserveHost, RservePort, NoRserveDepend ency, Poolvar, DisableSpeedup
java be.ac.vub.bsb.cooccurrence.cmd.CooccurrenceAnaly ser --method ensemble --input /Users/karoline/Docum ents/Documents_Karoline/BSB_Lab/CoNetProject/DEMO/ arctic_soils.txt --matrixtype abundance --thresholdgues sing edgeNumber --guessingparam 1000.0 --resamplem ethod shuffle_rows --ensemblemethods correl_pearson/ correl_spearman/sim_mutInfo/dist_bray/dist_kullbacklei bler --max 3 --format gdl --stand col_norm --minetdis c equalfreq --minetmiestimator mi.shrink --kernelwidth 0.25 --edgethreshold 0.05 --nantreatment none --nant reatmentparam 1 --networkmergestrategy union --input format biomtable --features /Users/karoline/Documents /Documents_Karoline/BSB_Lab/CoNetProject/DEMO/arcti

Help

Close

GO

Generate command line call

Settings loading/saving

Demo

Load GDL network

Load

Help   About CoNet

click here to generate command line call

- copy-paste first java command line call (first line starting with java and ending with thresholds.txt) into a text editor, add the path to the CoNet jar file via -cp argument, copy the extended command into a shell and enter
- **threshold file** will be created in temporary directory
- repeat the same steps for the second java command line call (second line starting with java)
- **network file** (ending in .gdl) will be generated in current directory

Example of a (simplified) command line call with jar file included (do not copy-paste this example into a shell):
java be.ac.vub.bsb.cooccurrence.cmd.CooccurrenceAnalyser **-cp /Applications/Cytoscape_v2.8.0/plugins/CoNet.jar** --method ensemble --input arctic_soils.txt --matrixtype abundance --thresholdguessing edgeNumber --guessingparam 1000.0 --ensemblemethods correl_pearson/correl_spearman/sim_mutInfo/dist_bray/dist_kullbackleibler --stand col_norm --minetdisc equalfreq --inputformat biomtable --features arctic_soils_features.txt --multigraph --higherleveltaxa --transposefeatures --matchfeaturesamples --topbottom --filter row_minocc/noinclusivetaxalinks --filterparameter 20.0 --output thresholds.txt

Optional: Load command line result into Cytoscape
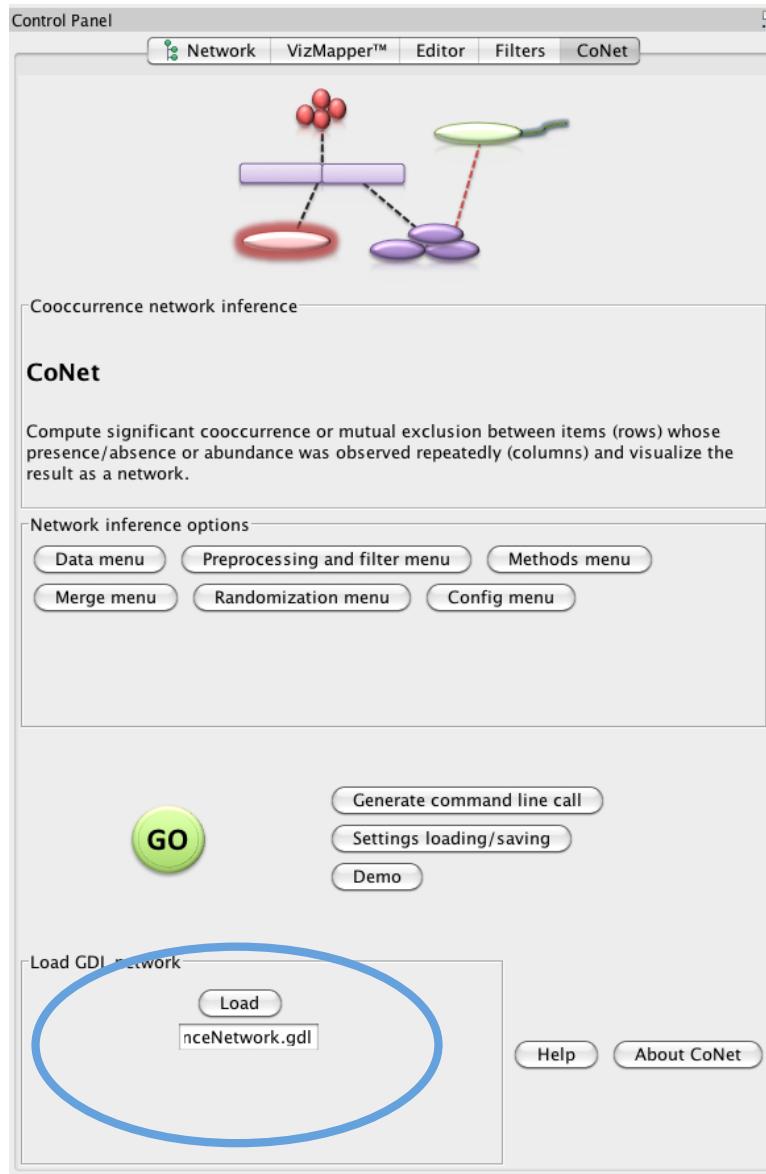
select gdl network
file to load

