MEGAN-DB – The MEtaGenome ANalyzer DataBase

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Abstract

The sequencing of genomic or transcribed DNA from environmental samples ("metagenomics") allows investigating the structure, function and metabolism of environmental communities on the molecular level. Comparative analyses between multiple metagenomes become increasingly informative due to the large, rapidly growing number of available metagenomic sequences from varying sources (soil, water, intestine, sludge, etc.).

MEGAN-DB provides a comprehensive repository of metagenomes and their taxonomic and functional profiles (see Fig. 1). Exploration of the database contents as well as comparative analyses are facilitated by a user-friendly web portal, providing versatile tools and an integration into the MEGAN software (see Fig. 2). MEGAN-DB offers direct data access to the meta-data through webservices and to MEGAN input files via FTP. Users may upload new metagenomes for permanent integration into MEGAN-DB or for single conversion into MEGAN files.

Frequent updating of MEGAN-DB with respect to new metagenomes as well as new reference sequences will facilitate comparative taxonomic and functional interpretation of metagenomes considering the whole publicly available metagenomic sequence space. MEGAN-DB is freely available to academic and commercial users via http://megan-db.org.
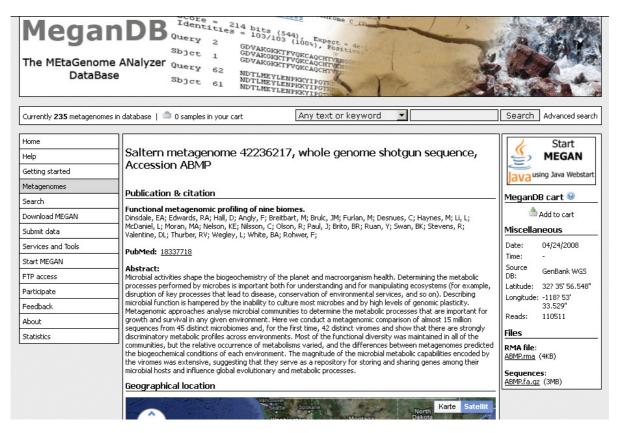
Figure 1: Screenshot of the metagenome entry webpage in MEGAN-DB for "saltern metagenome" with accession ABMP. MEGAN-DB displays various meta-data for each metagenome, e.g. geographic location, sequence size and publication details.
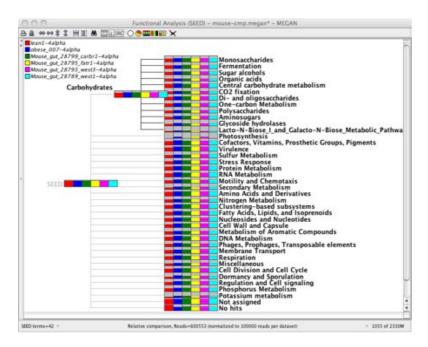

Figure 2: Comparative analyses of functional modules in lean and obese mouse gut metagenomes with MEGAN.