Soil microbe group abundances (DP1.10109.001)

Measurement

Semi-quantitative estimates of bacterial, archaeal and fungal abundance from soil samples.

Collection methodology

Samples are collected and sub-sampled in the field by horizon type (organic and mineral) to a maximum depth of 30 cm, and are frozen on dry ice in the field. After intermediate storage in ultra-low temperature freezers, they are shipped to an external laboratory which uses two targeted Quantitative Polymerase Chain Reaction (qPCR) analysis runs to produce the abundance estimates for: 1) bacteria and archaea, 2) fungi.

Samples are processed using established qPCR workflows that give estimates of abundance for each microbial group (bacteria/archaea and fungi). The exact qPCR primer sequences used may change over time as improved primers are developed.

For information about disturbances, land management activities, and other incidents that may impact data at NEON sites, see the Site management and event reporting (DP1.10111.001) data product.

Data package contents

mga_labSummary: Summary data on laboratory methods for qPCR results in soil samples
mga_soilLabSummary: Summary data on laboratory methods for qPCR results in soil samples
mga_batchResults: Batch-level results of analysis of gene copy number in soil samples
mga_soilBatchResults: Batch-level results of analysis of gene copy number in soil samples
mga_soilGroupAbundances: Laboratory results of gene copy number data in soil samples
variables: Description and units for each column of data in data tables
readme: Data product description, issue log, and other metadata about the data product
validation: Description of data validation applied at the points of collection and ingest

Data quality

As much as possible, soil microbe group abundance data follows the Minimum Information of Quantitative Real-Time PCR Experiments (MIQE) metadata and data quality assurance/quality control (QA/QC) guidelines. Batch-level quality control outcomes and long-term analytical standards and performance data can be found in the mga_batchResults and mga_labSummary tables, in the expanded data package.
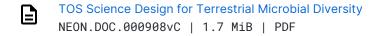
Table joining

Table 1	Table 2	Join by field(s)
mga_batchResults	mga_soilGroupAbundances	batchID
mga_soilGroupAbundances	sls_soilCoreCollection	geneticSampleID
mga_labSummary	Any other table	Join not recommended. Data resolution does not match other tables.

Documentation

NEON DNA Extraction Standard Operating Procedure v.7
BMI_dnaExtractionSOP_v7 | 242.2 KiB | PDF

TOS Science Design for Terrestrial Microbial Diversity
NEON.DOC.000908vC | 1.7 MiB | PDF

TOS Protocol and Procedure: SLS – Soil Biogeochemical and Microbial Sampling
NEON.DOC.014048vO | 3.6 MiB | PDF

NEON User Guide to Microbe Group Abundances (DP1.10109.001; DP1.20277.001; DP1.20278.001)
NEON_MGA_userGuide_vC | 497 KiB | PDF

For more information on data product documentation, see:
https://data.neonscience.org/data-products/DP1.10109.001

Citation

To cite data from Soil microbe group abundances (DP1.10109.001), see citation here:
https://data.neonscience.org/data-products/DP1.10109.001
For general guidance in citing NEON data and documentation, see the citation guidelines page:
https://www.neonscience.org/data-samples/guidelines-policies/citing