

Periphyton, seston, and phytoplankton collection (DP1.20166.001)

Measurement

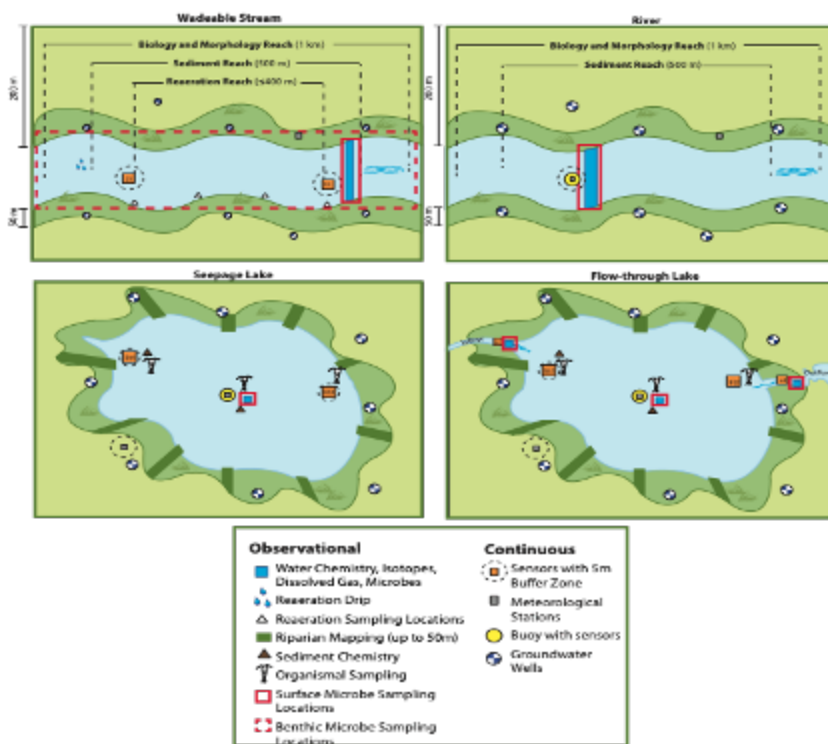
Identification, counts, and biomass of microalgae from benthic and water column collections per sample, per volume (cells L⁻¹ and ash-free dry mass g L⁻¹), and per benthic area (cells m⁻² and ash-free dry mass g m⁻²)

Collection methodology

Samples are collected at 24 wadeable stream sites, 7 lake sites, and 3 river sites. Samples are collected three times per year, roughly spring, summer, and fall. Benthic samples are collected by scrubbing substrata found in the dominant or subdominant habitat types and adding a known volume of rinsewater. Seston collection in wadeable streams is a simple grab in a 1L container. Phytoplankton are collected in lakes and rivers using a Kemmerer or Van Dorn sampler. Samples are subsampled, preserved, and sent to an external facility for identification.

Site type	Benthic samples	Water column
Stream	3 in subdominant habitat	1 near sensor set 2 for chlorophyll/AFDM only
Lake	5 in littoral zone	3 near buoy, inlet, and outlet sensors
River	5 in littoral zone	1 near buoy, 2 in river channel

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.



Spatial layout of sampling at streams, rivers, and lakes.

Data package contents

alg_taxonomyRaw: Periphyton, seston, and phytoplankton identifications by expert taxonomists - raw

alg_biomass: Periphyton, seston, and phytoplankton biomass data

alg_fieldData: Periphyton, seston, and phytoplankton field collection data from streams, lakes, and non-wadeable streams

alg_biovolumes: Biovolumes for algal taxonomy

alg_archive: Aquatic algae archived subsamples

alg_qualityCheck: Aquatic algae quality data

alg_taxonomyProcessed: Periphyton, seston, and phytoplankton identifications by expert taxonomists - desynonymized

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

10% of algal taxonomy samples are quality checked by the taxonomist, indicated in qcTaxonomyStatus. Percent similarity (PSc) must be >85% and percent difference in enumeration (PDE) <5% to pass the minimum quality objectives, else data are reconciled.

Standard calculations

For wrapper functions to download data from the API, and functions to merge tabular data files across sites and months, see the [neonUtilities R package](#).

The periphyton and phytoplankton taxonomic counts come from an external lab in the field `algalParameterValue`. This field should be coupled with `algalParameterUnit`.

The taxonomic count data with `algalParameterUnit = cellsPerBottle` are not corrected for preservative volume or benthic area. Data users will need to refer to the `benthicArea` presented in the `alg_fieldData` table and apply this correction to get the number of algal cells per stream, lake, or river bottom. All taxon records from a sample should be summed and divided by the `benthicArea` prior to reporting the total abundance per m².





NEON suggests using `algalParameter = 'cell density'` for the calculations above. See Data Product User Guide for specific equations and detailed descriptions of `algalParameters`.

Table joining

Table 1	Table 2	Join by field(s)
<code>alg_fieldData</code>	<code>alg_biomass</code>	<code>parentSampleID</code>
<code>alg_biomass</code>	<code>alg_taxonomyProcessed</code>	<code>sampleID</code>
<code>alg_biomass</code>	<code>alg_taxonomyRaw</code>	<code>sampleID</code>
<code>alg_fieldData</code>	<code>alg_taxonomyProcessed</code>	Requires intermediate table: join via <code>alg_biomass</code> table
<code>alg_fieldData</code>	<code>alg_taxonomyRaw</code>	Requires intermediate table: join via <code>alg_biomass</code> table
<code>alg_qualityCheck</code>	<code>alg_taxonomyProcessed</code>	<code>sampleID</code> , <code>algalAnalysisMethod</code>
<code>alg_qualityCheck</code>	<code>alg_taxonomyRaw</code>	<code>sampleID</code> , <code>algalAnalysisMethod</code>
<code>alg_taxonomyProcessed</code>	<code>alg_taxonomyRaw</code>	Join not recommended. These tables contain identifications of the same samples with possibly differing higher-order taxonomy; see User Guide.

Table 1	Table 2	Join by field(s)
alg_archive	Any other table	Join not recommended. This table is an account of subsamples shipped to the biorepository.
alg_biovolumes	Any other table	Join not recommended. Data resolution does not match other tables.

Documentation

-  [Standard Operating Procedures and Protocols for Algal Taxonomic Identification](#)
CU_algalTaxonomy_V2 | 1.3 MiB | PDF
-  [Soft Bodied Algae and Diatom Identification, Enumeration, and Processing Standard Operating Procedure](#)
EcoAnalysts_algalTaxonomy_V1 | 393.2 KiB | PDF
-  [AOS Protocol and Procedure: ALG – Periphyton and Phytoplankton Sampling](#)
NEON.DOC.003045vG | 3.2 MiB | PDF
-  [NEON User Guide to Periphyton and Phytoplankton Collection \(NEON.DP1.20166\)](#)
NEON_algalCollection_userGuide_vD | 595.4 KiB | PDF

For more information on data product documentation, see:
<https://data.neonscience.org/data-products/DP1.20166.001>

Citation

To cite data from Periphyton, seston, and phytoplankton collection (DP1.20166.001), see citation here:
<https://data.neonscience.org/data-products/DP1.20166.001>
For general guidance in citing NEON data and documentation, see the citation guidelines page:
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