



Chinese Academy of Sciences

Qingdao Institute of BioEnergy and BioProcess Technology



MetaSee

A Metagenomic Visualization toolbox

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BOSC2013

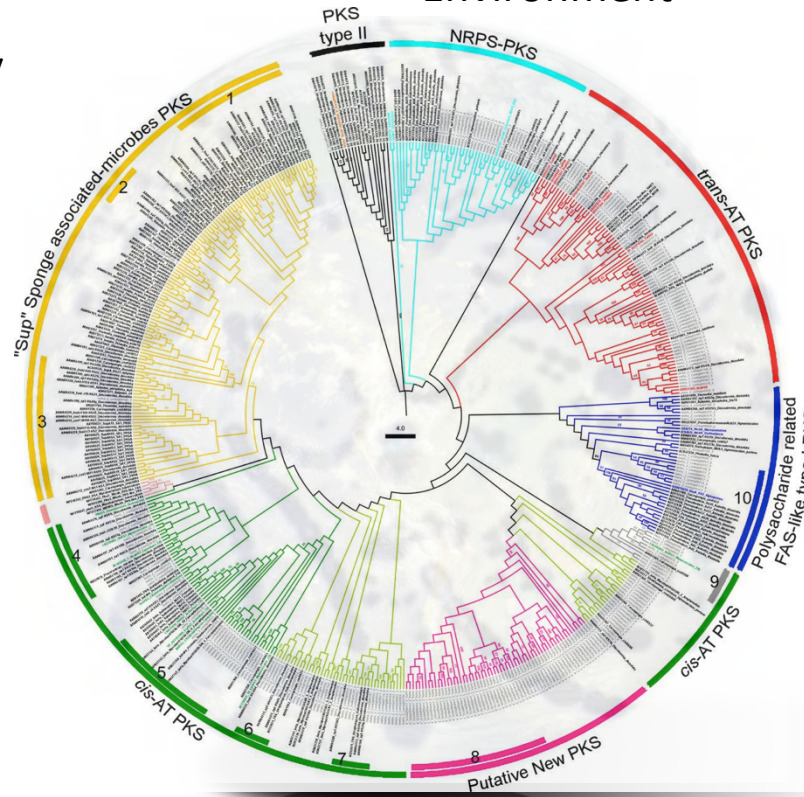
Metagenome



Bio-Energy



Environment



Wine Industry



Health



Ocean Research

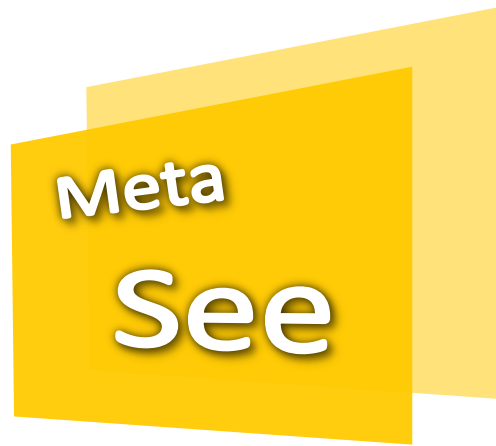


Agriculture



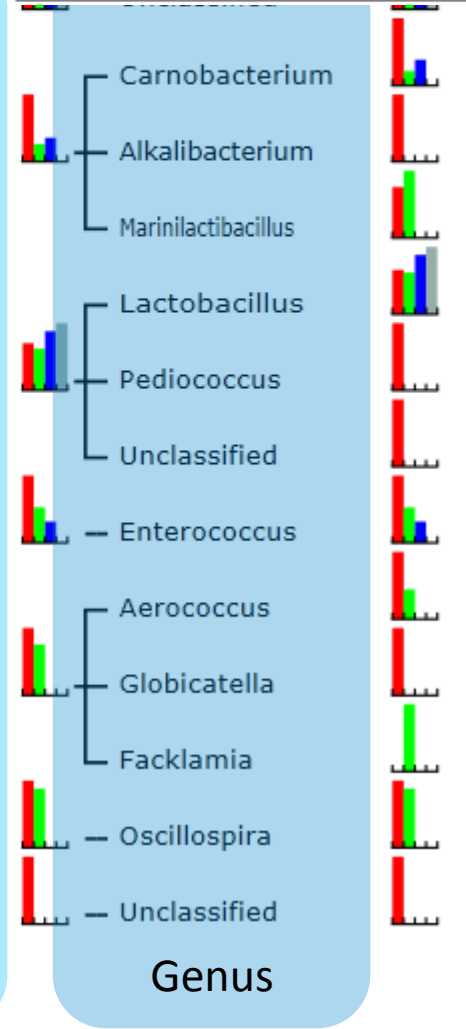