Click

Compute permutations

row-wise permutation with 100 iterations

enable renormalization
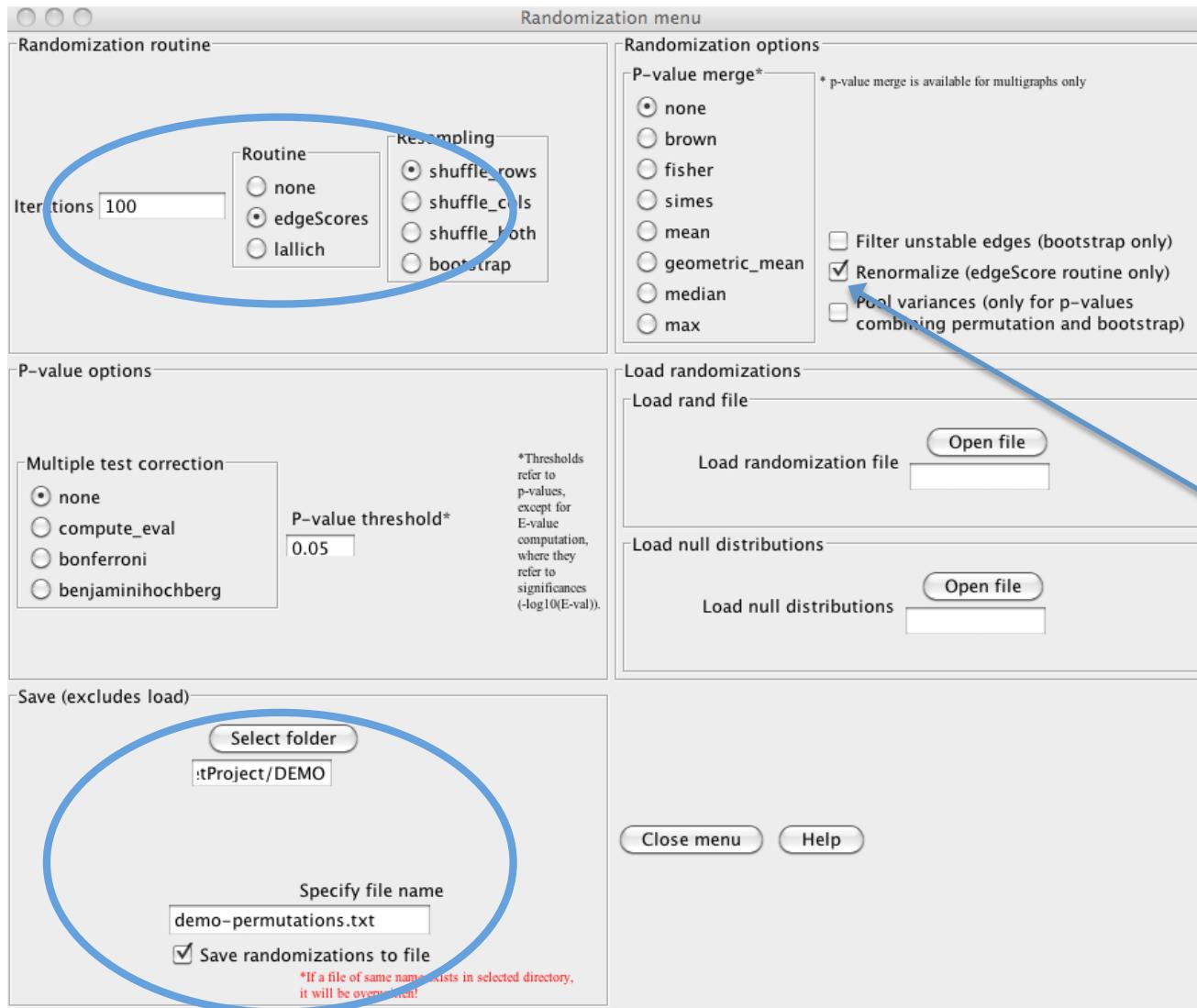
save permutation scores to a file

