Dynamic networks

1. Generate biom files from sequencing data for each primer pair
2. Subsample according to rarefaction curve is not needed for network analysis, as it is integrated into the script
3. Generate biom vs biom table to calculate a network for each genotype per month --> OTU\_correlation\_list.txt (windows formatted text)
4. Modified version: /projects/dep\_psl/grp\_kemen/programs/perl\_scripts/general\_useful/Amplicon-Processing/Networking/OTUs/Find\_OTU\_correlations\_NoFilt\_mod.pl

don’t source qiime before running the script!!

1. Use following commands to run on the cluster to source Perl and R mods for calculation:

|  |
| --- |
| # export PERL5LIB=$PERL5LIB:/projects/dep\_psl/grp\_kemen/programs/PerlMods/Statistics-R-0.33/lib/:/projects/dep\_psl/grp\_kemen/programs/PerlMods/Regexp-Common-2013031301/lib/:/projects/dep\_psl/grp\_kemen/programs/PerlMods/  # export PATH=/projects/dep\_psl/grp\_kemen/programs/R-3.3.1/bin:$PATH  # export R\_LIBS="/projects/dep\_psl/grp\_kemen/programs/myRLibs/" |

1. Make mapfile with replicate number, see /projects/dep\_psl/grp\_kemen/programs/perl\_scripts/general\_useful/Amplicon-Processing/Networking/OTUs/otu\_correlations\_list\_all.txt
2. Run perl /projects/dep\_psl/grp\_kemen/programs/perl\_scripts/general\_useful/Amplicon-Processing/Networking/OTUs/Find\_OTU\_correlations\_mod.pl otu\_correlation\_list.txt
3. Make Master\_Edge and Node dirs. and tables :

mkdir ./Correlation\_Resubmission\_Test\_NoFilt/All\_NodeTables/

mkdir ./Correlation\_Resubmission\_Test\_NoFilt/All\_EdgeTables/

ls ./Correlation\_Resubmission\_Test\_NoFilt/\*vs\*/Node\*4.txt | xargs cat > ./Correlation\_Resubmission\_Test\_NoFilt/All\_NodeTables/Master\_NodeTable4.txt

ls ./Correlation\_Resubmission\_Test\_NoFilt/\*vs\*/Node\*5.txt | xargs cat > ./Correlation\_Resubmission\_Test\_NoFilt/All\_NodeTables/Master\_NodeTable5.txt

ls ./Correlation\_Resubmission\_Test\_NoFilt/\*vs\*/Node\*6.txt | xargs cat > ./Correlation\_Resubmission\_Test\_NoFilt/All\_NodeTables/Master\_NodeTable6.txt

ls ./Correlation\_Resubmission\_Test\_NoFilt/\*vs\*/Node\*7.txt | xargs cat > ./Correlation\_Resubmission\_Test\_NoFilt/All\_NodeTables/Master\_NodeTable7.txt

ls ./Correlation\_Resubmission\_Test\_NoFilt/\*vs\*/Edge\*4.txt | xargs cat > ./Correlation\_Resubmission\_Test\_NoFilt/All\_EdgeTables/Master\_EdgeTable4.txt

ls ./Correlation\_Resubmission\_Test\_NoFilt/\*vs\*/Edge\*5.txt | xargs cat > ./Correlation\_Resubmission\_Test\_NoFilt/All\_EdgeTables/Master\_EdgeTable5.txt

ls ./Correlation\_Resubmission\_Test\_NoFilt/\*vs\*/Edge\*6.txt | xargs cat > ./Correlation\_Resubmission\_Test\_NoFilt/All\_EdgeTables/Master\_EdgeTable6.txt

ls ./Correlation\_Resubmission\_Test\_NoFilt/\*vs\*/Edge\*7.txt | xargs cat > ./Correlation\_Resubmission\_Test\_NoFilt/All\_EdgeTables/Master\_EdgeTable7.txt

1. Run clean-up tables to withdraw true correlations: perl /projects/dep\_psl/grp\_kemen/programs/perl\_scripts/general\_useful/Amplicon-Processing/Networking/OTUs/CleanUp\_Tables\_Simple\_NoSelfEdges\_mod.pl

run from dir before ./ Correlation\_Resubmission\_Test\_NoFilt

1. Header moves somewhere else, can’t open in excel otherwise formatting is shit, use this command on the Master Tables instead:

perl -e 'open(in1,"Master\_EdgeTable6\_cleaned.txt"); while(<in1>){ if(/OrgID/){ $header=$\_}else{push @lines,$\_;}} print "$header"; print join("",@lines) ' > Master\_EdgeTable6\_cleaned\_header.txt

perl -e 'open(in1,"Master\_NodeTable6\_cleaned.txt"); while(<in1>){ if(/ID/){ $header=$\_}else{push @lines,$\_;}} print "$header"; print join("",@lines) ' >Master\_NodeTable6\_cleaned\_header.txt

1. Load the edge and node tables into cytoscape and calculate statistics on the network. These can then be output as a file with properties of each node. For cytoscape settings use the L6, genus-level, network:

#Import Network from File choose your Master\_EdgeTable6\_cleaned\_header\_L6.txt and manually assign Source and Target node

# Then import table from file and choose your Master\_NodeTable6\_cleaned\_header.txt and pick your network and set edge and node table

Previously used settings:

# Edge Property|Parameter|Cont/Discrete|Value-Setting|Value-Setting

# Type| Slope|Discrete|Neg-Dashed|Pos-Solid

# Color|Slope|Discrete|Neg-Black|Pos-Orange

# Transparency|stm\_rsqadj|Continuous|3-30|7.0274-15

# Width|stm\_rsqadj|Continuous|3-0|7.0274-15

# Node Property|Parameter|Cont/Discrete|Value-Setting|Value-Setting|Value-Setting

# Size|Degree|Continuous|0-10|53-50|

# Color|Kingdom|Discrete|Bacteria-Blue|Chromalveolata-Green|Fungi-Red

# Border|EndoEpi|Discrete|Endo-Black|Epi-None