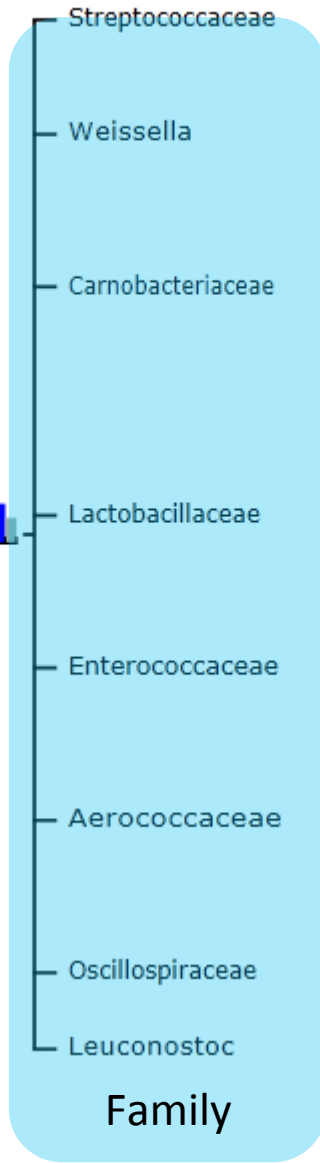
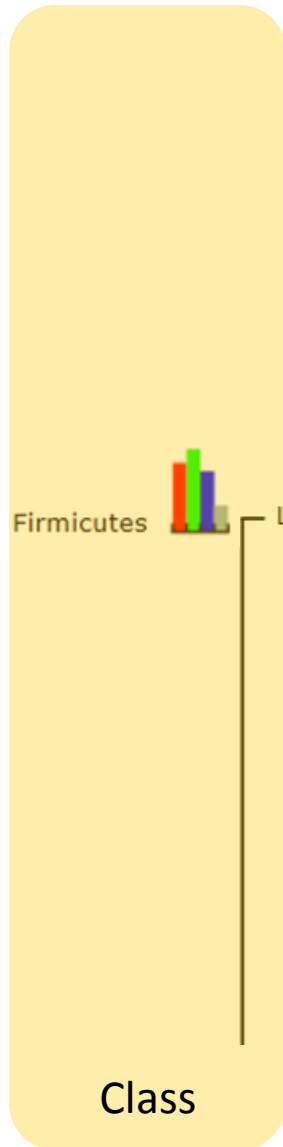
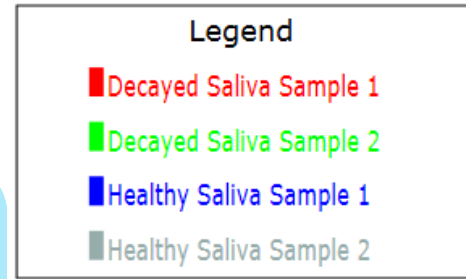
Bio-Security





MetaSee¹ is an extendable toolbox that facilitates the interactive visualization of metagenomic samples.

¹Song, et al., *MetaSee: An interactive and extendable visualization toolbox for metagenomic sample analysis and comparison*, PLOS ONE, 2012



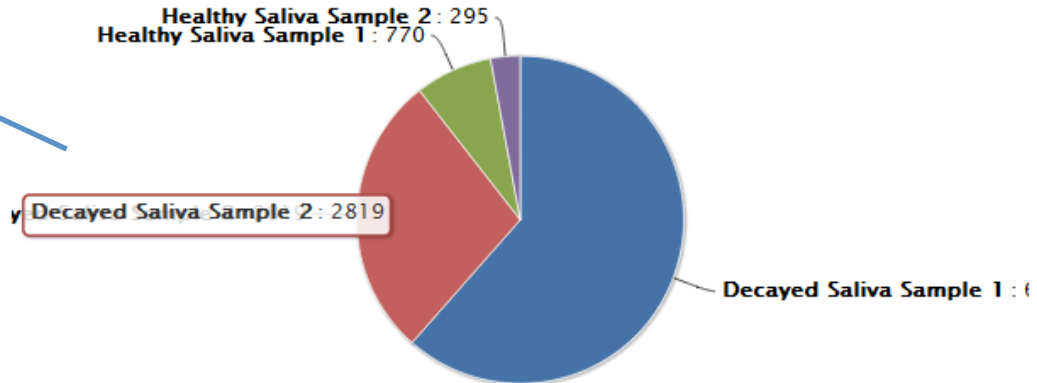
.....

