# F1000Research

SOFTWARE TOOL ARTICLE

# CoNet app: inference of biological association networks using Cytoscape [version 1; referees: 2 approved with reservations]

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## Abstract

Here we present the Cytoscape app version of our association network inference tool CoNet. Though CoNet was developed with microbial community data from sequencing experiments in mind, it is designed to be generic and can detect associations in any data set where biological entities (such as genes, metabolites or species) have been observed repeatedly. The CoNet app supports Cytoscape 2.x and 3.x and offers a variety of network inference approaches, which can also be combined. Here we briefly describe its main features and illustrate its use on microbial count data obtained by 16S rDNA sequencing of arctic soil samples. The CoNet app is available at: http://apps.cytoscape.org/apps/conet.

This article is included in the Cytoscape apps channel.

## Open Peer Review

Referee Status: ☑☑

| | Invited Referees | |
|---|---|---|
| | **1** | **2** |
| REVISED **version 2** published 14 Oct 2016 | | |
| **version 1** published 27 Jun 2016 | ☑ report | ☑ report |

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Comments (0)

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**Competing interests:** The authors declare that they have no competing interests.

## Introduction

Modern sequencing technology in combination with dedicated analysis pipelines allows determining the relative abundances of microbial community members, thereby obtaining microbial count data. Such community profiling experiments have been carried out for thousands of samples from a variety of ecosystems, ranging from the world's oceans (Bork *et al.*, 2015) to the human gut (Falony *et al.*, 2016; The Human Microbiome Project Consortium, 2012).

The analysis of species abundance patterns has a long tradition in ecology (Connor & Simberloff, 1979; Diamond, 1975; Gotelli & McCabe, 2002). More specifically, co-occurrence analysis detects significant co-occurrences or mutual exclusions across samples, which are interpreted as representing ecological relationships such as mutualism or competition or being due to similar responses to environmental factors. Co-occurrence analysis is an instance of network inference, an exploratory data analysis technique that attempts to unravel relationships between objects from repeated observations. The large number of microbial count tables resulting from the multitude of recent sequencing projects (e.g. Bork *et al.*, 2015; Falony *et al.*, 2016; Gilbert *et al.*, 2014; The Human Microbiome Project Consortium, 2012) opens the way to unraveling the complex relationships between microorganisms from their abundances across samples. CoNet was developed to carry out microbial network inference, but its generic design makes it applicable to any data set where objects have been observed repeatedly.

## Methods/Implementation

The CoNet app wraps the CoNet command line tool. The command line and Cytoscape 2.× app version are implemented in Java 1.6, whereas the Cytoscape 3.× app version requires Java 1.7.

### Implementation challenges and decisions

In general, the CoNet app is designed with minimum contact to Cytoscape, to ensure consistent behavior across different Cytoscape versions and to ease porting to future Cytoscape versions. The CoNet app is linked to Cytoscape only via its main menu and graph visualization classes. The Cytoscape-version-specific implementation of the graph visualization class is loaded via reflection at run time and is entirely separated from graph generation.

A major challenge for the implementation of the CoNet app is inclusion of the large number of options available in CoNet, which allows users to customize each network inference step, from data preprocessing via threshold setting, network construction and assessment of significance. This problem was solved by implementing a single user input handling class, which collects and checks user input from the various menus and submits it to CoNet once the GO button is pushed. This design allows to export and to read in user settings files, which make experiments carried out with the CoNet app more reproducible.

Another challenge is the command line support. Network inference from large data sets is not feasible within Cytoscape and CoNet is best run on command line for these cases. To facilitate this step for the inexperienced user, the current settings of the CoNet app can be exported as a command line call, by clicking the "Generate command line call" button. This call can then be executed on command line by including the CoNet jar file in the class path. Networks generated on command line can be loaded either via Cytoscape network import functions (if saved in gml format ((Himsolt)) or more conveniently via the CoNet app (if saved in the custom gdl format). The CoNet app's manual includes a step-by-step tutorial for command line usage.

The CoNet app also integrates the popular network inference R Bioconductor package minet (Meyer *et al.*, 2008). We decided to integrate it loosely via Rserve, a Java-R bridge capable of transferring R objects to Java and *vice versa* (http://rforge.net/Rserve/). Thus, advanced users can install and launch the Rserve server in R and configure the Rserve client settings (i.e. host and port) in CoNet app's configuration menu. The CoNet app's manual explains Rserve installation and usage.

Finally, we also implemented solutions for error and help display. The CoNet app displays help pages in html format, which allows the user to follow links within these pages. The CoNet app's pdf manual is compiled from the help pages using prince (http://www.princexml.com/). Each menu is linked to its specific help page, easing navigation.

When an error has been captured, an error report is generated that includes the error message as well as the CoNet app's current settings.

