MiSAFE

The Development and Validation of Microbial Soil Community Analyses
for Forensics Purposes

FP7 Theme 10: Security Call: FP7-SEC-2012-1

Work Programme: Topic SEC-2012.7.2-1. Open topic for Small and Medium
Enterprises: "Advancing contemporary forensic methods and equipment"

Report D5.9
Final version of software

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Approved by Work Package Manager of WP5:

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Table of Contents

Involved partners   01 HUJI, 03 CLCB, 04 ECL, 05 JHI

1. Objectives

This work encompasses T5.1.1-T5.1.8
The aim was to provide a total software solution including algorithmic functionality, user interface and documentation.

2. Significant results:

These tasks have been accomplished.

In the appendix, the material describing the software on QIAGEN Bioinformatics homepage (www.qiagenbioinformatics.com/MGM) is included.

CLC Microbial Genomics Module (MGM)

Explore the profile of microbial communities.

The expansion of NGS technology is accelerating in all directions with ever increasing variety of applications. In few application areas are samples and data more complex than when exploring the intricate world of microbial communities and their interplay with seemingly all aspects of life.

Now you can explore the composition of microbial communities and identify profiles that are indicative of patient health, changing yields of agricultural crops or livestock, or of the emergence of public health threats.

Supported Features:
The module extends the range of supported NGS applications with tools to study microbiome composition based on 16S rRNA- and other commonly used metagenome derived amplicon data.

- Microbiome Analysis via OTU-clustering of 16S rRNA or other amplicon data.
- OTU-clustering and taxonomic annotation using common reference databases such as Greengenes, Silva and UNITE.
- Stacked and area charts and zoomable sunburst diagrams to explore and compare the taxonomic composition of samples, or sample groups.
- A range of statistical tools, for instance to reveal differential abundance of OTUs, estimation of alpha- and beta diversities, or to carry out PERMANOVA analysis. Principal Coordinate Analysis (PCoA) results can be explored in 3D in the context of the sample metadata.
- Compatible also with T-RFLP data

The platform supports data from Illumina, 454, Ion Torrent and Sanger instruments.

- data from single read libraries
- paired read data strictly from libraries with overlapping paired reads.

Here are some additional MGM resources
to make the most of your trial.

the MGM please contact us

[The MGM plugin manual](#)
[The MGM quick guide](#)
[The MGM tutorial](#)

Last Name:

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Question:

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Sample to Insight

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