Specific Taxon

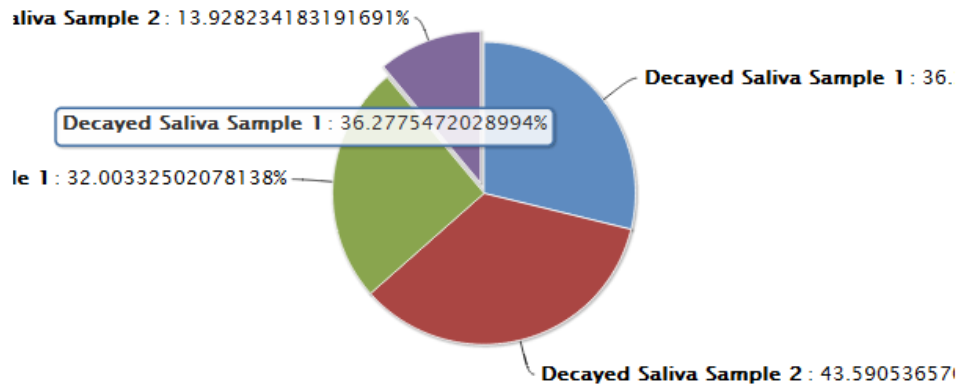
Abundance

- root
- Bacteria
 - Proteobacteria
 - Firmicutes
 - Lactobacillales
 - Bacillales
 - Clostridia
 - Unclassified
 - Mollicutes
 - Unclassified
 - Actinobacteria
 - Bacteroidetes
 - Fusobacteria
 - Acidobacteria
 - Cyanobacteria
 - Spirochaetes
 - Chlorobi
 - Chloroflexi
 - Ferribacter
 - Gulbenkianus
 - Thermus
 - Aquificae
 - Planctomycetes
 - Gemmatimonadetes
 - Deferribacteres
 - Verrucomicrobia
 - Thermolithobacter
 - Antarctic

Absolute Abundance



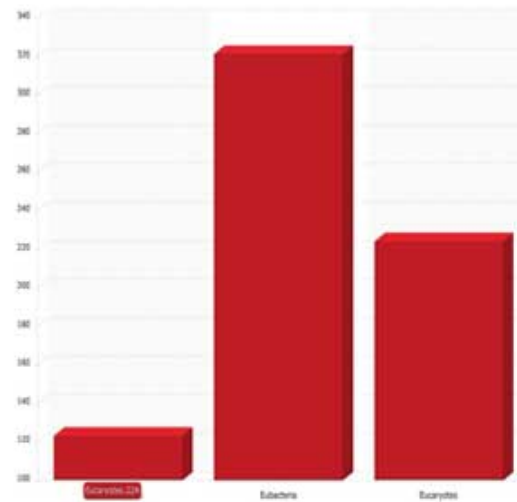
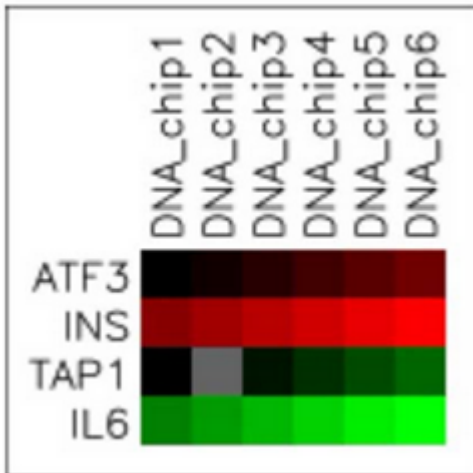
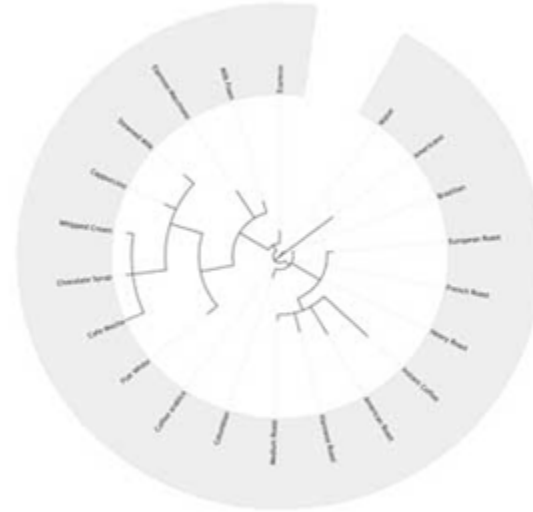
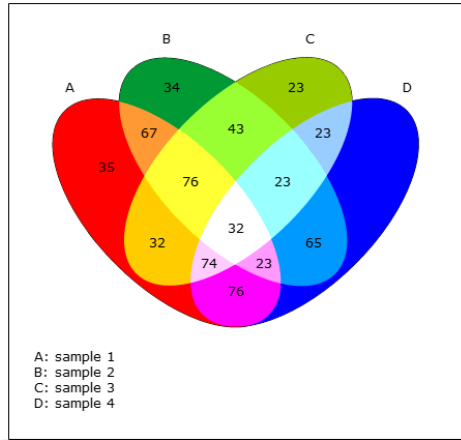
Relative Abundance



Plug-ins

Statistical tools

Press Ctrl+P, you can get a vectorgraph.