### Network inference workflow

CoNet takes a presence/absence, count or abundance matrix as input, where rows represent the objects of interest and columns their observations across locations or time points. Optionally, a second input matrix can be provided. This is of interest when two different measurements have been made for the same samples, for instance counts of microorganisms and concentrations of metabolites. CoNet's output consists of a network where significantly associated objects are connected by edges.

Depending on the data type, a number of filters needs to be applied. For instance, for 16S rDNA count data, taxa with too few non-zero observations need to be removed and the data needs to be normalized or rarefied to account for sequencing depth differences. In the next step, the user can select from a number of different correlations (Pearson, Spearman, Kendall), similarities (mutual information, Steinhaus, distance correlation etc.) or dissimilarities (Kullback Leibler, Euclidean, Bray Curtis, Jensen-Shannon *etc.*) to score the association strength between the objects. For presence/absence (also termed incidence) data, the hypergeometric distribution or Jaccard distance can be chosen for the same purpose. CoNet's special strength is its capability to combine multiple such measures and/or to combine these measures with other network inference algorithms, e.g. those implemented in minet. The idea behind such an ensemble approach to network inference is to exploit the fact that different methods make different mistakes. If erroneous edges predicted by one method are not supported by the others, they can be filtered out, thereby reducing the number of false positives. The

thresholds for the measures can be either set manually (using sliding windows for bounded measures) or automatically, by specifying the desired number of edges in the output network. The network can then be displayed either as a multigraph (with as many edges between two objects as selected measures) or as a graph (where scores of individual measures are combined). Optionally, the significance of the associations can be computed, *e.g.* with a permutation test. Multiple testing correction can be performed with either Bonferroni or Benjamini-Hochberg procedures. Figure 1 summarizes this workflow.

### Special features
CoNet offers a series of features that distinguish it from other network inference tools, such as its support for object groups. This feature allows a user to assign objects to different groups (*e.g.* metabolites and enzymes). Relationships can then be inferred only between different object types (resulting in a bipartite network) or only within the same object type. CoNet's treatment of two input matrices is built upon this feature.

Furthermore, CoNet can handle row metadata, which allows for instance to infer links between objects at different hierarchical levels (*e.g.* between order Lactobacillales and genus Ureaplasma)

while preventing links between different levels of the same hierarchy (e.g. Lactobacillales and Lactobacillaceae). CoNet can also parse sample metadata such as temperature or oxygen concentration, which are then correlated with the objects in the input matrix while being excluded from normalization. In addition, CoNet recognizes abundance tables generated from biom files (McDonald *et al.*, 2012) and, in its Cytoscape 3.× version, reads biom files in HDF5 format directly, using the BiomIO Java library (Ladau). Phylogenetic lineages in these tables are automatically parsed and displayed as node attributes of the resulting network. CoNet also computes a few node properties, such as a node's total edge number as well as the number of positive and negative edges, the total row sum and the number of samples in which the object was observed (e.g. was different from zero or a missing value).

To ease the selection of suitable preprocessing steps, CoNet can display input matrix properties and recommendations based on them. Importantly, CoNet can also handle missing values, by omitting sample pairs with missing values from the association strength calculation. Finally, CoNet supports a few input and output network formats absent in Cytoscape, including adjacency matrices (import), dot (the format of GraphViz (http://www.graphviz.org/)) and VisML (VisANT's format (Hu *et al.*, 2013)) (both for export).
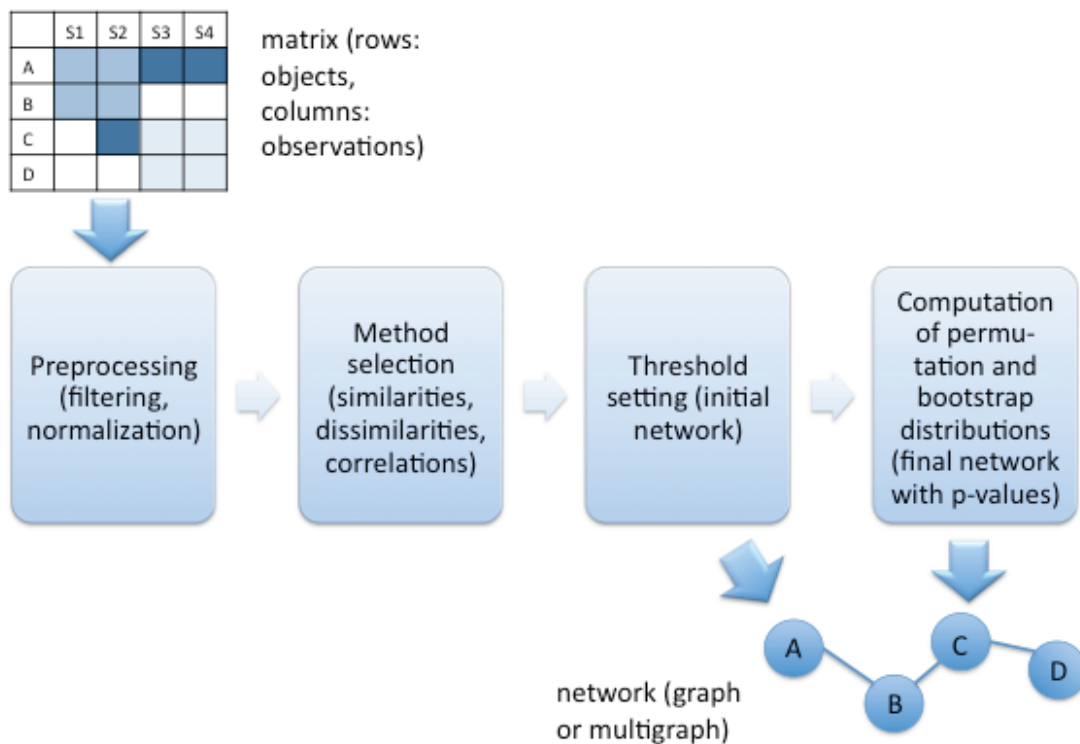


