Algae 1 pager draft

Tuesday, February 11, 2020   2:40 PM

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

What is measured?
Identification and counts of microalgae from benthic and water column collections per sample, per volume, and per benthic area
Biomass (ash-free dry mass in g/m2)

Collection methodology
Where: Samples are collected at 24 wadeable stream sites, 7 lake sites, and 3 river sites
When: Three times per year, roughly spring, summer, and fall
How: 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	5 in dominant habitat 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

What do I get?
- alg_fieldData - field parent data, also used in DP1.20163.001
- alg_biomass - biomass data calculated at the domain support facility; sample volume and preservative information for taxonomic samples sent to lab
- alg_taxonomyProcessed – processed taxonomy data, where taxonomic names are converted to synonyms via the NEON taxon table
- alg_taxonomyRaw – raw taxonomy data raw, where taxonomic names are returned directly from the taxonomist [expanded package]
- alg_archive - archive data table describing types of samples and identifiers sent to the biorepository [expanded package]
- alg_biovolumes – algal biovolume table per scientificName, deprecated and not updated after 2018 [expanded package]
- Variables (...variables...csv): Description and units for each column header
- Readme (...readme...csv): Data product description, file naming convention, change log, and more

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 Mminimum quality objectives, else data are reconciled.

Common data manipulation
Step 1: Convert to algal cells per L and correct for preservative volume when algalParameterUnit = countPerBottle (cells/L)
Step 2: Correct for benthicArea using calculation from Step 1 (cells/m2)

NEON suggests using algalParameter = 'cell density' for the calculations above. See DPUG for detailed descriptions of algalParameters.

samplingImpractical records in the fieldData table indicate instances where samples could not be collected due to environmental conditions.

Table joining instructions

Table 1	Table 2	Join by field
alg_fieldData	alg_biomass	parentSampleID
alg_biomass	alg_taxonomyProcessed or alg_taxonomyRaw	sampleID
alg_taxonomyProcessed or alg_taxonomyRaw	alg_biovolume	scientificName

Where can I find out more?

Document	Description
NEON.DOC.003045	Field sampling protocol
NEON_algalCollection_userGuide	Data Product User Guide
NEON.DOC.001152	Aquatic Sampling Design
NEON Biorepository at ASU [link]	Samples are deposited at the bioarchive after taxonomic analysis (permanent slides, preserved soft algae, freeze-dried diatoms)

How do I cite this data in my publications?
(citation will be autogenerated)