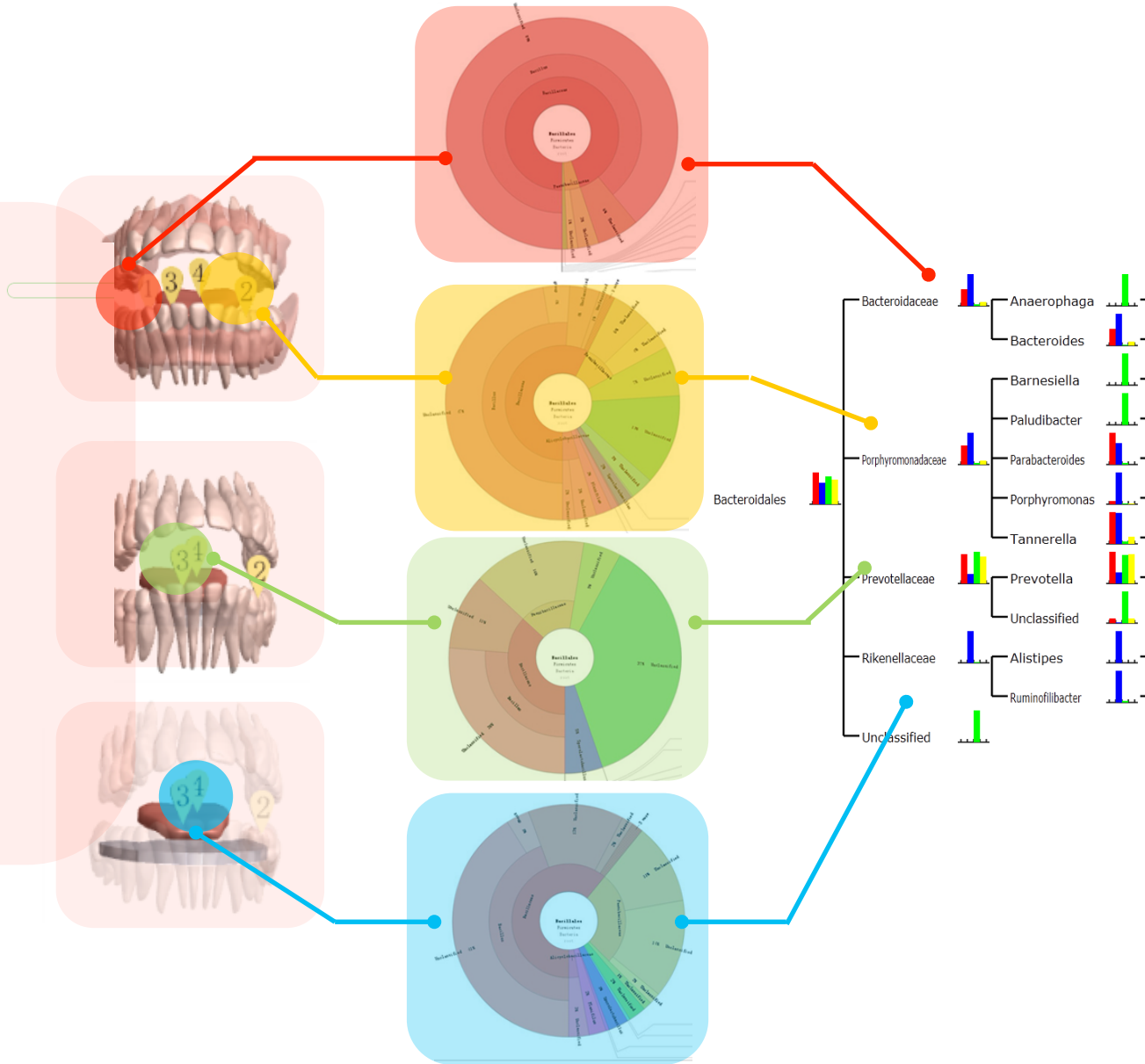


Application

Digital Mouth

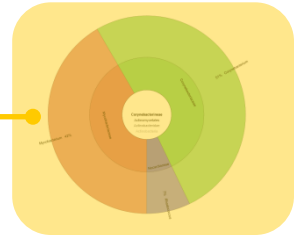