**Figure 1. Network inference workflow in CoNet.**

## Results

### Use case: microbial relationships in the arctic soil

We demonstrate the abilities of the CoNet app on a real-world example taken from the Qiita database (The Qiita Development Team, 2015). The Qiita database, which merges the previously separated QIIME and EMP databases, is a rich resource for processed 16S rDNA sequence data: each study is accompanied by a microbial count file in biom format computed from the raw sequence data with the QIIME pipeline (Caporaso *et al.*, 2010).

In our example, we will demonstrate how to build an association network from microbial count data obtained from arctic soil samples (Chu *et al.*, 2010). This data set was chosen for its sample number (sufficient to compute associations but short run times) as well as for the biological insights that are gained from the network analysis. The example showcases the CoNet app's ability to compute associations between higher taxonomic levels and to take environmental metadata into account, which is important for the interpretation of predicted microbial relationships.

In the Qiita database, the arctic soil study can be found under the title "Soil bacterial diversity in the Arctic is not fundamentally different from that found in other biomes" (study identifier: 104, see Supplementary material). This data set consists of 52 soil samples from the arctic tundra, which were sequenced with Roche FLX using primers targeting the V1V2 region of the 16S rDNA. The processed data can be downloaded from the Qiita study page (in Data Types, click on 16S, then click on the URL appearing below, expand the Files network, click on the file object containing BIOM in its name and then download the file with suffix .biom). The study also provides a mapping file with sample metadata (on the Qiita study page, click Sample Information and then the Sample Info button). We extract the pH of each sample by loading the sample information file into Excel, selecting the sample_name and ph columns and saving them to a separate, tab-delimited file.

### Combining multiple measures

The CoNet app is composed of the main window and several menus, including a "Data" menu with input and output options, a "Preprocessing and filter" menu, a "Methods" menu to select network construction methods, a "Merge" menu where the user can specify how results from different network construction methods should be merged, a "Randomization" menu for the assessment of edge significance and finally a "Config" menu for configuration.

In the following, we will build a network from the arctic tundra biom file. First, in the "Data" menu, the arctic tundra biom file is selected and the option "Biom file in HDF5" is enabled (direct biom file parsing is only supported in the Cytoscape 3.× version of the CoNet app). In the sub-menu "Metadata and Features", the option "explore links between higher-level taxa" is enabled together with the option "Parent-child exclusion" to compute correlations between higher-level taxa while preventing edges between taxa within the same lineage (e.g. Lactobacillales and Lactobacillaceae). Sample metadata (pH in this case) are passed to the CoNet app via the "Select file" button in the "Features" corner of the "Metadata and Features" sub-menu. Both "Transpose" and "Match samples" need to be enabled to convert sample metadata into rows and to match sample metadata identifiers to biom file identifiers.

In the "Preprocessing and filtering" menu, the parameter "row_minocc" is set to 20 to discard taxa with less than 20 non-zero values across samples. The sum of the discarded rows can be kept by enabling "Keep sum of filtered rows". In addition, "col_norm" is activated to divide each matrix entry by the sum of its corresponding column, thus avoiding the inference of spurious links due to sequencing depth differences.

In the "Methods" menu, Pearson, Spearman, Bray Curtis, Kullback Leibler and mutual information are selected. Their thresholds can be automatically set such that 1,000 top-scoring and 1,000 bottom-scoring edges (for anti-correlations) are included for each measure in the initial network, by typing "1000" as the value of the edge selection parameter and enabling "Top and bottom" in the "Threshold setting" sub-menu. At this stage, pushing "GO" will result in a multigraph, where microbial taxa are connected by up to five different measure-specific edges.

