METAREP
JCVI Metagenomics Reports

An open source tool for high-performance comparative metagenomics

JCVI Metagenomics Reports (METAREP) is a new open source tool for **high-performance comparative metagenomics**. It provides a suite of web based tools to help scientists to **view, query, browse, and compare metagenomics** annotation data derived from ORFs called on metagenomics reads or assemblies.

METAREP supports browsing of functional and taxonomic assignments. Users can either specify fields, or logical combinations of fields to **filter and refine datasets**. Users can compare multiple datasets at various functional and taxonomic levels applying statistical tests as well as hierarchical clustering, multidimensional scaling and heatmaps.

For each of these features, **tab delimited files can be exported** for downstream analysis. The web site is optimized to be user friendly and fast.
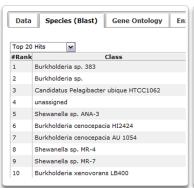
▼ **View**
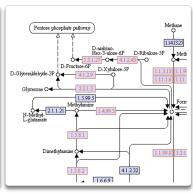top summaries by data type

▼ **Query**
use SQL-like query syntax

▼ **Browse**
NCBI Taxonomy, GO, Kegg pathways

▼ **Compare**
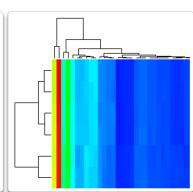datasets using plots and statistical tests

Feature Summary ▶

- **Handle extremely large datasets.** Uses scalable high-performance search engine (we have indexed 300 million annotation entries, but much larger volumes can be handled).

- **Compare 20+ datasets at the same time.** Use various compare options including statistical tests and plot options to visualize dataset difference at various taxonomic and functional levels.

- **Use statistical tests** such as METASTATS (White et al.), a modified non-parametric t-test to compare two sample populations (e.g. metagenomics samples from healthy and diseased individuals).

- **Export publication-ready graphics.** Export heatmaps, hierarchical clustering and multi-dimensional scaling plots in PDF format.

- **Analyze KEGG metabolic pathways.** Summaries include enzyme highlights on KEGG maps, pathway enzyme distributions and statistics about pathway coverage at various pathway levels.

- **Search using a SQL-like query syntax.** Build your query using 14 different fields that can be combined logically.

- **Drill down into data** using METAREP's NCBI Taxonomy, Gene Ontology, Enzyme Classification or KEGG Pathway browser.

- **Install your own METAREP version.** Flexible central configuration, METAREP and 3rd party code base is completely open source.

- **Cross-link function with phylogeny.** Slice your data at various taxonomic and/or functional levels. For example, search for all bacteria or exclude eukaryotes or search for a certain (GO/EC ID)/taxonomic combination.

- **Generic data format.** Data types that can be populated include a free text functional description, best BLAST hit information, as well as GO ID, EC ID, and HMMs.

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