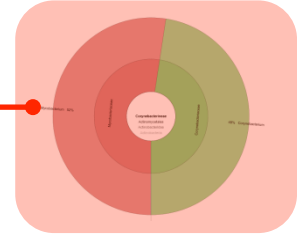
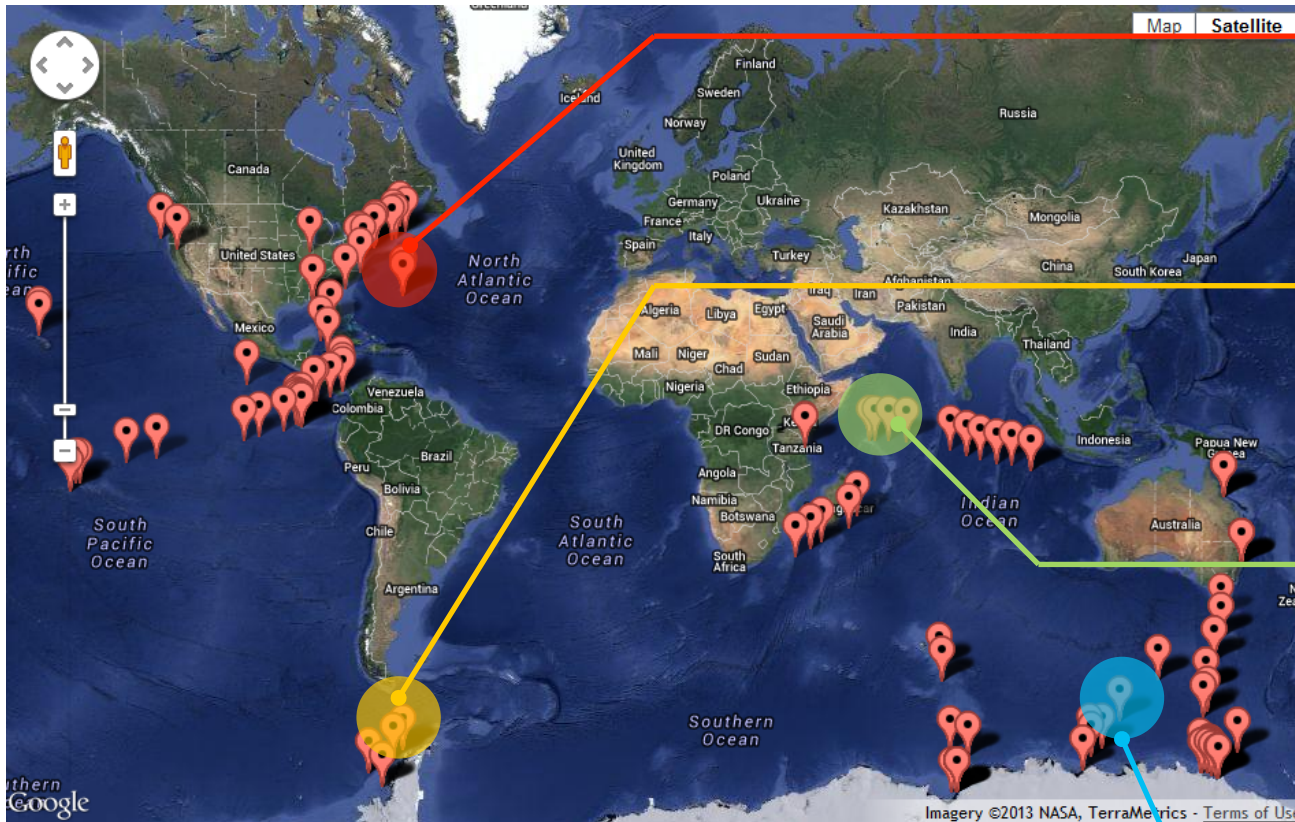
Oral metagenomic research, powered by WebGL

