

Correlation and Co-occurrence Networks in Taxonomic Classification

Jim Brunner

September 5, 2017

1 Introduction

[5][3][6][2][7][9][1][10][4]

2 Network Construction

2.1 Correlation construction

We construct an undirected, weighted graph with nodes from the set of taxa in the GOTTCHA output of metagenomic samples. Edges correspond to correlation between taxa across samples. If \mathbf{x} is the vector of abundances of a certain taxa, and \mathbf{y} is the vector of abundances of another, we compute the correlation of these two vectors (with N samples):

$$\rho_{xy} = \frac{1}{N} \frac{(\mathbf{x} - \mu_x \mathbf{1}) \cdot (\mathbf{y} - \mu_y \mathbf{1})}{\sigma_x \sigma_y}$$

where μ_x is the mean abundance of taxa x , and σ_x is the standard deviation of abundance of taxa x across samples. These correlations can be efficiently computed from a matrix whose columns correspond to the GOTTCHA output (in taxa abundance) of metagenomic samples, and rows corresponding to the abundances of taxa across samples. Finally, if \mathbf{r}_i is the vector of abundances of taxa i , and \mathbf{r}_k is a vector of abundances of taxa k , we compute

$$w_{ik} = \begin{cases} \rho_{\mathbf{r}_i \mathbf{r}_k} & \rho_{\mathbf{r}_i \mathbf{r}_k} \geq 0.8 \\ 0 & \rho_{\mathbf{r}_i \mathbf{r}_k} < 0.8 \end{cases}$$

and take an edge from taxa i to taxa k with weight w_{ik} (where an edge with weight 0 implies no edge).

Alternatively, we can first “thresh-hold” the abundances given, converting to binary presence/absence data. To do this, we find the mean of all non-zero abundance values μ_{nz} , and take

$$r_{ij}^* = \begin{cases} 1 & r_{ij} \geq 0.01\mu_{nz} \\ 0 & r_{ij} < 0.01\mu_{nz} \end{cases}$$

where r_{ij} is the the abundance of taxa i in sample j . The network is then constructed using correlation just as before.

Again, we check the significance of each edge, removing edges that have a high probability of occurring in a null model. We check this using Monte-Carlo simulation by estimating $p_{ik} \approx P(\rho_{\mathbf{r}_i^{\text{null}} \mathbf{r}_k^{\text{null}}} > \rho_{\mathbf{r}_i \mathbf{r}_k})$. In construction, we take enough Monte-Carlo trials for a 95% confidence interval of length 0.03. We then adjust edges so that

$$p_{ik} > 0.05 \Rightarrow w_{ik} = 0$$

2.2 Null Model

Rather than simply generate an Erdős-Rényi random graph with some chosen parameter, we generate a graph that more closely reflects the idea of random data. That is, we start with random data that resembles our real data, and then generate a graph. The random data is generated in the following way. Let

$$N_j = |\{i : r_{ij} \neq 0\}|$$

and

$$P_i = \frac{|\{j : r_{ij} \neq 0\}|}{|\{(i, j) : r_{ij} \neq 0\}|}$$

then take

$$\hat{r}_{ij} = \text{binom}(N_j, P_i)$$

as randomly generated abundance data. The values N_i are the counts of appearances of taxa i , while the values P_j are the proportions of all appearances which happen within each sample.

Then, we construct our null model graph from this random data. If $\hat{\mathbf{r}}_i$ is the vector of random “abundances” of taxa i , the null graph has edges

$$w_{ik}^{null} = \frac{1}{N} \frac{(\hat{\mathbf{r}}_i - \hat{\mu}_i \mathbf{1}) \cdot (\hat{\mathbf{r}}_k - \hat{\mu}_k \mathbf{1})}{\hat{\sigma}_i \hat{\sigma}_k}$$

The null model’s use of a binomial random variable can be interpreted in the following way. A “success” for a taxa/sample pair is an appearance of the taxa in the sample. The number of trials is the number of times the taxa appears in the data set. The probability of success is the proportion of all appearances which happen within the sample. This does have some drawbacks: notably that it does not preserve total abundance, or even total appearances. It allows more than one “success” for a single taxa/sample pair, which could be interpreted as higher abundance. Our “random samples” should be scaled by average abundances of a taxa across samples to “look like” real data. This doesn’t effect correlation, because $Cov(ax, by) = abCov(x, y)$, and $\sigma_x = Cov(x, x)^{1/2}$, implying that $w_{ik} = Cor(\hat{\mathbf{r}}_i, \hat{\mathbf{r}}_k) = Cor(a\hat{\mathbf{r}}_i, b\hat{\mathbf{r}}_k)$.

In [8], this model is called the “binomial model”. Interestingly, that paper argues that an “edge swapping” model is more accurate, but slower to construct and so less suitable for Monte-Carlo methods. A random permutation of the data used in [4].