Click

Compute bootstraps

100 bootstrap iterations
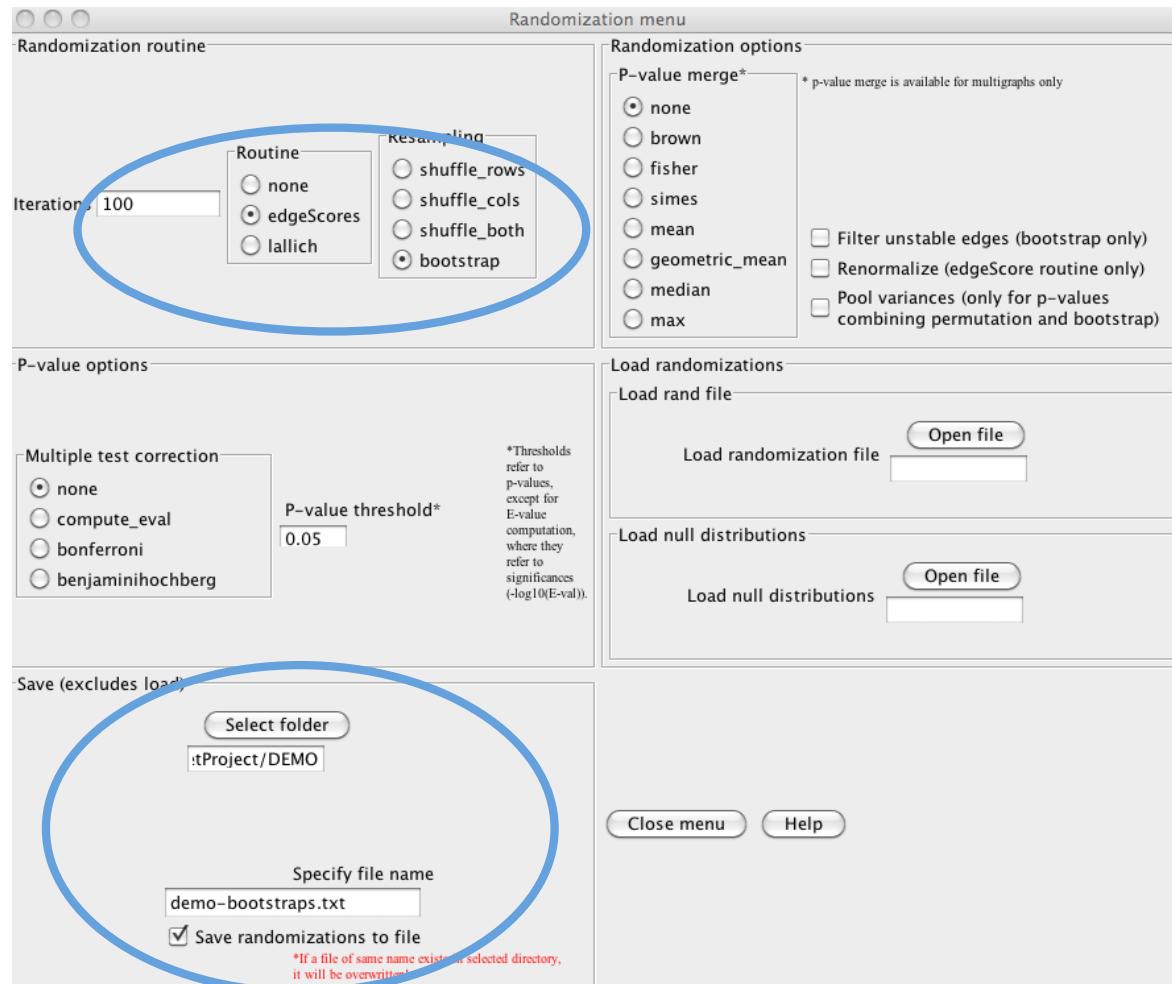
save bootstrap scores to a file

