



Chinese Academy of Sciences

Qingdao Institute of BioEnergy and BioProcess Technology



MetaSee

A Metagenomic Visualization toolbox

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BOSC2013

Metagenome



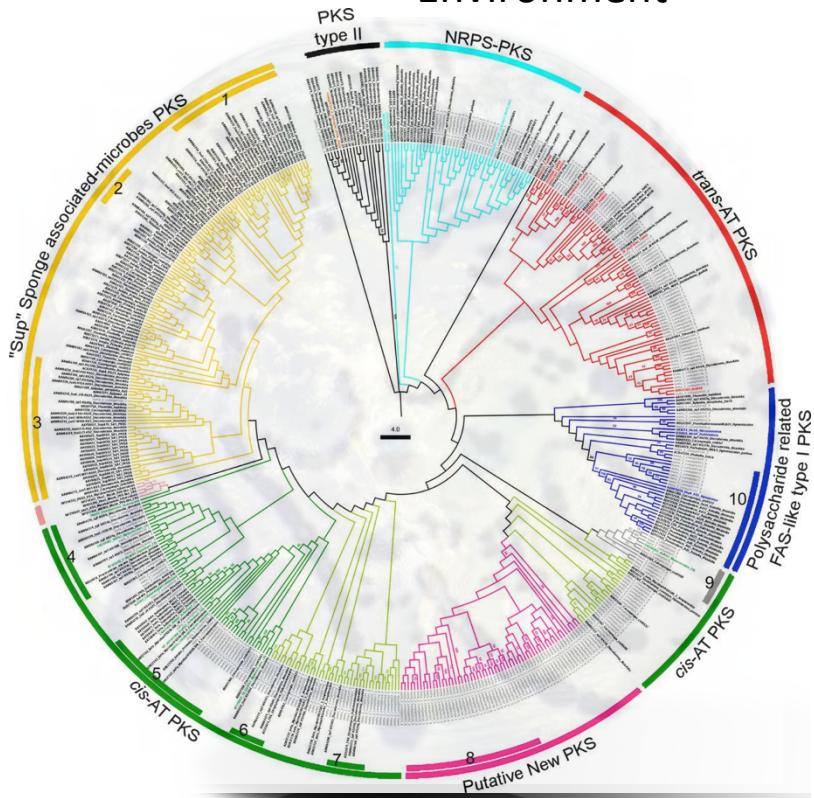
Bio-Energy



Environment



Health



Agriculture



Bio-Security



Wine Industry



Ocean Research



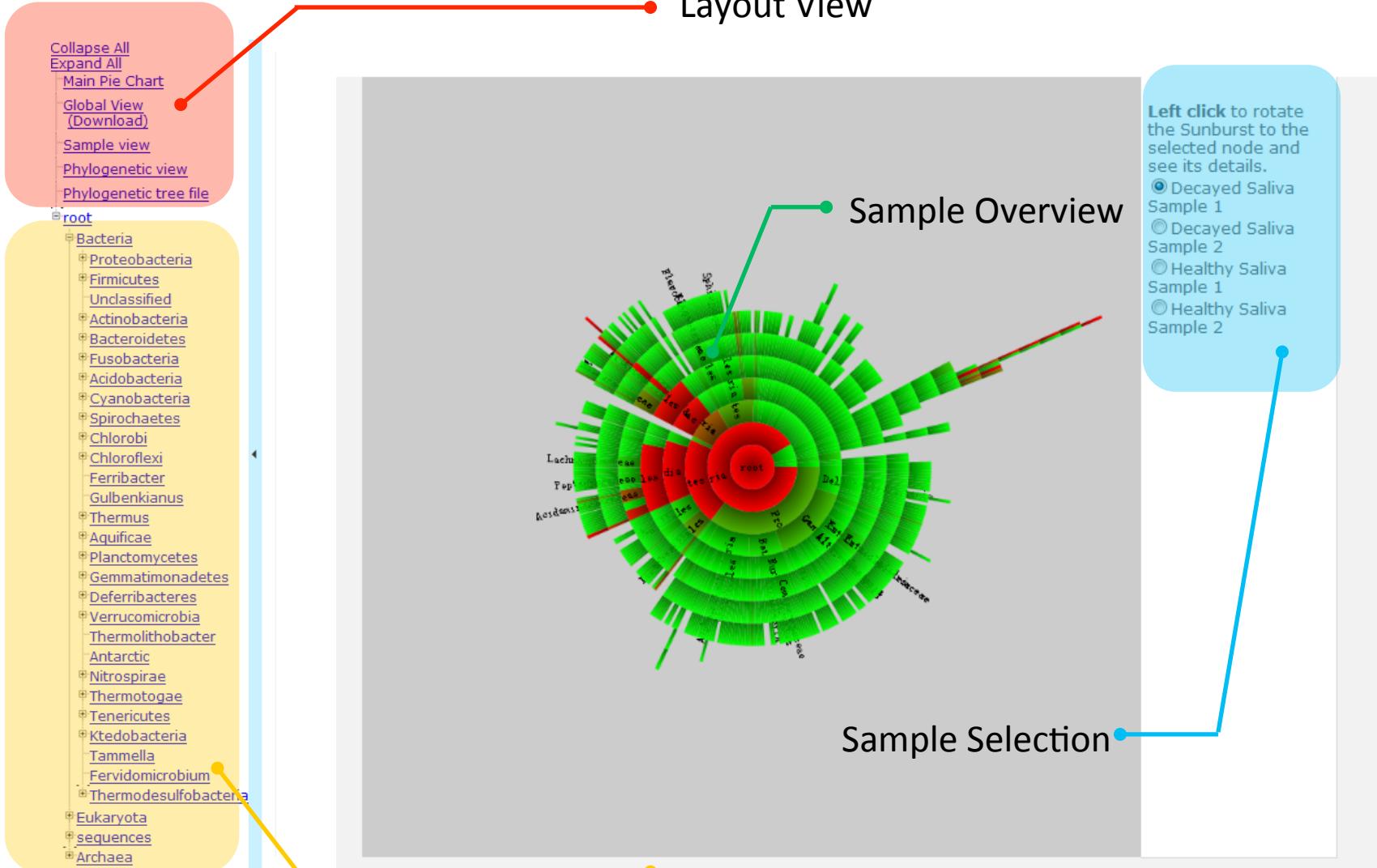


MetaSee¹ is an extendable toolbox that facilitates the interactive visualization of metagenomic samples.