### Assessment of edge significance

The significance of edges, that is their p-values, is computed in two CoNet launches, the first of which generates the permutation distributions and an intermediate network and the second the bootstrap distributions and the final network.

For the first launch, the user selects the "edgeScores" routine in the "Randomization" menu, with "shuffle_rows" as resampling parameter, and enables "Renormalize" (for details on renormalization, see Faust *et al.*, 2012). The user then specifies a folder and a file name to export permutation scores and enables "Save randomizations" in the "Save" corner of the "Randomization" menu. Pushing "GO" will then launch the computation of edge- and measure-specific permutation distributions. Permutation alone is sufficient to set p-values on the edges, but we found that a combination of permutation and bootstrap is more stringent (Faust *et al.*, 2012). Thus, the network generated in this first step should be considered as an intermediate result.

In order to compute bootstrap distributions and the final network, the user prepares a second CoNet launch, by selecting the "bootstrap" resampling method and a p-value merging method, for instance "brown" (Brown 1975), in the "Randomization" menu. P-value merging will unite measure-specific p-values for the same edge into a single edge-specific p-value. "Renormalize" is disabled and "benjaminihochberg" is selected as the multiple testing correction method. In the "Save" corner of the "Randomization" menu, another file name should be specified to store bootstrap distributions in a separate file. P-values of the final network are computed from both permutation and bootstrap distributions, thus previously generated permutation distributions have to be loaded into the CoNet app. This is done by selecting the permutation file generated in the previous step with the "Load null distributions" button. Pushing "GO" will then result in the final network, shown in Figure 2A.

The CoNet app does not layout resulting networks, to leave the choice of the (potentially time-consuming) layout algorithm to the user. Here, the "Organic" layout from yFiles was applied and nodes were colored according to their class using Cytoscape's node coloring functionality.
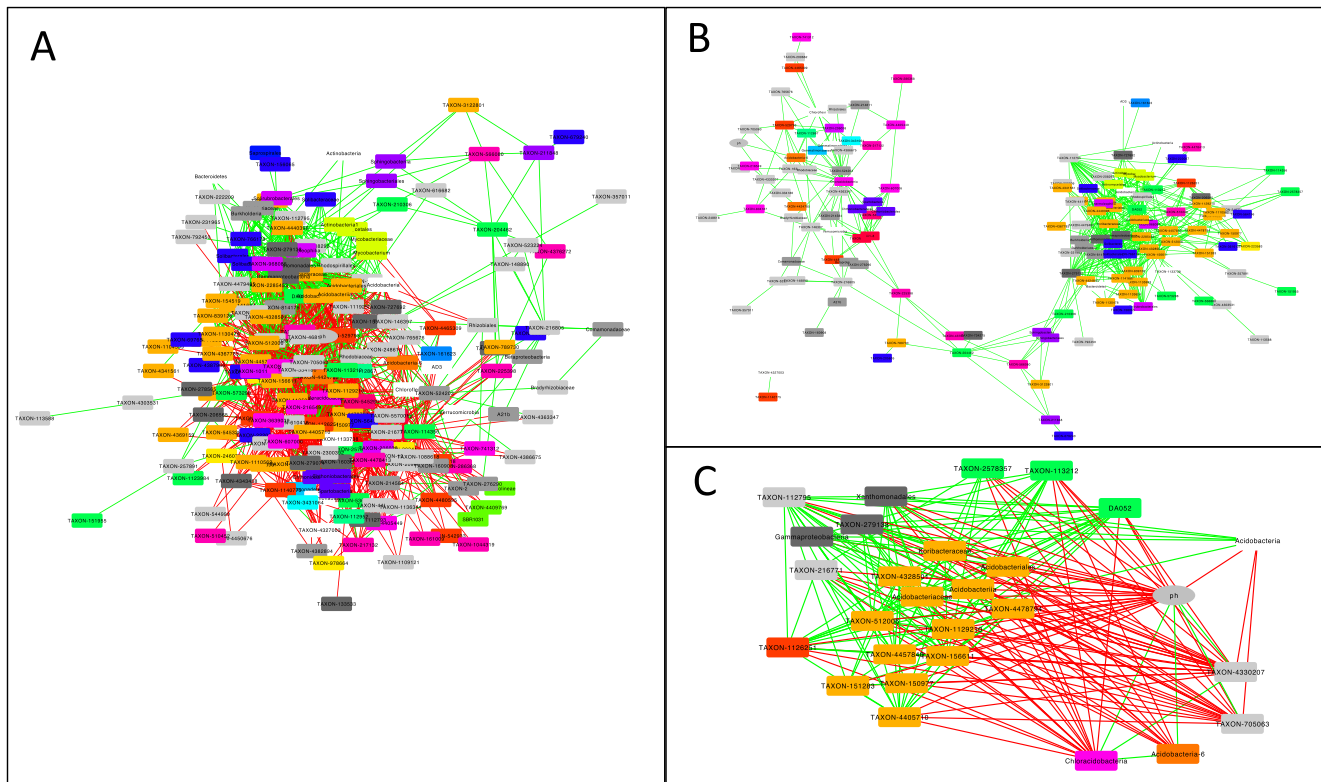
**Figure 2. A**: Result network obtained for bacterial counts from the arctic soil 16S rDNA example data set, downloaded from the Qiita database. **B**: Same as A, but with negative edges discarded. The remaining edges form clusters with different microbial composition. **C**: Neighbors of the pH node form two clusters: one correlated and the other anti-correlated to pH, which reflects the opposite pH preferences of the cluster members.