Click

GO

Build final network
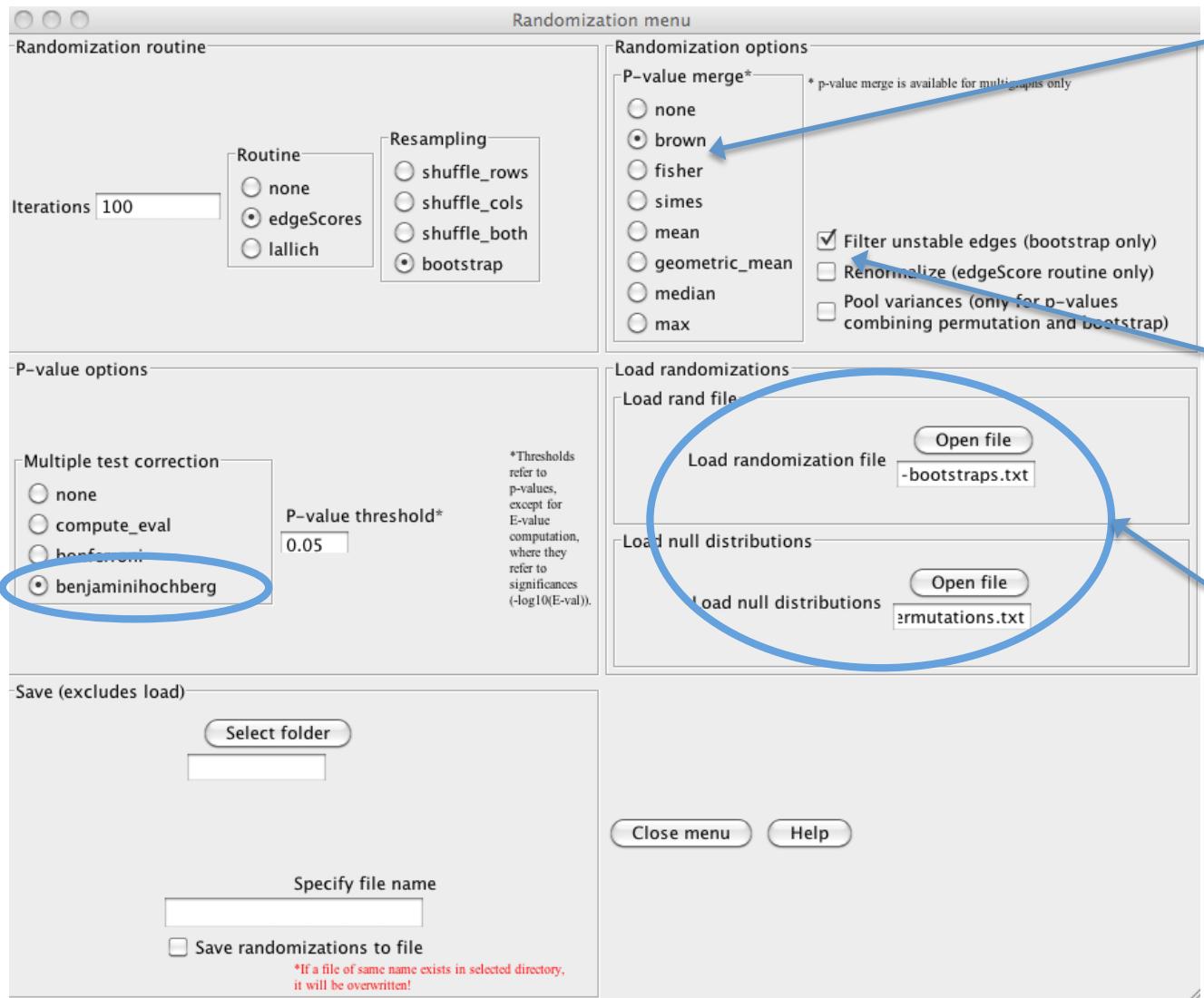
Beautify the network