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

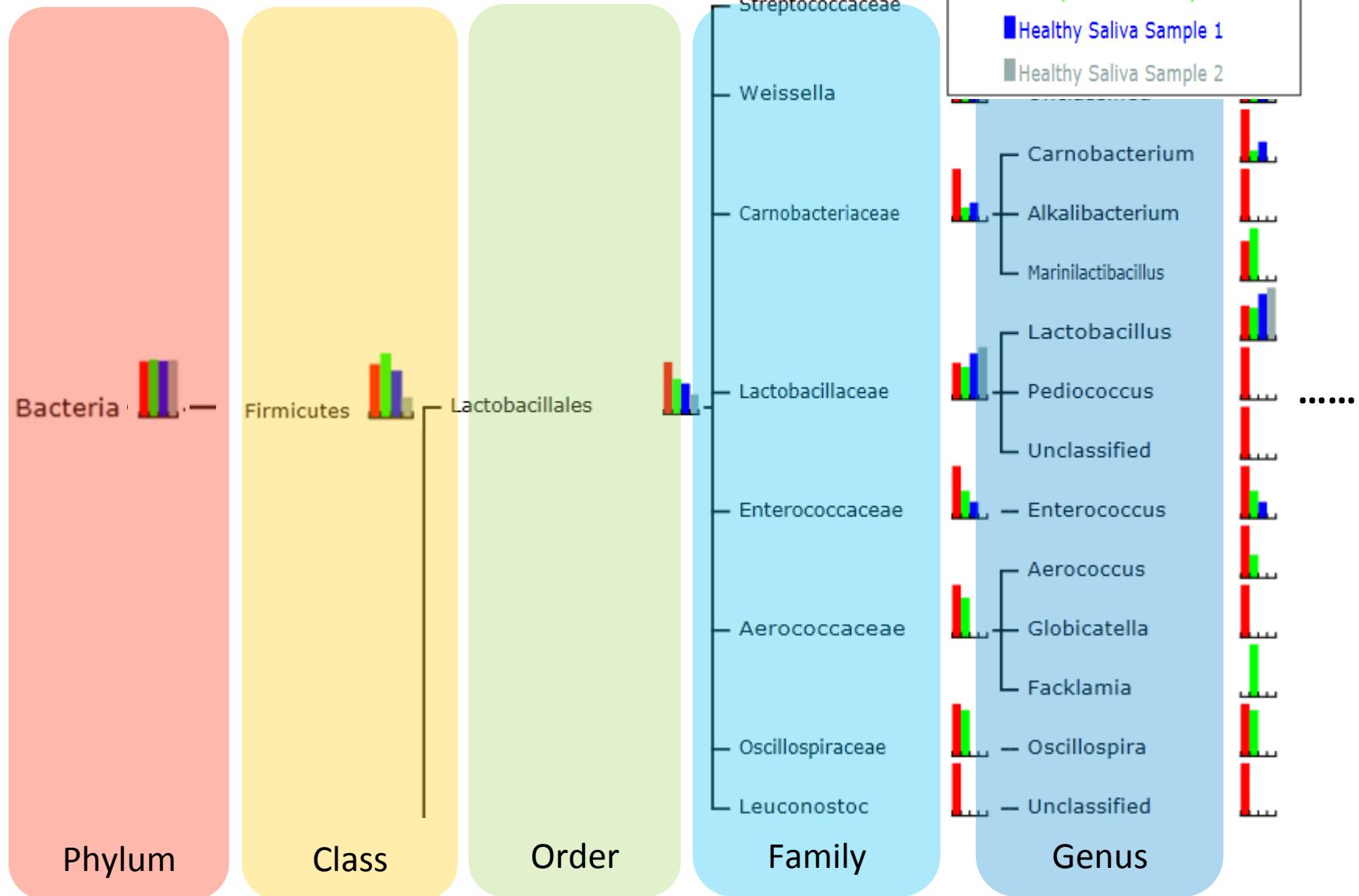
Main Index Page

Over view and link to all pages



Global View

Powered by SVG



Sample View

Powered by Krona²



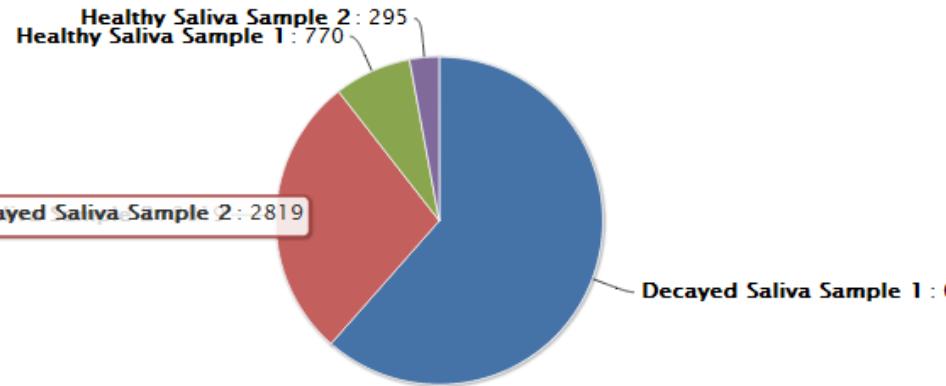
²Ondov B, et al., Interactive metagenomic visualization in a Web browser. BMC Bioinformatics 2011.

