

Surface water microbe metagenome sequences (DP1.20281.001)

Measurement

Shotgun metagenomic DNA sequence data and sample processing metadata for surface water microbes.

Collection methodology

Samples are collected annually during the period of peak productivity. Between 1-3 samples are collected based on the habitat type and level of stratification of the water body. Water is filtered using aseptic methods and filters are frozen in the field on dry ice. Samples are transported and stored frozen. Samples are shipped on dry ice to an external facility for analysis.

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

mms_swMetagenomeSequencing: Surface water metagenomics sequencing metadata
mms_swRawDataFiles: Surface water metagenomics raw sequence data
mms_swMetagenomeDnaExtraction: Laboratory metadata from surface water DNA extraction for metagenomics sequencing
amc_fieldGenetic: Field data for the genetic sample of surface water microbes
amc_fieldSuperParent: Field data for the parent sample of surface water microbes
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

Sequence data are generated in batches of multiple samples, which are parsed into separate files on a per-sample basis. For bidirectional sequencing runs, 2 sequence files are created per sample, one for each sequencing read direction.

Samples must achieve a minimum number of sequences of sufficient quality in order to pass QAQC. Samples must also pass QAQC checks during the various processing steps. Samples that do not meet these QAQC criteria will be noted as "Fail" in the qaqcStatus fields in the respective data tables, or may include additional quality flags.

Table joining

| Table 1 | Table 2 | Join by field Table 1 | Join by field Table 2 |
|--------------------------------|--------------------------------|---|-----------------------|
| amc_fieldGenetic | mms_swMetagenome DnaExtraction | metagenomicSampleID | genomicsSampleID |
| mms_swMetagenome DnaExtraction | mms_swMetagenome Sequencing | dnaSampleID | dnaSampleID |
| mms_swMetagenome Sequencing | mms_metagenomeDnaExtraction | dnaSampleID | dnaSampleID |
| mms_swRawDataFiles | mms_swMetagenome DnaExtraction | dnaSampleID | dnaSampleID |
| mms_swRawDataFiles | mms_swMetagenome Sequencing | dnaSampleID | dnaSampleID |
| amc_fieldGenetic | amc_fieldSuperParent | parentSampleID | parentSampleID |
| amc_fieldGenetic | mms_swMetagenome Sequencing | Requires intermediate table: join via mms_swMetagenomeDnaExtraction table | |
| amc_fieldGenetic | mms_swRawDataFiles | Requires intermediate table: join via mms_swMetagenomeDnaExtraction table | |
| amc_fieldSuperParent | mms_swMetagenome DnaExtraction | Requires intermediate table: join via mms_fieldGenetic table | |
| amc_fieldSuperParent | mms_swMetagenome Sequencing | Requires intermediate table: join via mms_fieldGenetic and mms_swMetagenomeDnaExtraction tables | |

| Table 1 | Table 2 | Join by field Table 1 | Join by field Table 2 |
|----------------------|--------------------|---|-----------------------|
| amc_fieldSuperParent | mms_swRawDataFiles | Requires intermediate table: join via mms_fieldGenetic and mms_swMetagenomeDnaExtraction tables | |

Documentation



[NEON DNA Extraction Standard Operating Procedure v.7](#)

BMI_dnaExtractionSOP_v7 | 242.2 KiB | PDF



[NEON Aquatic Sampling Strategy](#)

NEON.DOC.0011152vB | 931.8 KiB | PDF



[AOS Protocol and Procedure: AMC – Aquatic Microbial Sampling](#)

NEON.DOC.003044vE | 1.6 MiB | PDF



[NEON User Guide for Surface Water Microbe Cell Count \(NEON.DP1.20138\)](#)

NEON_cellCount_userGuide_vC | 622.7 KiB | PDF



[NEON User Guide to Microbial Metagenome Sequences \(DP1.10107.001; DP1.20279.001; DP1.20281.001\)](#)

NEON_metagenomes_userGuide_vE | 1.2 MiB | PDF

For more information on data product documentation, see:

<https://data.neonscience.org/data-products/DP1.20281.001>

Citation

To cite data from Surface water microbe metagenome sequences (DP1.20281.001), see citation here:

<https://data.neonscience.org/data-products/DP1.20281.001>

For general guidance in citing NEON data and documentation, see the citation guidelines page:

<https://www.neonscience.org/data-samples/guidelines-policies/citing>