2.3 Significance of the network

The networks connected by the methods above would not occur in randomized data, and so there is some significance to these networks. In a Monte-Carlo simulation, networks are generated according to the null mode in order to estimate the following

- $P(\mu_d < \mu_d^{null})$, where μ_d is the mean degree of the nodes of a network
- $P(\sigma_d < \sigma_d^{null})$, where σ_d is the variance of degrees of the nodes of a network
- $P(\lambda_{max} < \lambda_{max}^{null})$, where λ_{max} is the largest eigenvalue of the adjacency matrix
- $P(\lambda_{min} < \lambda_{min}^{null})$, where λ_{min} is the smallest eigenvalue of the adjacency matrix
- $P(|\mathcal{E}| < |\mathcal{E}^{null}|)$

The result with 10,000 Monte Carlo trials show that it was extremely rare for a network constructed from the null model to have higher mean degree, higher degree variance, larger maximum eigenvalue, smaller minimum eigenvalue, or more edges. This suggests that the networks constructed from real data would be very unexpected according to the null model.

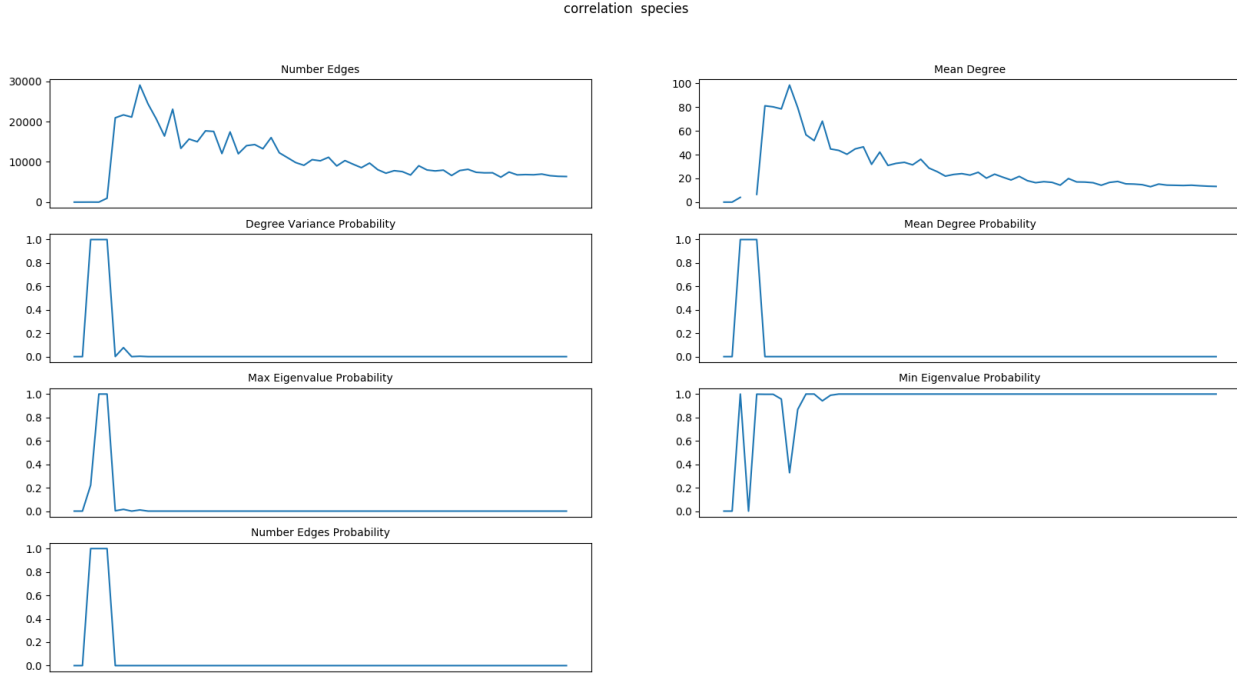


Figure 1: The result of Monte-Carlo estimation of the likelihood of various network statistics, as well as the number of edges and mean degree. The networks were made from correlations using randomly drawn subsets of increasing size of the data at the species level, from 1 sample to 60 samples. Samples were GOTTCHA output of data from (FIND OUT). For each network, 1000 random trials were generated according to the above null model in order to estimate likelihood of statistics.

3 Taxonomic Classification Analysis

We would like to identify taxa likely to be present in a sample, given an initial estimate of abundances of taxa. Inspired by spectral clustering, we may solve the diffusion equation on the graph in order to identify nodes that are likely present, given the sample data. The diffusion equation is

$$\frac{\partial}{\partial t} u(v, t) = Lu(v, t)$$

where v takes values in the vertex set of the graph. Then, we encode “known” information in the initial values.