1. Layout the network with yFiles

Layout

⬇
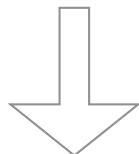
yFiles

⬇
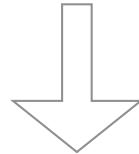
Organic

2. Color phyla with the VizMapper
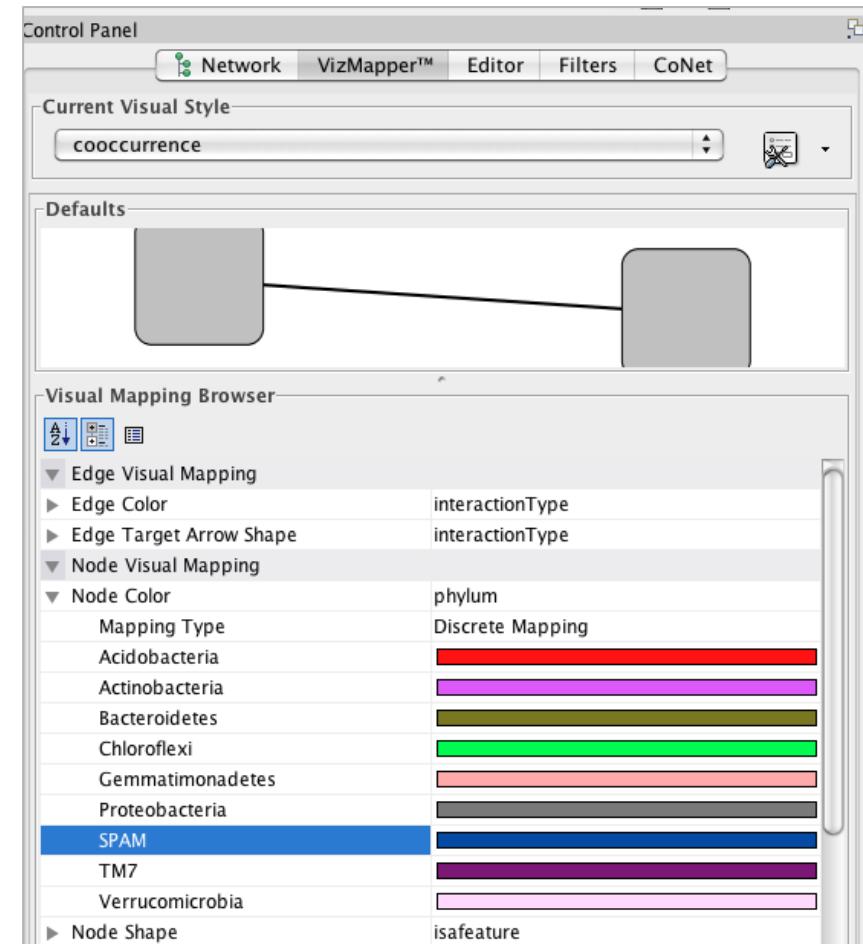