Specific Taxon

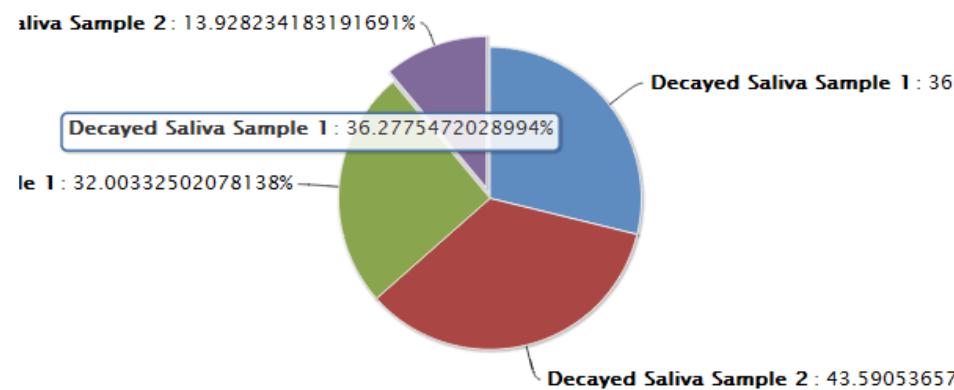
Abundance



Absolute Abundance



Relative Abundance



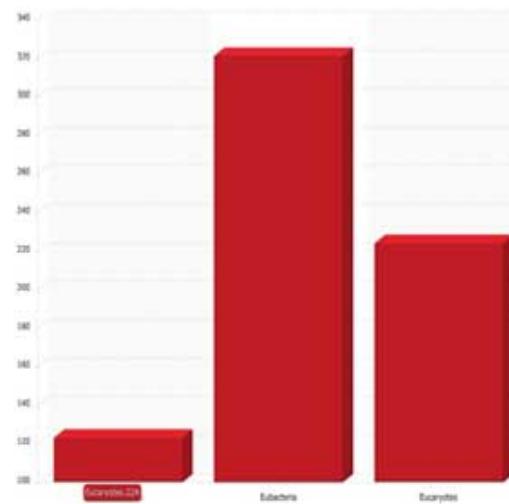
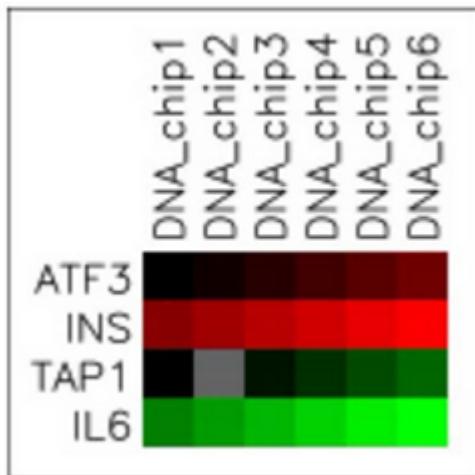
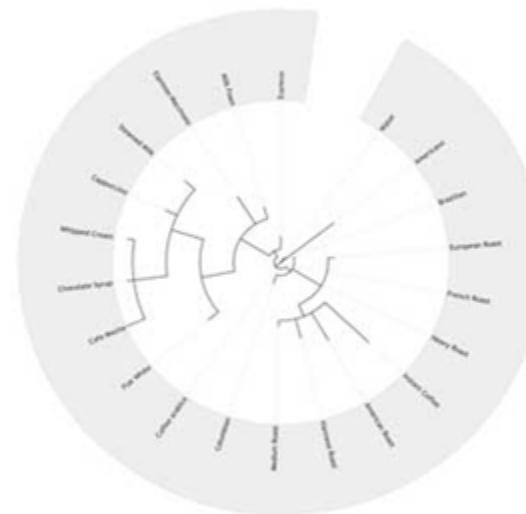
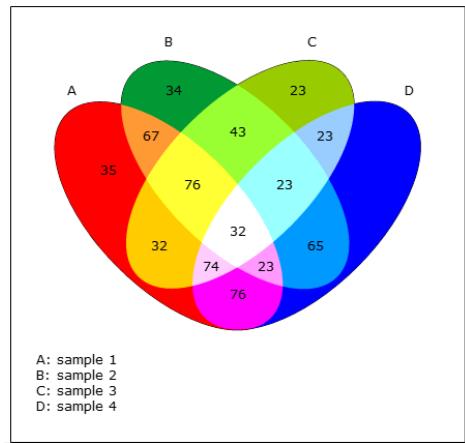
Meta

See

Plug-ins

Statistical tools

Press **Ctrl+P**, you can get a vectorgraph.