Method 1 (Initial Value Problem). Let $u_i(t)$ be the solution at node v_i to the discrete diffusion problem

$$\frac{d}{dt} \mathbf{u}(t) = -L\mathbf{u}$$

where L is the graph Laplacian with initial conditions $u_i = 1$ if node v_i is known to be “on”, $u_j = 0$ if v_j is known to be “off”, and $u_k = 0.5$ (or 0, or perhaps encoded with some confidence in $[0, 1)$) if v_k is unknown. I then normalize the initial vector so that it represents a probability distribution on the nodes. Then, if \mathbf{K} is the information “known” and the values of v_k and v_l are unknown,

$$\int_0^\infty u_k(t) dt - \int_0^\infty u_l(t) dt > 0 \Rightarrow P(v_k = 1 | \mathbf{K}) > P(v_l = 1 | \mathbf{K})$$

These comparisons are easily computed. Solutions to the diffusion equation are of the form

$$\mathbf{u} = \sum_{i=1}^a c_i \mathbf{1}_{cc} + \sum_{i=a+1}^n c_i e^{-\lambda_i t} \boldsymbol{\xi}_i$$

where a is the number of connected components of the graph, and $\lambda_i, \boldsymbol{\xi}_i$ are eigenvalue, eigenvector pairs of L . Note that each eigenvalue $\lambda_i \geq 0$, with $\lambda_i > 0$ for $i = a + 1, \dots, n$ [11]. Then, assuming there is some initial mass on the

connected component containing v_1 and v_2 ,

$$\int_0^\infty u_k(t)dt - \int_0^\infty u_l(t)dt = \sum_{i=a+1}^n c_i(\xi_{ki} - \xi_{li}) \int_0^\infty e^{-\lambda_i t} dt = \sum_{i=a+1}^n \frac{c_i}{\lambda_i}(\xi_{li} - \xi_{ki})$$

and $\mathbf{c} = \mathbf{V}^{-1}\mathbf{u}(0)$. Therefore, it is straightforward to compute and compare the transitive terms of the solution:

$$\int_0^\infty \left(u_k(t) - \sum_{i=1}^a c_i \right) dt = \sum_{i=a+1}^n \frac{c_i}{\lambda_i} \xi_{ki} \quad (1)$$

We can relate this method to spectral clustering. Spectral clustering uses computes a k -means clustering algorithm on the rows for a matrix of the first k eigenvectors ξ_k . Thus, spectral clustering uses a distance metric from the inner product

$$\|u_l\|_s = (\mathbf{V}^T)_l^T \begin{pmatrix} \mathbf{I}_{k \times k} & 0 \\ 0 & \mathbf{0}_{n-k \times n-k} \end{pmatrix} (\mathbf{V}^T)_l$$

and clusters nodes l and m if $\|u_l - u_m\|_s$ is small, or

$$\langle u_m, u_l \rangle_{sc} = (\mathbf{V}_m^T)^T \begin{pmatrix} \mathbf{I}_{k \times k} & 0 \\ 0 & \mathbf{0}_{n-k \times n-k} \end{pmatrix} \mathbf{V}_l^T \quad (2)$$

is large. Similarly, inspection of eq. (1) reveals that we will rank nodes highly when

$$\langle \mathbf{V}^{-1}\mathbf{u}(0), u_l \rangle_{ivp} = (\mathbf{V}^{-1}\mathbf{u}(0))^T \mathbf{\Lambda}^{-1} \mathbf{V}_l^T \quad (3)$$

is large. Notice that the ordering of the eigenvalues insures that the terms on the diagonal of $\mathbf{\Lambda}^{-1}$ decay along the diagonal, and all terms are positive, making this matrix and the matrix used in eq. (1) similar. We are in some sense then asking about how close a node is to the initial condition given in a metric similar to that used in spectral clustering. In fact, if we have as an initial condition $\mathbf{u}(0) = \mathbf{V}\mathbf{V}_m^T$, this metric is very close to that used in spectral clustering.

This method provides a ranking of taxa which attempts to estimate an ordering of the probabilities

$$\mathbb{P}(t_i \in S | m(S))$$

where $t_i \in S$ indicates taxa i is present in a sample, and $m(S)$ is the GOTTCHA output for the sample.

3.1 Matching samples to networks

Suppose we have different networks built from different types of data - i.e. healthy and unhealthy, or different regions, etc. We would like to match a sample with the network that makes most the sense. That is, we would like to say that a sample is more likely to be from one type of data than the other based on the network.