Result network
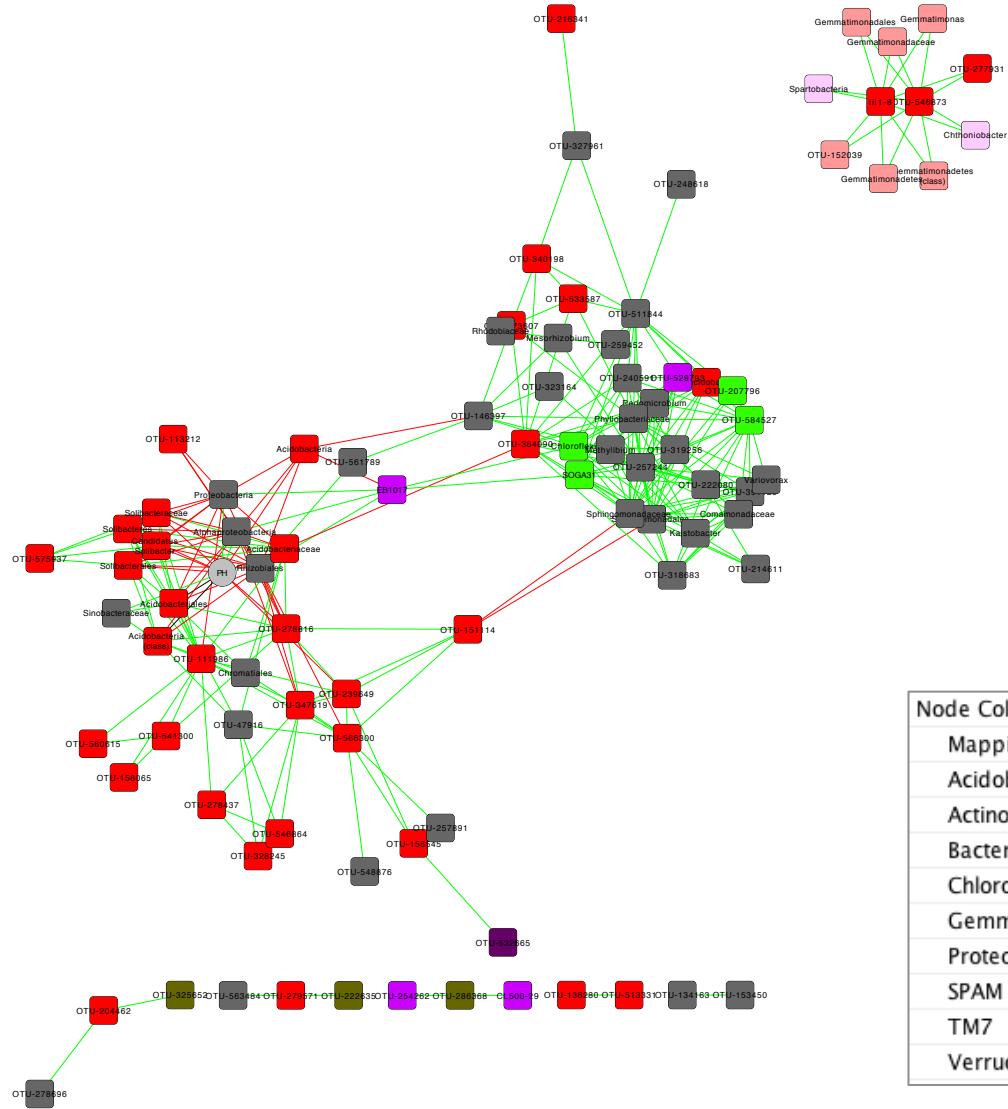
Node Color	phylum
Mapping Type	Discrete Mapping
Acidobacteria	
Actinobacteria	
Bacteroidetes	
Chloroflexi	
Gemmatimonadetes	
Proteobacteria	
SPAM	
TM7	
Verrucomicrobia	

