

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>.

MeganDB
The MEtaGenome ANalyzer DataBase

Currently 235 metagenomes in database | 0 samples in your cart

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Saltern metagenome 42236217, whole genome shotgun sequence, Accession ABMP

Publication & citation

Functional metagenomic profiling of nine biomes.
Dinsdale, EA; Edwards, RA; Hall, D; Angly, F; Breitbart, M; Brulic, JM; Furlan, M; Desnues, C; Haynes, M; Li, L; McDaniel, L; Moran, MA; Nelson, KE; Nilsson, C; Olson, R; Paul, J; Brito, BR; Ruan, Y; Swan, BK; Stevens, R; Valentine, DL; Thurber, RV; Wegley, L; White, BA; Rohwer, F;

PubMed: 18337718

Abstract:
Microbial activities shape the biogeochemistry of the planet and macroorganism health. Determining the metabolic processes performed by microbes is important both for understanding and for manipulating ecosystems (for example, disruption of key processes that lead to disease, conservation of environmental services, and so on). Describing microbial function is hampered by the inability to culture most microbes and by high levels of genomic plasticity. Metagenomic approaches analyse microbial communities to determine the metabolic processes that are important for growth and survival in any given environment. Here we conduct a metagenomic comparison of almost 15 million sequences from 45 distinct microbiomes and, for the first time, 42 distinct viromes and show that there are strongly discriminatory metabolic profiles across environments. Most of the functional diversity was maintained in all of the communities, but the relative occurrence of metabolisms varied, and the differences between metagenomes predicted the biogeochemical conditions of each environment. The magnitude of the microbial metabolic capabilities encoded by the viromes was extensive, suggesting that they serve as a repository for storing and sharing genes among their microbial hosts and influence global evolutionary and metabolic processes.

Geographical location

Vancouver Seattle Spokane Montana North Dakota Karte Satellit

Start MEGAN
Java using Java Webstart

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Miscellaneous

Date: 04/24/2008
Time: -
Source: GenBank WGS
DB:
Latitude: 32° 35' 56.548"
Longitude: -118° 53' 33.529"
Reads: 110511

Files

RMA file:
ABMP.rma (4KB)

Sequences:
ABMP.Fa.gz (3MB)

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.