Once permutation and bootstrap distributions have been computed, network generation can be quickly repeated by loading both distributions via the "Load null distributions" and "Load randomization file" buttons, respectively. Figure 2B shows the same network re-generated from pre-computed distributions, but with "positive edges only" enabled in the "Preprocessing and filter" menu. Figure 2C displays the neighbors of the pH node, which were selected and instantiated as a separate network using Cytoscape's node selection function "First neighbors of selected nodes" for undirected networks.

The computation of permutation and bootstrap distributions took ~5 minutes each for 100 iterations on a standard laptop.

Input and settings files for the use case can be found in the Supplementary material.

## Discussion
### Insights into arctic soil microbiota
After removal of negative edges, the arctic soil network forms two prominent clusters (Figure 2B), which are enriched with representatives of different classes, such that one cluster features mostly members of the Solibacteres and Acidobacteria, whereas the other consists mostly of Alphaproteobacteria and Chloracidobacteria. When examining the neighbors of the pH node (Figure 2C), members of the former cluster are found to be anti-correlated to pH, whereas members of the latter are correlated to it. Thus,

network analysis helps to identify pH as a major driving factor for microbial soil communities, as has been found previously (Fierer & Jackson, 2006). The correlations with pH have also been described by the authors of the soil study (Chu *et al.*, 2010). However, network analysis adds more details (correlations are computed on lower taxonomic levels) and discovers additional taxonomic groups impacted by pH, e.g. Chloracidobacteria. Furthermore, network inference suggests candidates for cross-feeding. For instance, the neighboring nodes of *Bradyrhizobium*, a nitrogen fixer that produces ammonium, may represent taxa that depend on ammonium as main nitrogen source.

### Related apps
The CoNet app offers mostly similarity-based network inference. Complementary apps that implement various Bayesian network inference algorithms are Cyni Toolbox (http://www.proteomics. fr/Sysbio/CyniProject), bayelviraApp (http://apps.cytoscape.org/ apps/bayelviraapp) and MONET (Lee & Lee, 2005). ARACNE (http://apps.cytoscape.org/apps/aracne) exploits mutual information to build networks (Margolin *et al.*, 2006). ExpressionCorrelation (http://www.baderlab.org/Software/ExpressionCorrelation) and MetaNetter (http://apps.cytoscape.org/apps/metanetter) also offer similarity-based network inference techniques, in case of the former specialized to gene expression and in the latter to metabolomics data. Results from these different network inference approaches could be combined with Cytoscape tools such as Merge Networks.

## Conclusion

In this article, we have demonstrated the CoNet app on a typical 16S data set. Alternative use cases are for instance the inference of function networks (*i.e.* co-occurrence of orthologous gene groups) from metagenomics or metatranscriptomics data or taxon-metabolite networks from 16S and metabolomics data.

We hope that CoNet's integration into Cytoscape will lower the barrier for its employment by users less familiar with the command line version. Due to its flexibility and comprehensiveness, CoNet can be useful in a variety of applications and we thus hope it will find a broad user base.

## Software availability

CoNet app page: http://apps.cytoscape.org/apps/conet

CoNet tool web page: http://systemsbiology.vub.ac.be/conet

Latest source code: http://sourceforge.net/projects/conet/

Archived source code as at the time of publication: Zenodo, Biological network inference in Cytoscape, doi: 10.5281/zenodo.55715 (Faust & Raes, 2016)

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## Author contributions

K.F. developed the Cytoscape plugin, J.R. initiated and supervised the work. K.F. wrote the paper. Both authors agreed to the final content of the article.

## Competing interests

The authors declare that they have no competing interests.

## Supplementary material

Use case data in CoNet app: inference of biological association networks using Cytoscape.

This file contains microbial count data, sample metadata, permutation settings and bootstrap settings associated with this submission. Description of each dataset is provided in the text file.

Click here to access the data.