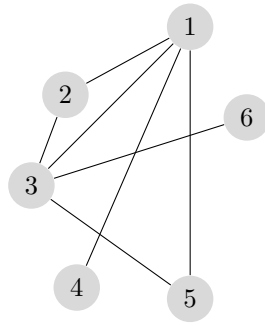
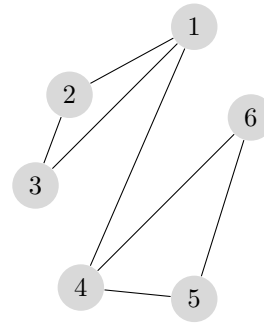
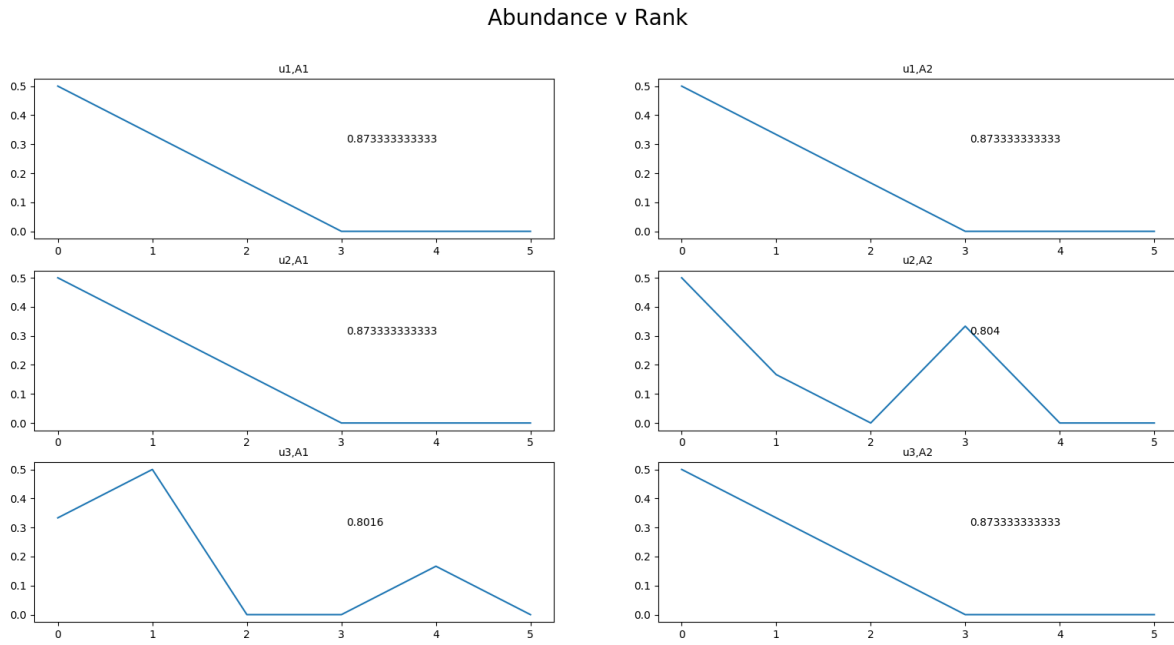
If the sample “fits” a network well, method 1 should return nodes ranked highly which have nonzero and perhaps high abundance. If we imagine a sample is created by performing a random walk on a graph and recording the nodes most often visited, method 1 should identify nodes that the random walk “should” have seen often. If there are a bunch of those missing from the sample, we might think the network is not the right one. We could consider the map from rank to abundance, and integrate this against a kernel that weights towards the high ranks. Let \mathbf{s} be the sample abundances (so s_i is the abundance of organism i), and $\boldsymbol{\sigma}$ the ranking. We take

$$F(\mathbf{s}, \boldsymbol{\sigma}) = \frac{1}{\|\mathbf{s}\|} \sum_{i=1}^n c^{\sigma_i/n} s_i$$

where $c < 1$. Given a sample, we get ranking from a network N_j . Let $\boldsymbol{\sigma}^j(\mathbf{s})$ be the ranking given by diffusion on network j . Then,

$$F_j(\mathbf{s}) = F(\mathbf{s}, \boldsymbol{\sigma}^j(\mathbf{s})) = \frac{1}{\|\mathbf{s}\|} \sum_{i=1}^n c^{\sigma_i^j/n} s_i$$

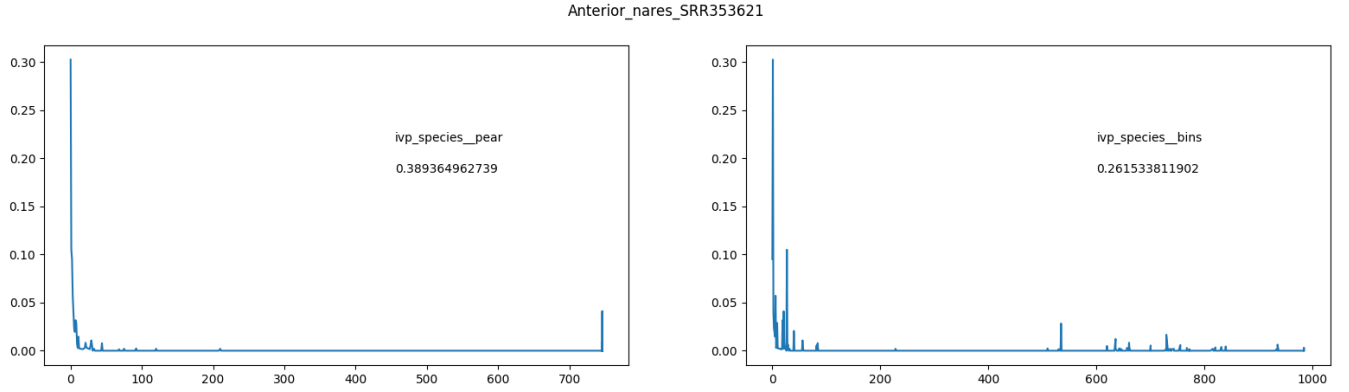
and we can attempt to optimize over the networks. We can then conjecture