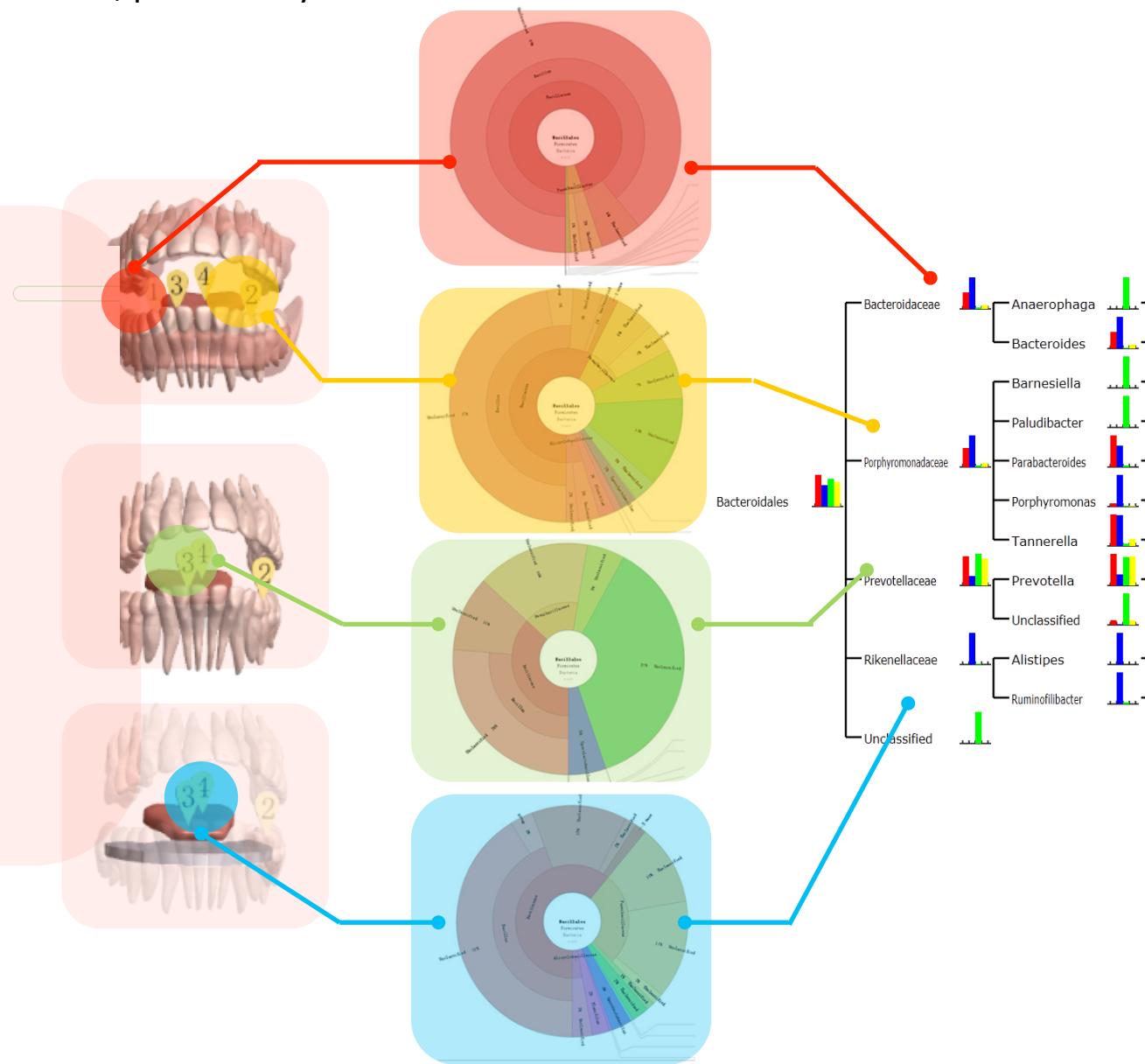
Meta
See

Application

Digital Mouth

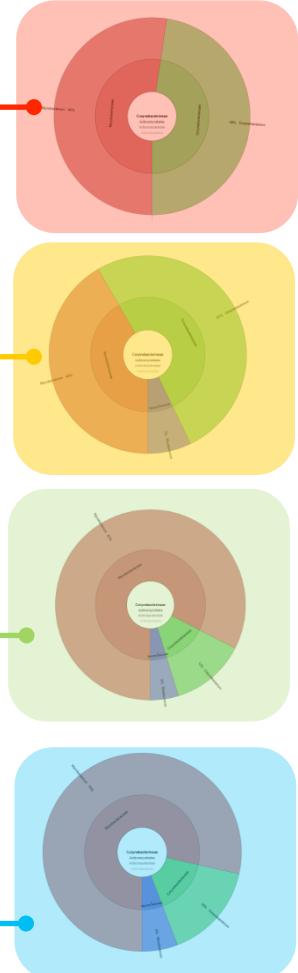