Interpretation of results
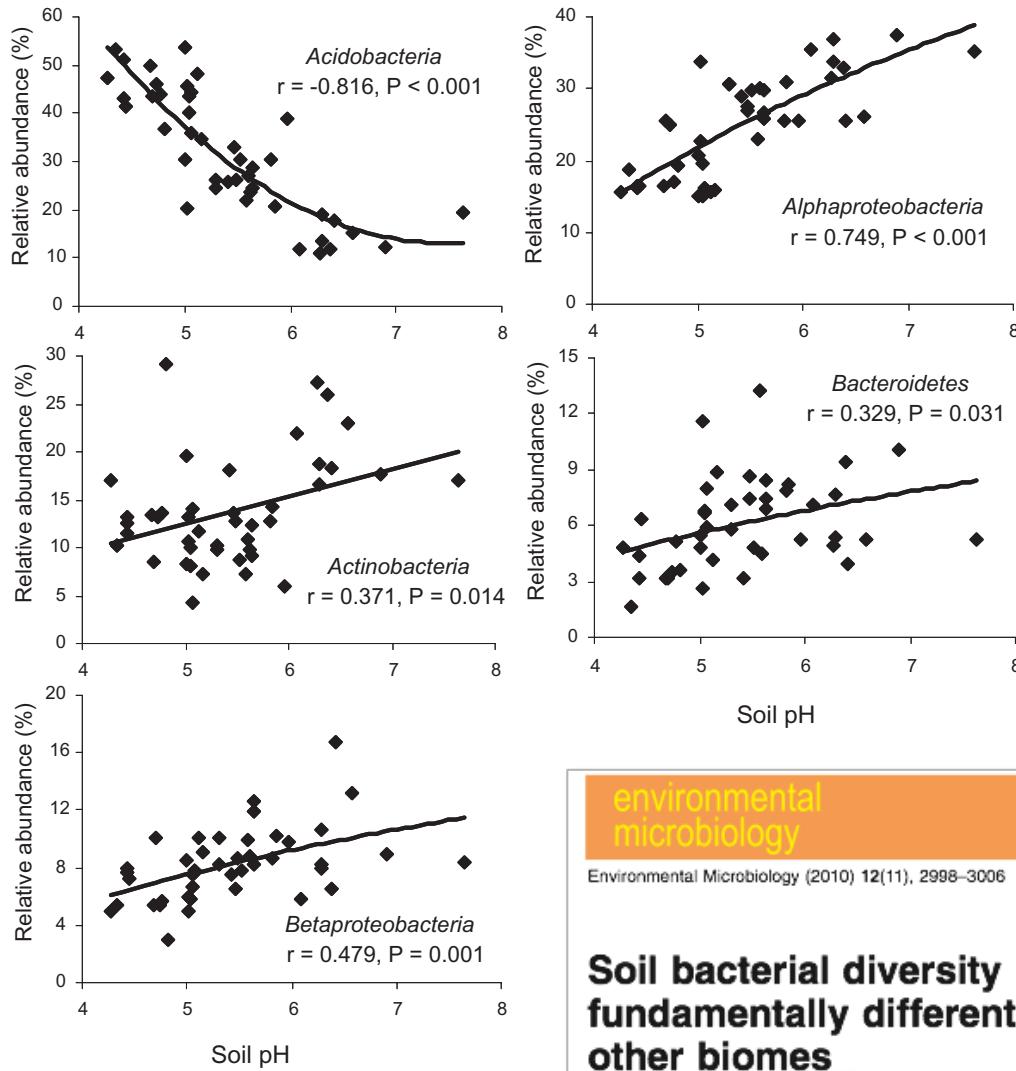
Anti-correlation between Proteobacteria OTUs and Acidobacteria OTUs is pH-driven.

Soil bacterial diversity in the Arctic is not fundamentally different from that found in other biomes

Next steps

- analyze network properties such as modularity, diameter, average cluster coefficient and node degree distribution using Cytoscape plugin "Network analysis"
- cluster network with Cytoscape plugins "CommFinder", "clusterMaker" or "MCODE"