(a) Network A_1 (b) Network A_2 **Figure 2:** Test networks.**Figure 3:** Results of sample assignment: u_1 cannot be decided, u_2 is assigned to network A_1 , and u_3 is assigned to network A_2 .

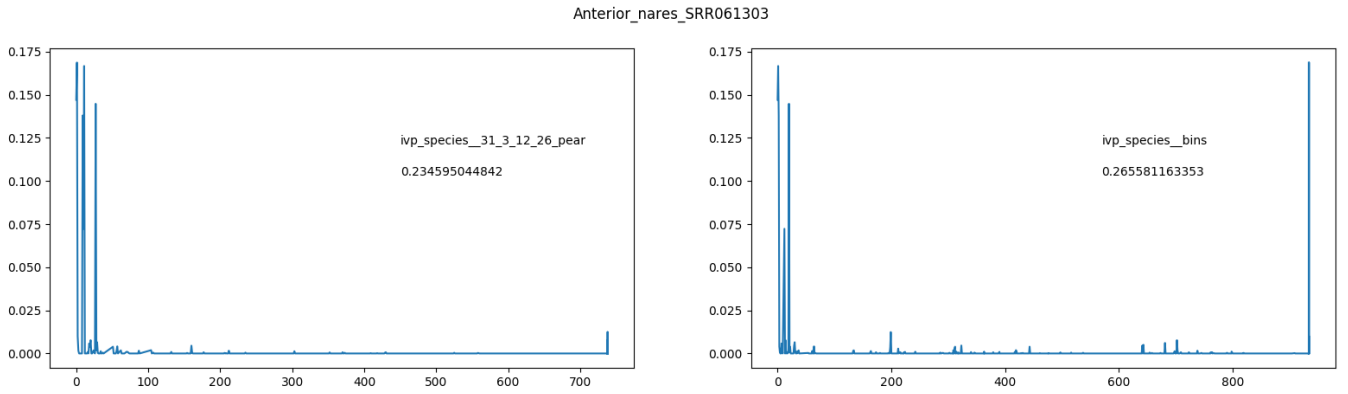
Conjecture 1. *Assume that $F_j(\mathbf{s}) > F_k(\mathbf{s})$. Then $P(\mathbf{s}|N_j) > P(\mathbf{s}|N_k)$.*

We begin with a very simple example. Consider the two networks shown in fig. 2. Using “samples” $u_1 = (1/6, 1/2, 1/3, 0, 0, 0)$, $u_2 = (1/6, 1/2, 0, 0, 1/3, 0)$, and $u_3 = (0, 0, 0, 1/6, 1/2, 1/3)$ gave results shown in fig. 3.

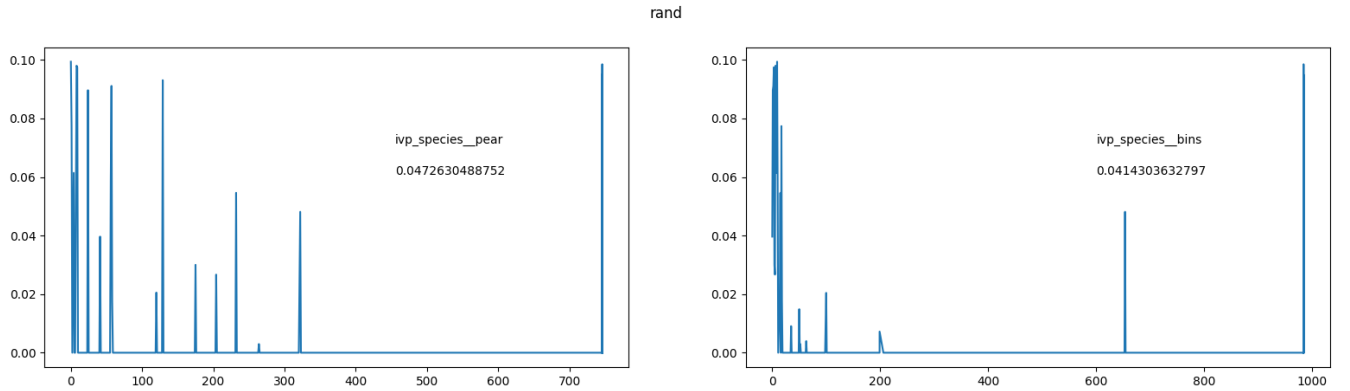
We performed the same experiment on a column of training data for the species level network, a column of data that was held out of the network building, and a randomly generated sample. The results, shown in fig. 4, have the training data and held out data more likely to “fit” the network than the random data.