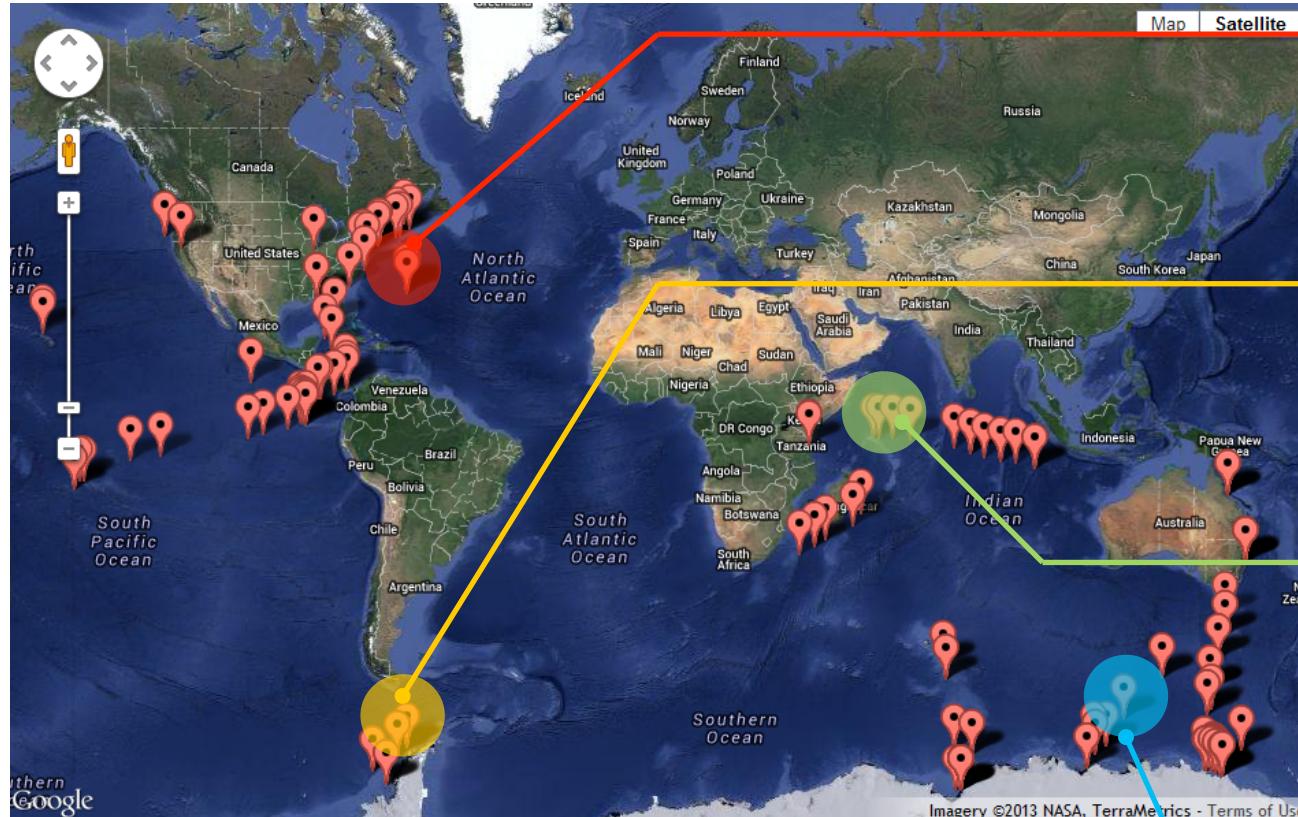
Oral metagenomic research, powered by WebGL

