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BBIO 393: Computational Biology  
Project 2 Proposal

## 1. Overview

This project will extend the insights from project 1, from [Jeff Gordon's \*A Core Gut Microbiome in Obese and Lean Twins\*](#). Given an input [.BIOM file](#) and mapping file, a network will be generated to visualize any differences that exist between lean and obese samples. This project will implement a monte-carlo method and the statistical significance of any insights will be focused upon. This visualization will be implemented in the original exploratory analysis script, which will undergo any necessary improvements/ optimization from project 1.

## 2. Inputs

The script will call a single [.BIOM file](#) and [mapping file](#) (39 features, with 281 samples). Once the nodes and edges are created, that will be used as an input to visualize the network.

## 3. Approach

The network could be defined with `make_otu_network.py` in a qiime virtual machine, or the network could be created from scratch. Visualization could be done through matplotlib, or cytoscape, depending on the complexity of the problem. Comparison to the random networks described in lecture will be conducted as well.

## 4. References

Qiime: <http://qiime.org/>

Qiita: <https://qiita.ucsd.edu/>

Gut Microbiome Dataset: <https://qiita.ucsd.edu/study/description/77>

Biom-Format: [http://biom-format.org/documentation/biom\\_format.html](http://biom-format.org/documentation/biom_format.html)

Cytoscape: [http://www.cytoscape.org/documentation\\_users.html](http://www.cytoscape.org/documentation_users.html)

Make\_otu\_network.py: [http://qiime.org/scripts/make\\_otu\\_network.html](http://qiime.org/scripts/make_otu_network.html)