## References

Bork P, Bowler C, de Vargas C, *et al*.: **Tara Oceans. *Tara* Oceans studies plankton at planetary scale. Introduction.** *Science.* 2015; **348**(6237): 873.
**PubMed Abstract** | **Publisher Full Text**

Caporaso JG, Kuczynski J, Stombaugh J, *et al*.: **QIIME allows analysis of high-throughput community sequencing data.** *Nat Methods.* 2010; **7**(5): 335–336.
**PubMed Abstract** | **Publisher Full Text** | **Free Full Text**

Chu H, Fierer N, Lauber CL, *et al*.: **Soil bacterial diversity in the Arctic is not fundamentally different from that found in other biomes.** *Environ Microbiol.* 2010; **12**(11): 2998–3006.
**PubMed Abstract** | **Publisher Full Text**

Connor EF, Simberloff D: **The Assembly of Species Communities: Chance or Competition?** *Ecology.* 1979; **60**(6): 1132–1140.
**Publisher Full Text**

Diamond JM: **Assembly of species communities.** In *Ecology and evolution of communities.* Cody M, Diamond JM eds., Harvard University Press, 1975; 342–444.
**Reference Source**

Falony G, Joossens M, Vieira-Silva S, *et al*.: **Population-level analysis of gut microbiome variation.** *Science.* 2016; **352**(6285): 560–564.
**PubMed Abstract** | **Publisher Full Text**

Faust K, Sathirapongsasuti JF, Izard J, *et al*.: **Microbial co-occurrence relationships in the human microbiome.** *PLoS Comput Biol.* 2012; **8**(7):

e1002606.
**PubMed Abstract** | **Publisher Full Text** | **Free Full Text**

Faust K, Raes J: **Biological network inference in Cytoscape.** *Zenodo.* 2016.
**Data Source**

Fierer N, Jackson RB: **The diversity and biogeography of soil bacterial communities.** *Proc Natl Acad Sci U S A.* 2006; **103**(3): 626–631.
**PubMed Abstract** | **Publisher Full Text** | **Free Full Text**

Gilbert JA, Jansson JK, Knight R: **The Earth Microbiome project: successes and aspirations.** *BMC Biol.* 2014; **12**: 69.
**PubMed Abstract** | **Publisher Full Text** | **Free Full Text**

Gotelli NJ, McCabe DJ: **Species Co-Occurrence: A Meta-Analysis of J. M. Diamond's Assembly Rules Model.** *Ecology.* 2002; **83**(8): 2091–2096.
**Publisher Full Text**

Himsolt M: **GML: A portable Graph File Format [Online].**
**Reference Source**

Hu Z, Chang YC, Wang Y, *et al.*: **VisANT 4.0: Integrative network platform to connect genes, drugs, diseases and therapies.** *Nucleic Acids Res.* 2013; **41**(Web Server issue): W225–W231.
**PubMed Abstract** | **Publisher Full Text** | **Free Full Text**

Ladau J: **Lightweight, portable library for working with HDF5 BIOM files using Java [Online].**
**Reference Source**

Lee PH, Lee D: **Modularized learning of genetic interaction networks from biological annotations and mRNA expression data.** *Bioinformatics.* 2005; **21**(11): 2739–2747.
**PubMed Abstract** | **Publisher Full Text**

Margolin AA, Nemenman I, Basso K, *et al.*: **ARACNE: An algorithm for the reconstruction of gene regulatory networks in a mammalian cellular context.** *BMC Bioinformatics.* 2006; **7**(Suppl 1): S7.
**PubMed Abstract** | **Publisher Full Text** | **Free Full Text**

McDonald D, Clemente JC, Kuczynski J, *et al.*: **The Biological Observation Matrix (BIOM) format or: how I learned to stop worrying and love the ome-ome.** *GigaScience.* 2012; **1**(1): 7.
**PubMed Abstract** | **Publisher Full Text** | **Free Full Text**

Meyer PE, Lafitte F, Bontempi G: ***minet*: A R/Bioconductor package for inferring large transcriptional networks using mutual information.** *BMC Bioinformatics.* 2008; **9**: 461.
**PubMed Abstract** | **Publisher Full Text** | **Free Full Text**

The Human Microbiome Project Consortium: **A framework for human microbiome research.** *Nature.* 2012; **486**(7402): 215–221.
**PubMed Abstract** | **Publisher Full Text** | **Free Full Text**

The Qiita Development Team: **Qiita: report of progress towards an open access microbiome data analysis and visualization platform.** In *14th Python in Science Conference (SCIPY 2015),* 2015.
**Reference Source**

# Open Peer Review

## Current Referee Status: [?] [?]

[?] **Alexander Eiler**

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Be more precious, here. "The idea behind such an ensemble approach to network inference is to exploit the fact that different methods make different mistakes."

These are different statistical inferences so based on the underlaying algorithms results will be different. Same may be better suited for parametric or none-parametric data, some perform better with larger or smaller sample numbers. The different methods have also different statistical power do identify significances. Some may produce more false positives or false negatives than others. Some guidance and references to statistical literature could be provided in the article.

I really liked to see an implementation that calculates false discovery rate (after Benjamin Hochberg) over all statistical comparisons.