Digital Mouth



Metagenomic Global Survey

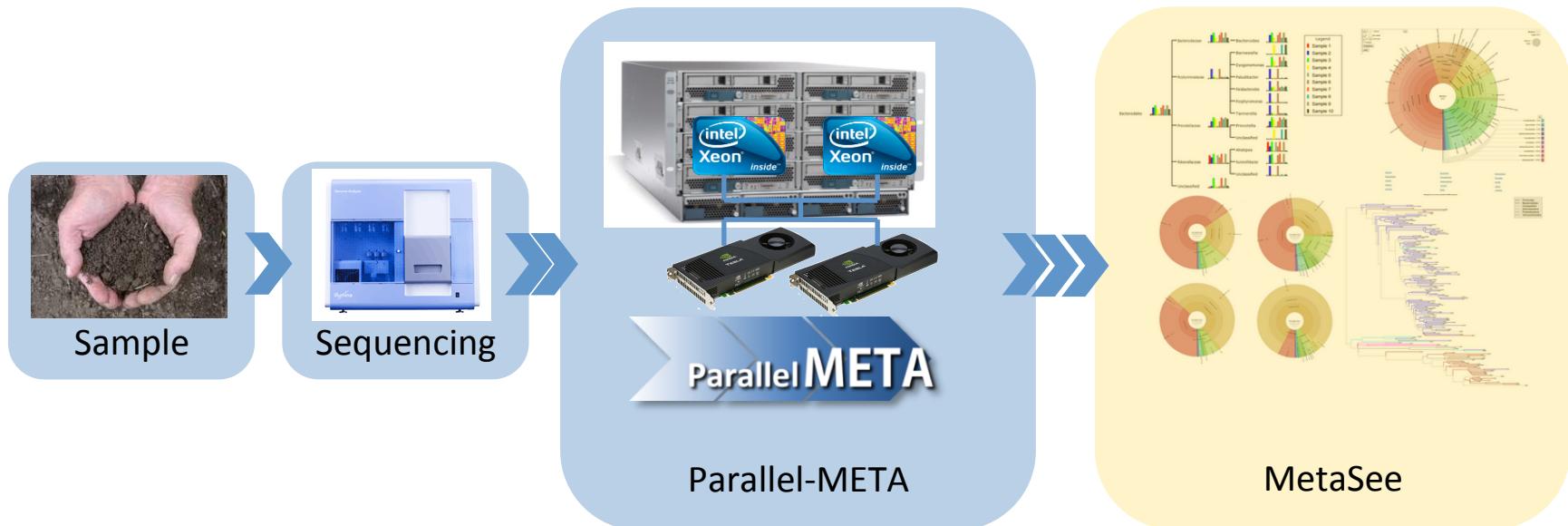
Global metagenomic structure comparison
powered by Google Map





- 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.

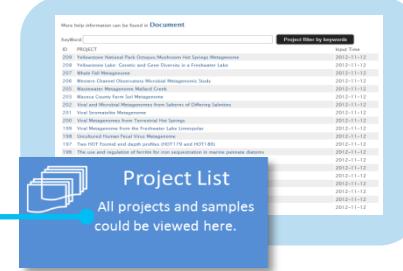
<http://www.computationalbioenergy.org/parallel-meta.html>



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



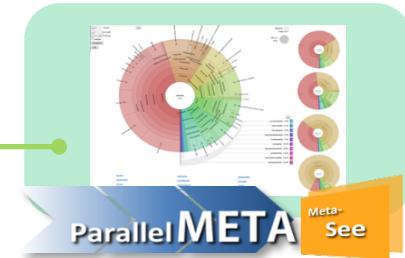
Home Project List Map Work Center Download