(a) Assignment of column of training data to networks built with binning (right) and with correlation (left).



(b) Assignment of column of held out data to networks built with binning (right) and with correlation (left).



(c) Assignment randomly generated data to networks built with binning (right) and with correlation (left). This random sample had 63 nodes chosen to be present, uniformly, and given an abundance drawn from a $\text{unif}[0, 0.1]$ distribution.

Figure 4: A training data column fits the network better than a randomly generated sample.

4 Validation

To validate this approach, we built correlation and thresholded correlation networks from GOTTCHA output of 1,367 samples from the NIH Human Microbiome Project (`08_14_14_57_networks`). We constructed a network using all of these samples, as well as networks for 6 body sites for which at least 50 samples were present in the full 1,367:

- Anterior Nares (168 samples)
- Buccal Mucosa (206 samples)
- Posterior Fornix (110 samples)
- Stool (288 samples)
- Supragingival Plaque (220 samples)
- Tongue Dorsum (223 samples)

For each network we assessed the significance of the statistics listed in section 2.3. (`stats.txt` in the folder with the networks.)

We analyzed 300 samples from the NIH Human Microbiome Project that were not used in the network training. We computed the fit score of each sample on a the networks made from the set of 1,367 samples, as well as the body site networks. We hoped to analyze the fit score's use in identifying the body site a sample was taken from. We compared fit of each sample across networks to identify the body site.

We also computed the fit on the full networks of simulated samples created using the null model describe in section 2.2.

For each sample, we also performed the following experiment. We set the taxa with n^{th} highest abundance in the sample to 0 abundance and used the diffusion method to find the rank of this taxa, for n from 1 to 100.

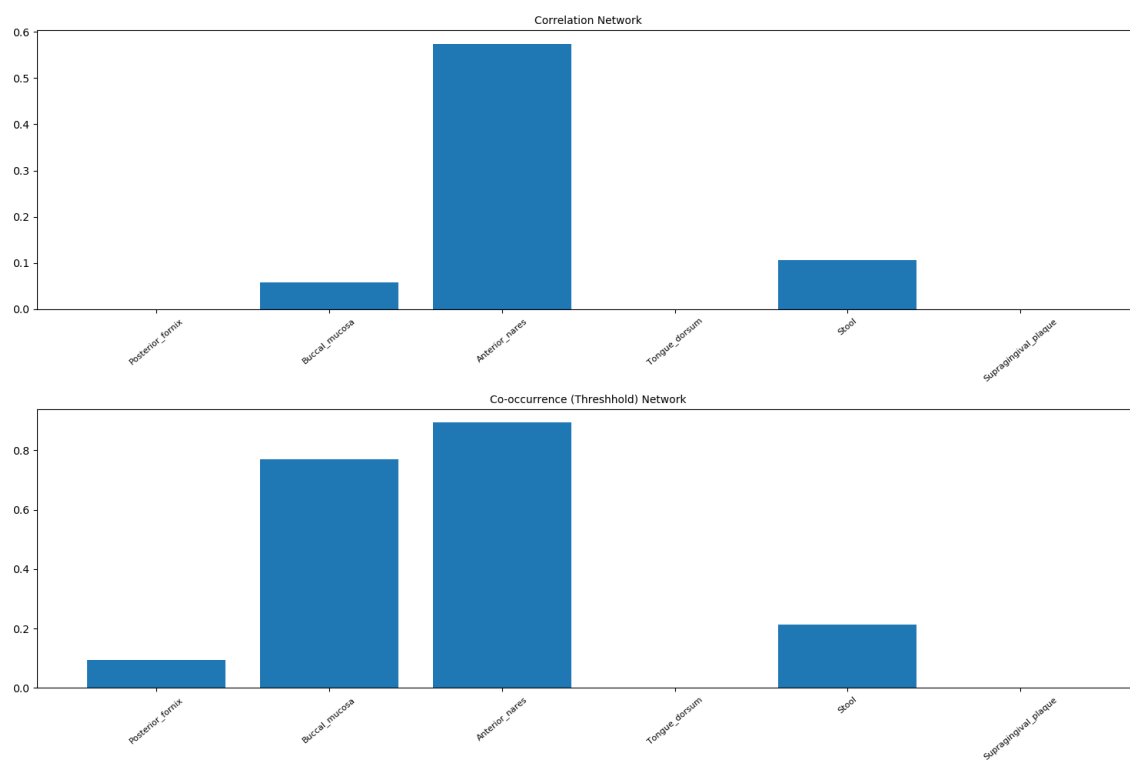
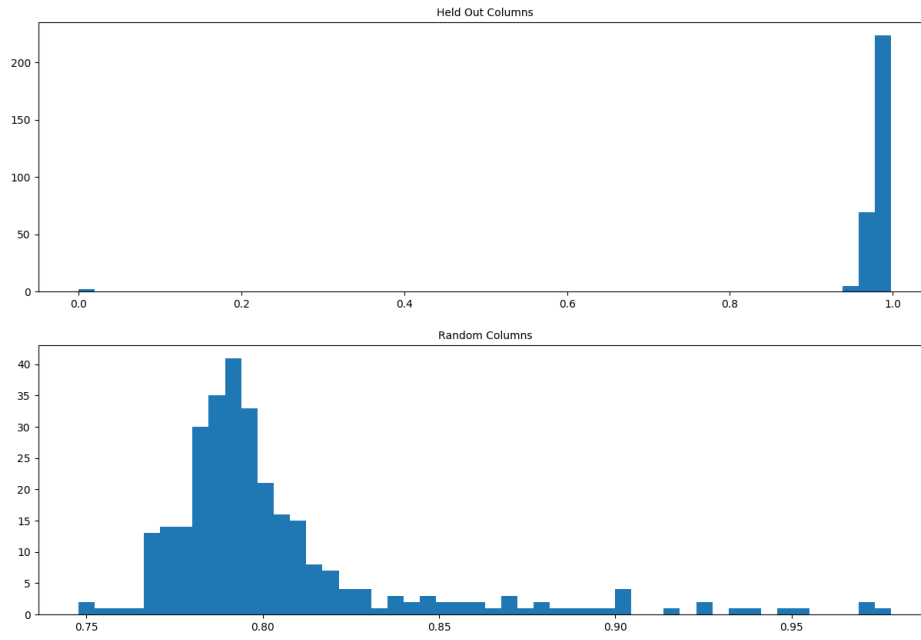