Digital Mouth



Metagenomic Global Survey

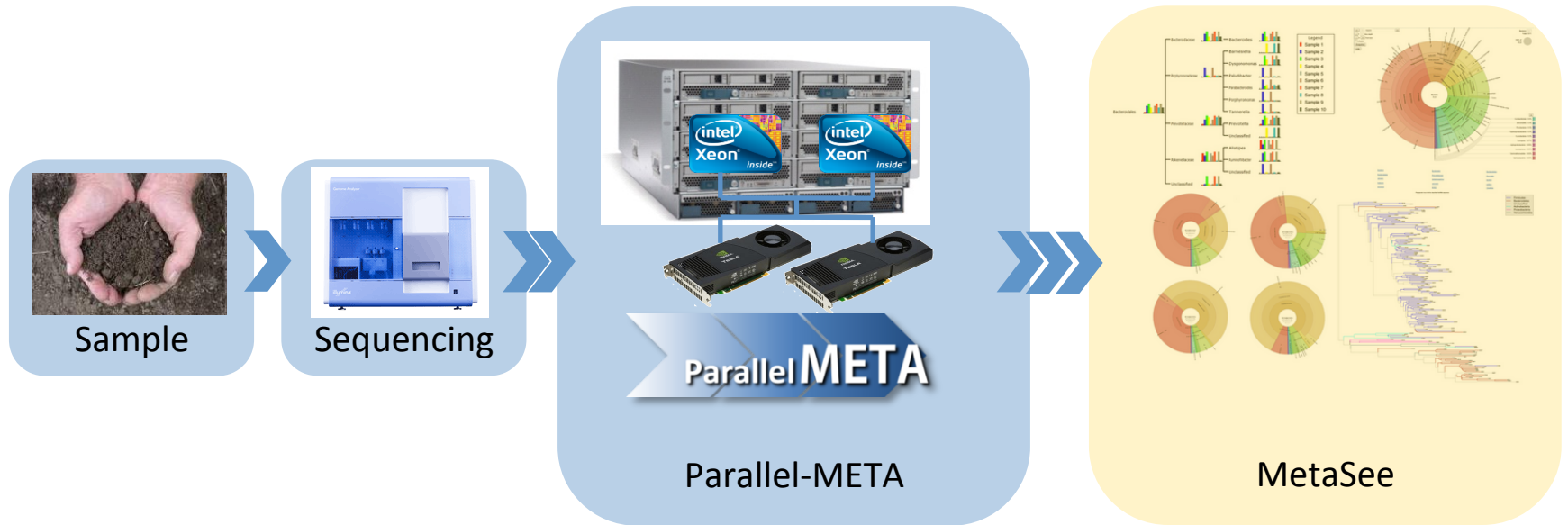
Global metagenomic structure comparison
powered by Google Map





● **Parallel-META³** is a GPGPU and Multi-Core CPU based software pipeline which can parallelly analyze massive metagenomic data, report the classification, construction and distribution on phylogenetic and taxonomic level.

<http://www.computationalbioenergy.org/parallel-meta.html>



³Su et al., *Parallel-META: Efficient metagenomic data analysis based on high-performance computation*, BMC Systems Biology, 2012.



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All projects and samples could be viewed here.

BEGC-SPIDER
Automatic information collection tool to update the database monthly

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Database

BEGC-SPIDER
Automatic information collection tool to update the database monthly

Updater

Parallel META
Meta-See

Structure Analysis

Meta-Storms
Meta-See

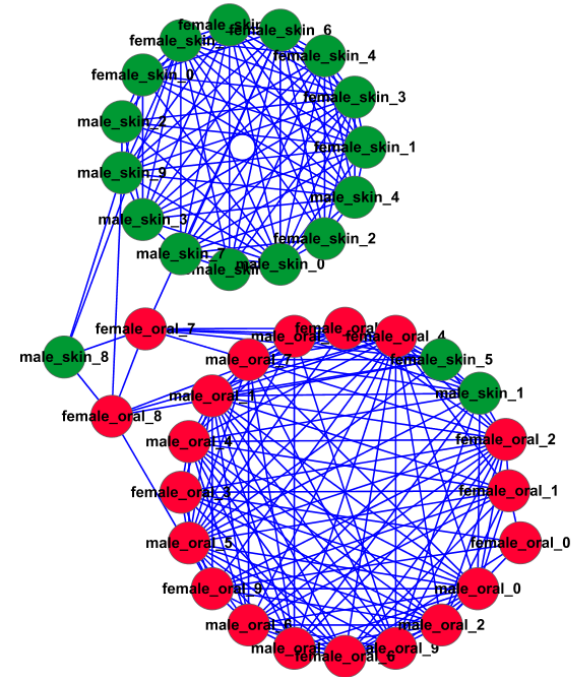
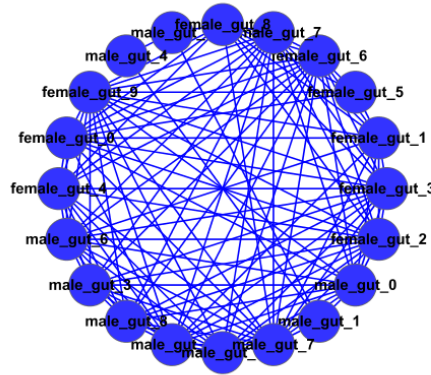
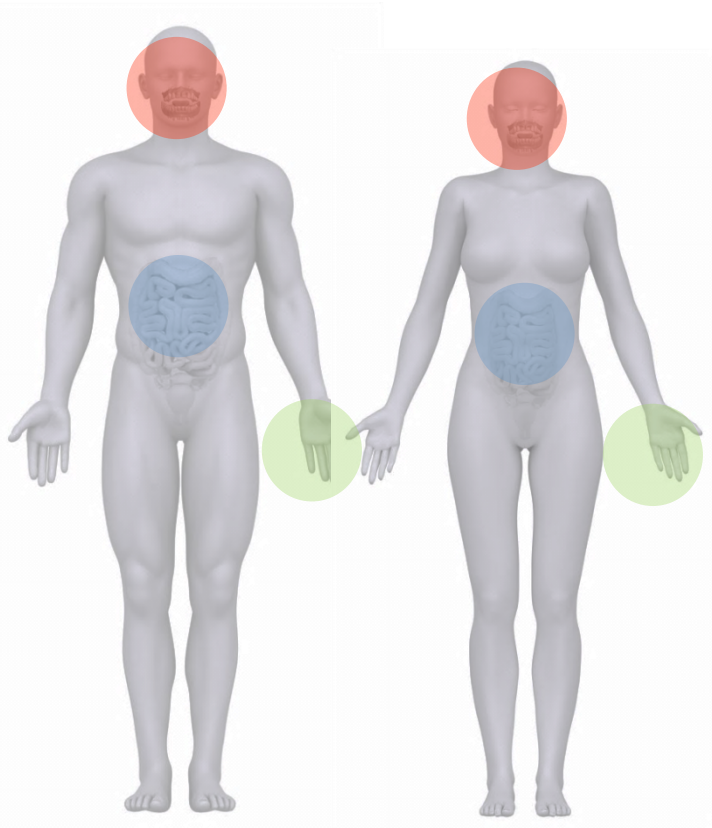
Sample Search⁴