Database



Updater



Structure Analysis



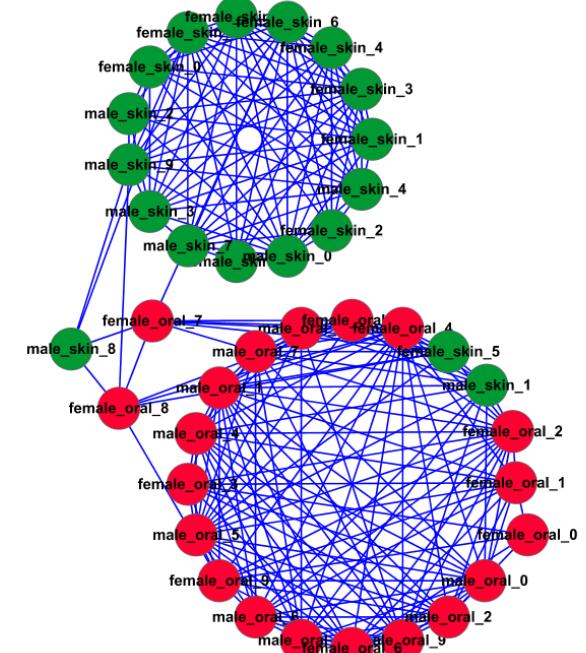
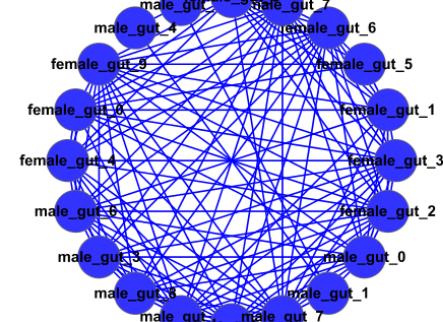
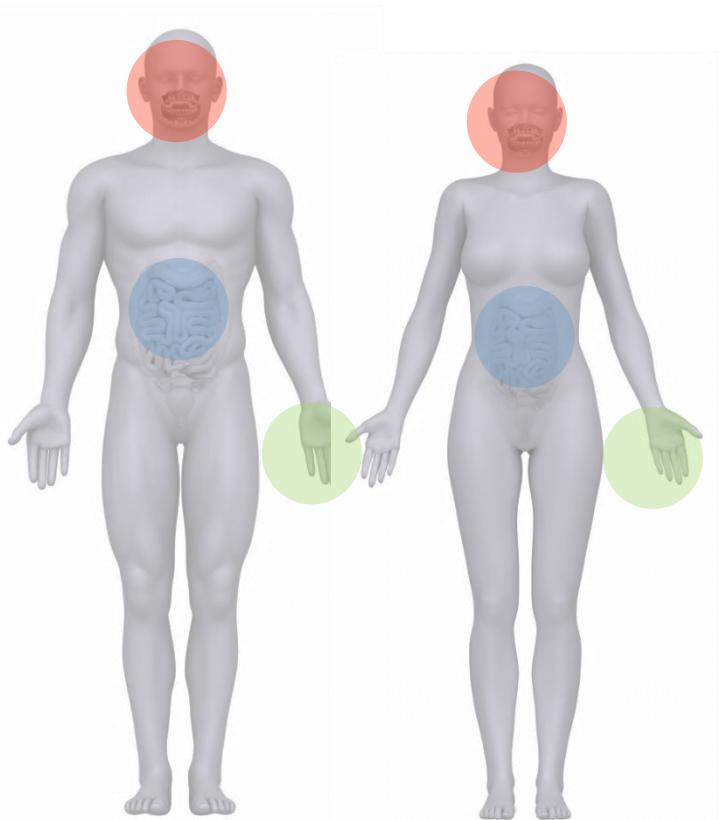
Sample Search⁴

● **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



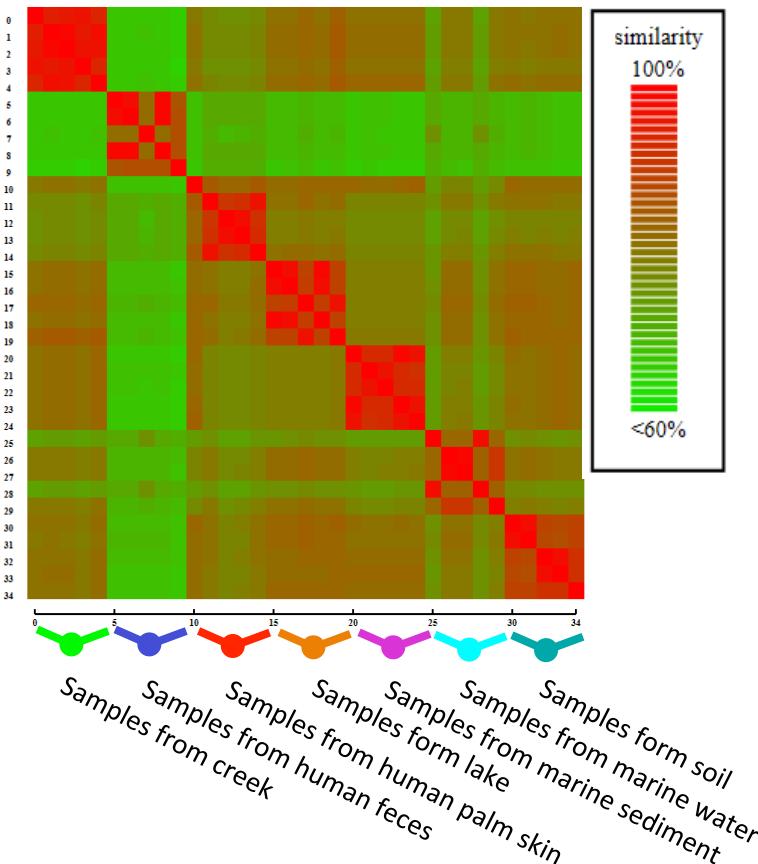
Samples form gut(feces)