**I have read this submission. I believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard, however I have significant reservations, as outlined above.**

*Competing Interests:* No competing interests were disclosed.

Author Response 07 Oct 2016

**Karoline Faust**, VUB, Belgium

"These are different statistical inferences so based on the underlaying algorithms results will be different."
Thanks for pointing this out. We have now added an overview table of the strengths and weaknesses of selected measures available in CoNet. We also added a paragraph that discusses the different ways in which these measures can be combined in CoNet.

"I really liked to see an implementation that calculates false discovery rate (after Benjamin Hochberg) over all statistical comparisons."
CoNet does allow computing false discovery rate over all statistical comparisons either by setting the number of initial edges sufficiently high or by setting the thresholds on the individual measures sufficiently low. We have added this remark to the article.
Despite the fact that multiple testing correction is in most cases only applied after edges are

discarded through initial filtering, CoNet is among the microbial network inference tools with the lowest false positive rates tested in Weiss et al., The ISME Journal 2016 ( https://www.ncbi.nlm.nih.gov/pubmed/26905627, supplementary Figure 10) .

*Competing Interests:* No competing interests were disclosed.

Referee Report 13 July 2016

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**Paul Wilmes**, **Anna Heintz-Buschart**
Luxembourg Centre for Systems Biomedicine (LCSB), University of Luxembourg, Luxembourg City, Luxembourg

The article describes a Cytoscape plugin "CoNet app" designed for the inference of networks from microbial abundance or incidence matrices. The effort combining a versatile network inference tool with a user-friendly and widely used network visualization and analysis framework, such as Cytoscape is very valuable to the community.

I would suggest certain improvements to the article to make it in itself more valuable for potential users to judge the applicability of the plugin to their datasets.

**Introduction:** As the authors of the plugin are well aware (being co-authors of "Correlation detection strategies in microbial data sets vary widely in sensitivity and precision" [1]), co-abundance or co-occurrence analysis is an approach to ecological data interpretation that is not without caveats and as such, the article is lacking both mention of limitations of the approach and references to the successful use cases of earlier versions of CoNet. I suggest including both in the introduction.

The introduction also does little to explain the approach to potential users who are not familiar with the concept. E.g. the sentence "More specifically, co-occurrence analysis detects significant co-occurrences or mutual exclusions across samples, which are interpreted as representing ecological relationships such as mutualism or competition or being due to similar responses to environmental factors." mixes up observations and analyses with interpretation. Similarly, relating to the first sentence of the introduction, microbial count data are not obtained from relative abundances, but microbial counts taken to infer relative abundances (the sentence is also ambiguous as to what these abundances are relative to). Furthermore, the second but last sentence of the introduction "The large number of microbial count tables resulting from the multitude of recent sequencing projects…" can be interpreted to advise for the co-analysis of results from different studies, which is most often not possible. These parts should be revised for clarity.

**Methods/Implementation:** More details on the algorithms would be useful, or alternatively references to other publications which describe CoNet, as relates to the following points:
- "its capability to combine multiple such measures and/or to combine these measures with other network inference algorithms",

- "CoNet can also parse sample metadata such as temperature or oxygen concentration, which are then correlated with the objects in the input matrix while being excluded from normalization." and

- "Phylogenetic lineages in these tables are automatically parsed". Also, what are positive and negative edges? How is mutual information integrated with measures which can be positive or negative?

**Use case**: It would be helpful to shortly describe the size of the dataset (number of OTUs and number of samples) as part of the sentence "This data set was chosen for its sample number (sufficient to compute associations but short run times) as well as for the biological insights that are gained from the network analysis." A general advice on the required sample number and or relationship between numbers of analyzed features and sample numbers would also be helpful. In addition, are the 100 iterations performed in this example a realistic number of iterations to be used in such an analysis?

The formulation "The significance of edges, that is their p-values" is a bit unfortunate. On a similar note, next to the permutations, is there a way in CoNet or the CoNet app to assess association strengths? An example of how the assessment of edge significance affects network size and structure would be informative.

Figures: The large heading in Figure 1 should be removed. Figure 2 would benefit from a heading. The labels of figure 2 are not legible. It is unclear from the text and not mentioned in the legend, how the "classes" used for coloring nodes are defined. Are these classes in the taxonomic sense or different kinds of data? The color scheme for positive and negative edges should be explained. In panel C, the pH node should be more clearly pointed out.

### Small comments:
The referenced "Brown 1975" does not appear in the references.

The capitalization of "P-value" is inconsistent.

As the buttons in the app are actually called that, refer to "Data menu", "Preprocessing and filter menu" etc.