● **Meta-Mesh** is a well-organized metagenomic database and analysis system that can automatically collect, integrate metagenomic samples and information, with web-service of **structure analysis, sample comparison and searching.**

⁴Su, et al., *Meta-Storms: Efficient Search for Similar Microbial Communities Based on a Novel Indexing Scheme and Similarity Score for Metagenomic Data*, Bioinformatics 2012



Human-associated habitat metagenomic samples

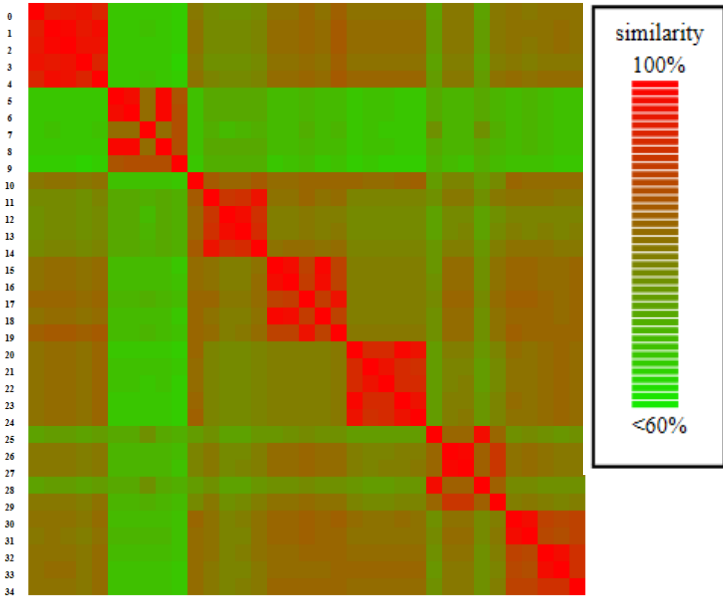


Clustering

- Samples from oral cavity
- Samples from gut(feces)
- Samples from skin

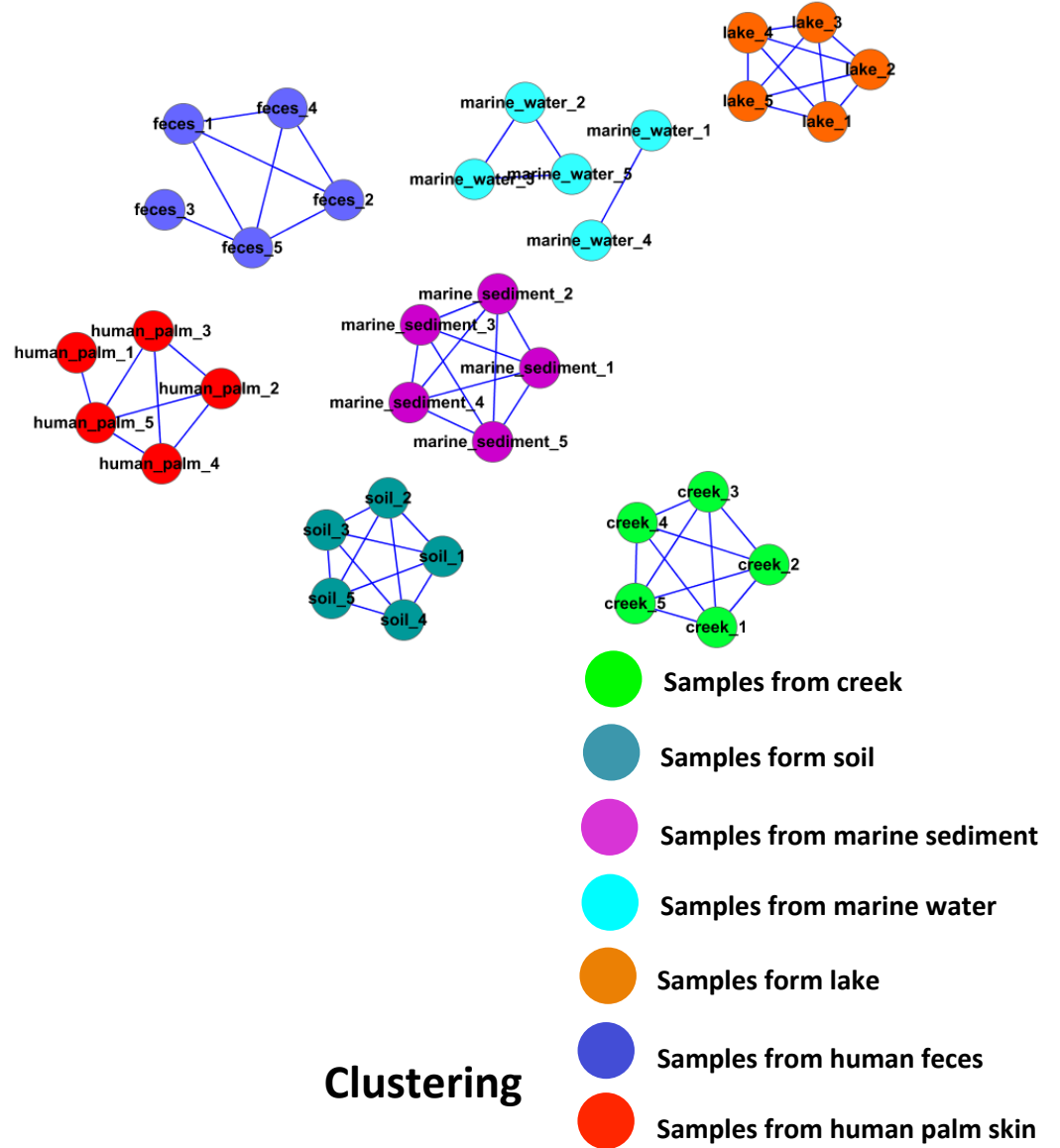


Environmental Samples

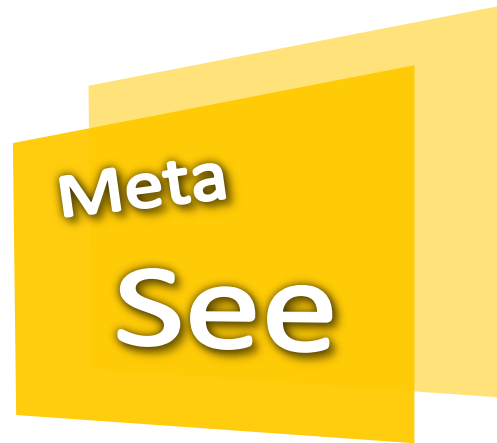


0 Samples from creek
 1 Samples from creek
 2 Samples from creek
 3 Samples from creek
 4 Samples from creek
 5 Samples from creek
 6 Samples from creek
 7 Samples from creek
 8 Samples from creek
 9 Samples from creek
 10 Samples from creek
 11 Samples from creek
 12 Samples from creek
 13 Samples from creek
 14 Samples from creek
 15 Samples from creek
 16 Samples from creek
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 31 Samples from creek
 32 Samples from creek
 33 Samples from creek
 34 Samples from creek

Similarity Matrix



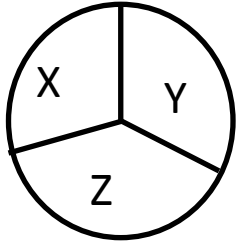
Clustering



The end

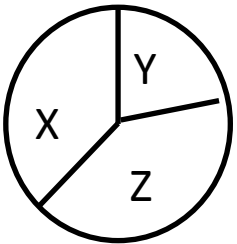
Powered by





X	30%
Y	40%
Z	30

Sample S1



X	40%
Y	20%
Z	40%

Sample S2

$$S1 = 20\% * (1 - 0.3) = 14\%$$

$$S2 = 10\% * (1 - 0.2) = 8\%$$