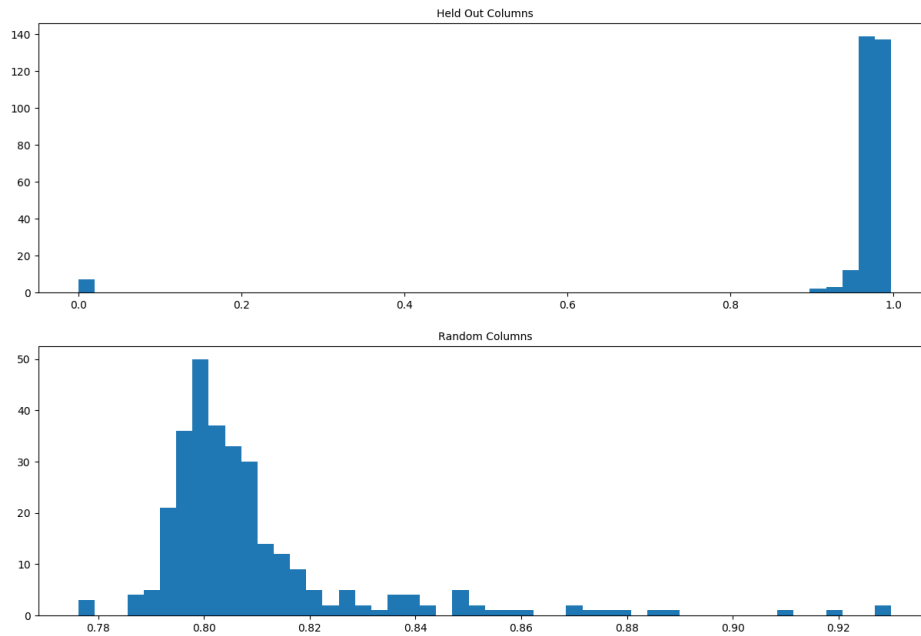
Figure 5: Proportion of samples from each body site that were correctly assigned to their body site by taking the best fit to the various body site networks (species level).