### References
1. Weiss S, Van Treuren W, Lozupone C, Faust K, Friedman J, Deng Y, Xia LC, Xu ZZ, Ursell L, Alm EJ, Birmingham A, Cram JA, Fuhrman JA, Raes J, Sun F, Zhou J, Knight R: Correlation detection strategies in microbial data sets vary widely in sensitivity and precision.*ISME J*. 2016; **10** (7): 1669-81 PubMed Abstract | Publisher Full Text

**We have read this submission. We believe that we have an appropriate level of expertise to confirm that it is of an acceptable scientific standard, however we have significant reservations, as outlined above.**

*Competing Interests:* No competing interests were disclosed.

Author Response 07 Oct 2016
**Karoline Faust**, VUB, Belgium

"The effort combining a versatile network inference tool with a user-friendly and widely used network visualization and analysis framework, such as Cytoscape is very valuable to the community."

We would like to thank the reviewer for this appreciation of our work.

**Introduction**

In response to the reviewers' comments, we have rewritten the introduction, thereby rephrasing problematic sentences, pointing out limitations of microbial network inference and citing the evaluation. We also added a paragraph in the discussion to mention applications of CoNet.

**Methods/Implementation**

- "its capability to combine multiple such measures and/or to combine these measures with other network inference algorithms",

We included an overview table comparing selected measures of association. We also added a paragraph on how measures can be combined in CoNet.

- "CoNet can also parse sample metadata such as temperature or oxygen concentration, which are then correlated with the objects in the input matrix while being excluded from normalization."

We improved this explanation of CoNet's treatment of sample metadata.

- "Phylogenetic lineages in these tables are automatically parsed".

We provided an example to better explain what we mean.

- Also, what are positive and negative edges? How is mutual information integrated with measures which can be positive or negative?

We added an explanation.

**Use case**

The OTU number was added to the following sentence (which already listed the sample number): *This data set consists of 4,022 operating taxonomic units and 52 soil samples from the arctic tundra, which were sequenced with Roche FLX using primers targeting the V1V2 region of the 16S rDNA.*

"A general advice on the required sample number and or relationship between numbers of analyzed features and sample numbers would also be helpful."

In general, the number of false positives increases with decreasing sample number. While assessment of significance counter-balances this effect, it is unreasonable to compute a correlation from a few observations only, even if it is strongly significant. However, we cannot provide a formula to compute where exactly to put the cut-off.

"In addition, are the 100 iterations performed in this example a realistic number of iterations to be used in such an analysis?"

We saw previously that there is no big difference between networks computed with 100 or 1000 iterations. The reason is that we are not computing p-values from a pure permutation test, where small p-values can only be reached by performing a sufficient number of iterations. Instead, we compute the p-value parametrically as the mean of the permutation distribution under the bootstrap distribution. Estimating the mean and standard deviation of normal distributions is less sensitive to iteration number than computing parameter-free p-values. We added this explanation to the text.

"The formulation "The significance of edges, that is their p-values" is a bit unfortunate. On a similar

note, next to the permutations, is there a way in CoNet or the CoNet app to assess association strengths? An example of how the assessment of edge significance affects network size and structure would be informative."

The p-value is an assessment of association strength. So are the scores of the measures themselves, e.g. Pearson's r and Spearman's rho, which are correlated with the p-value. We have added a remark explaining this to the text.
Assessing the significance usually discards edges from the initial network, in some cases even removing all initial edges. The number of edges removed depends on the initially selected thresholds. In the use case, the initial network consists of 10000 edges, 1546 of which remain after assessment of significance and merging of measure-specific p-values into a single p-value. The exact edge number in the final network may vary slightly from run to run, due to variations in the permutation and bootstrap distributions.

"Figures: The large heading in Figure 1 should be removed."

This heading was not intended as a Figure heading but as a heading to divide the text. We improved the layout and added headers to Figure 1 and 2.

"Figure 2 would benefit from a heading. The labels of figure 2 are not legible."

Our aim here was to show the networks as obtained with the CoNet app when executing the use case, but we understand the point of the reviewer. As a compromise, we have now removed the labels and added a class-level color code.

"It is unclear from the text and not mentioned in the legend, how the "classes" used for coloring nodes are defined. Are these classes in the taxonomic sense or different kinds of data?"

These are taxonomic classes. We clarified this in the caption of Figure 2.

"The color scheme for positive and negative edges should be explained."

We added an explanation of the color scheme in the main text and to the caption of Figure 2.

"In panel C, the pH node should be more clearly pointed out."

The pH node stands out by differing in shape from the taxon nodes. We have clarified this by adding a legend to Figure 2.

**Small comments:**
"The referenced "Brown 1975" does not appear in the references."

We excuse for this oversight. We have added the reference.

"The capitalization of "P-value" is inconsistent."

We now use p-value with a lower case p, unless it is the first word of a new sentence, where we use the upper case P.

"As the buttons in the app are actually called that, refer to "Data menu", "Preprocessing and filter menu" etc. "

Done

***Competing Interests:*** No competing interests were disclosed.