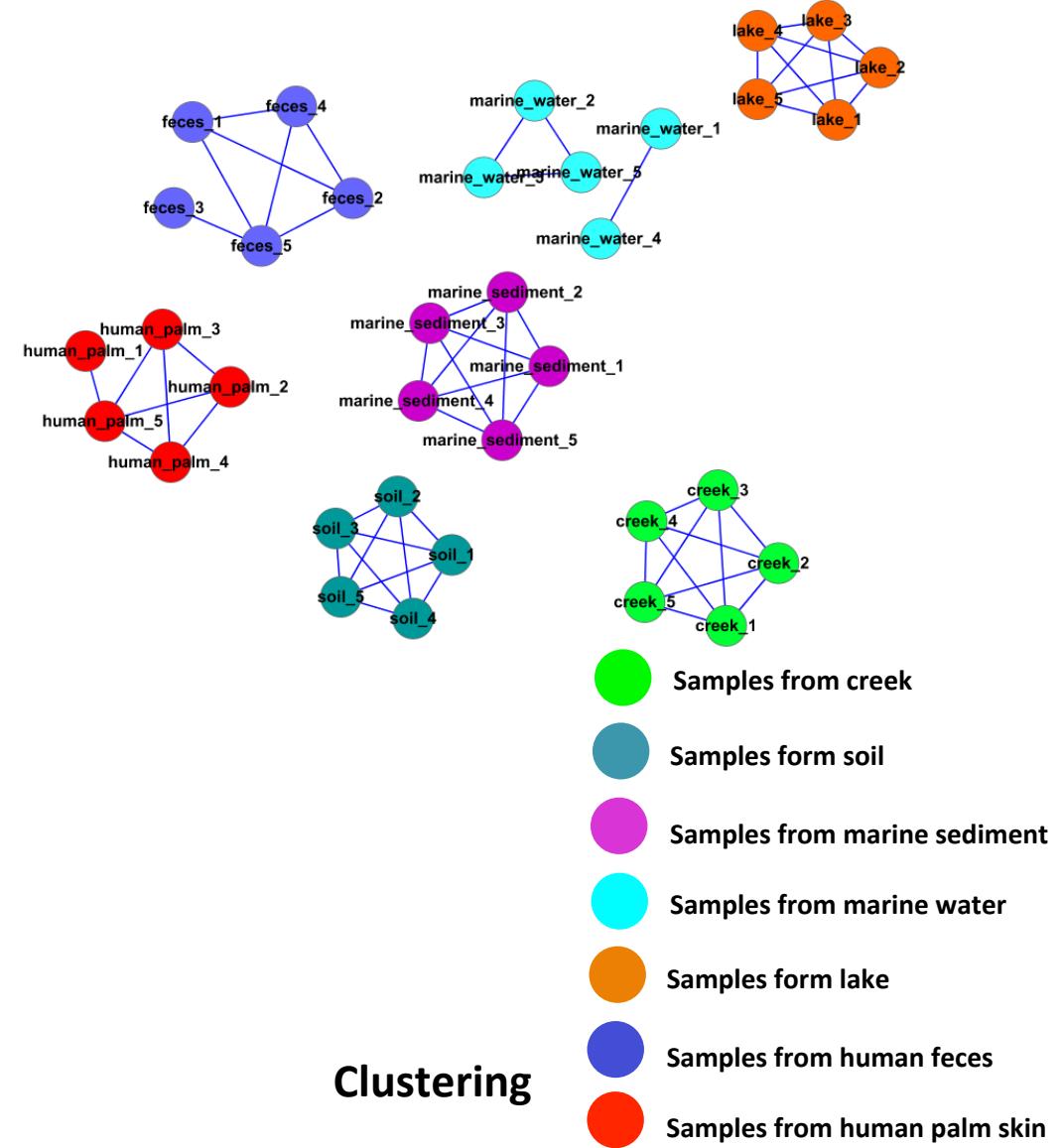
Samples from skin



Environmental Samples



Similarity Matrix

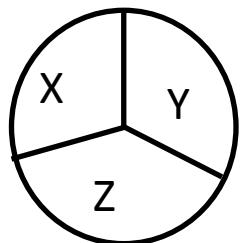




The end

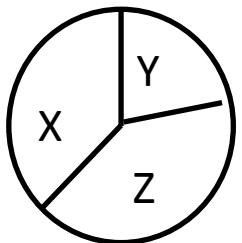
Powered by





X	30%
Y	40%
Z	30

Sample S1



X	40%
Y	20%
Z	40%

Sample S2