Full Correlation Network Fit



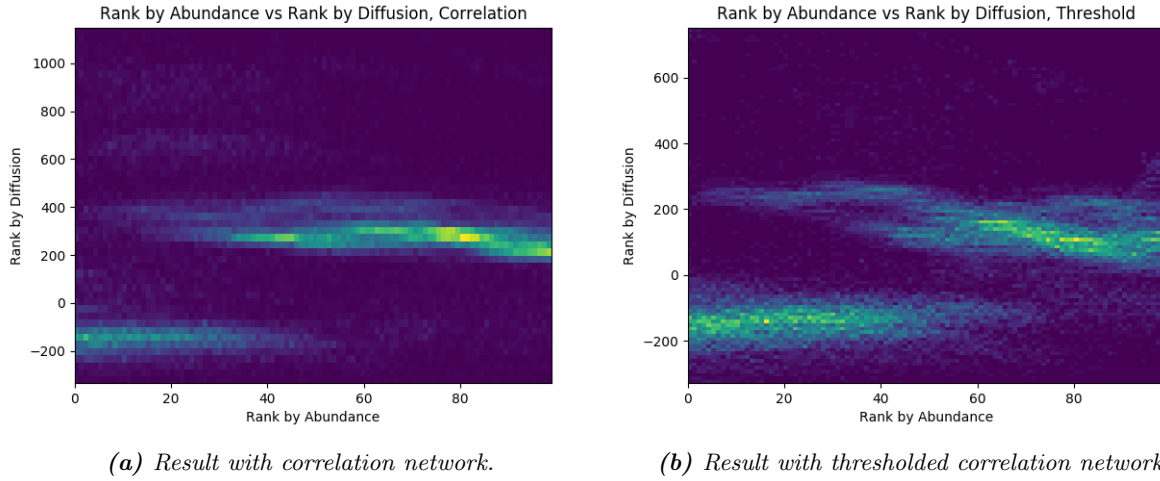
(a) *Correlation network*

Full Threshold Network Fit



(b) *Thresholded correlation network*

Figure 6: Network fit scores of 300 hold out columns (top) to the correlation network built with all of the data, and fit of 300 simulated samples (bottom) constructed using the null model described in section 2.2 (species level).



(a) Result with correlation network.

(b) Result with thresholded correlation network.

Figure 7: Results of set the taxa with n^{th} highest abundance in the sample to 0 abundance and used the diffusion method to find the rank of this taxa, for n from 1 to 100. The plots are histograms of the result, and the “diffusion rank” plotted is the node rank minus the number of non-zero values in the sample. Thus, a rank less than zero indicates the taxa is ranked higher (after being “removed” from the sample) than some taxa with non-zero abundance (species level).

5 Discussion

References

- [1] Aaron Clauset, M. E. J. Newman, and Cristopher Moore. Finding community structure in very large networks. *Phys. Rev. E*, 70:066111, Dec 2004.
- [2] Karoline Faust and Jeroen Raes. Microbial interactions: from networks to models. *Nature Reviews Microbiology*, 10:538–550, 2012.
- [3] Tracey Allen K. Freitas, Po-E Li, Matthew B. Scholz, and Patrick S.G. Chain. Accurate read-based metagenome characterization using a hierarchical suite of unique signatures. *Nucleic Acids Research*, 43(10), 2015.
- [4] Lianshuo Li, Zicheng Wang, Peng He, Shining Ma, Jie Du, and Rui Jiang. Construction and analysis of functional networks in the gut microbiome of type 2 diabetes patients. *Genomics Proteomics Bioinformatics*, 14:314 – 324, 2016.
- [5] Po-E Li, Chien-Chi Lo, Joseph J. Anderson, Karen W. Davenport, Kimberly A. Bishop-Lilly, Yan Xu, Sanaa Ahmed, Shihai Feng, Vishwesh P. Mokashi, and Patrick S.G. Chain. Enabling the democratization of the genomics revolution with a fully integrated web-based bioinformatics platform. *Nucleic Acids Research*, 45(1):67, 2017.
- [6] Zhanshan (Sam) Ma, Chengchen Zhang, Qingpeng Zhang, Jie Li, Lianwei Li, Linyi Qi, and Xianghong Yang. A brief review on the ecological network analysis with applications in the emerging medical ecology. In Terry J. McGenity, Kenneth N. Timmis, and Balbina Nogales Fernndez, editors, *Hydrocarbon and Lipid Microbiology Protocols*. Springer, 2016.
- [7] Kevin P. Murphy. *Machine Learning: A Probabilistic Perspective*. The MIT Press, 2012.
- [8] Heiko Mller and Francesco Mancuso. Identification and analysis of co-occurrence networks with netcutter. *PLOS ONE*, 3(9):1–16, 09 2008.
- [9] M. E. J. Newman. Analysis of weighted networks. *Phys. Rev. E*, 70:056131, Nov 2004.
- [10] Paul Shannon, Andrew Markiel, Owen Ozier, Nitin S Baliga, Jonathan T Wang, Daniel Ramage, Nada Amin, Benno Schwikowski, and Trey Ideker. Cytoscape: A software environment for integrated models of biomolecular interaction networks. *Genome Research*, 13(11):2498–2504, 11 2003.
- [11] Ulrike von Luxburg. A tutorial on spectral clustering. *Statistics and Computing*, 17(4):395–416, 2007.