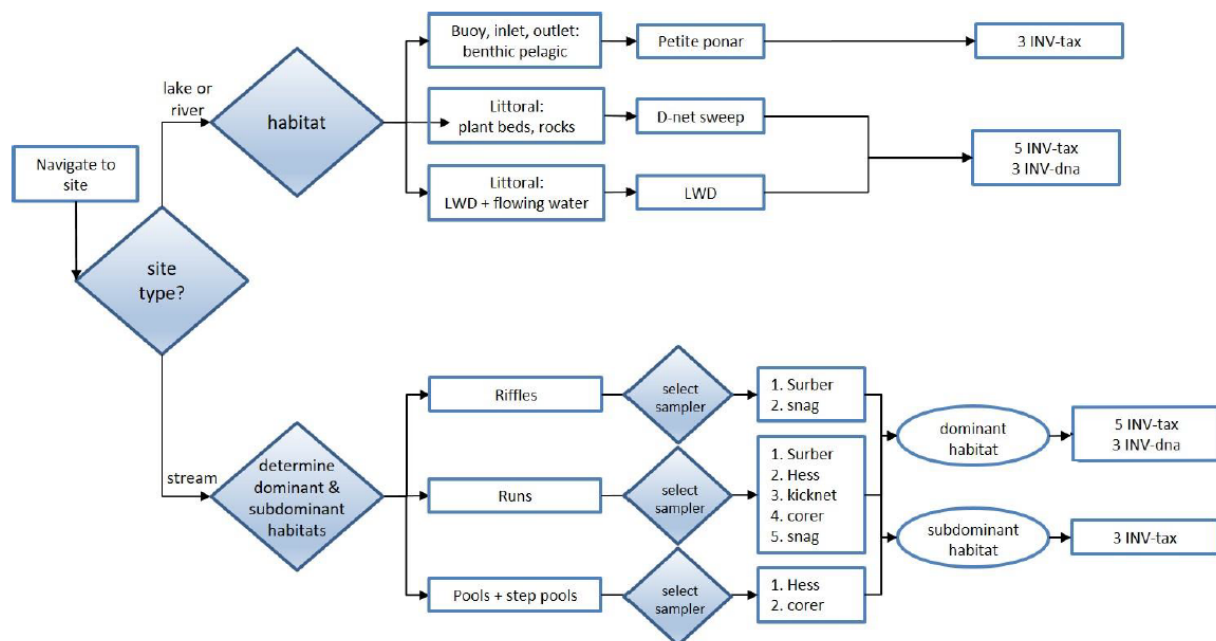# Macroinvertebrate collection (DP1.20120.001)

Measurement

Benthic macroinvertebrates in rivers, lakes and wadeable streams. This data product includes collection information and field metadata, as well as taxonomy and counts per taxon and per size class.

Collection methodology

Benthic macroinvertebrates are collected three times annually (roughly spring, summer and fall) at 24 wadeable stream sites, 7 lake sites and 3 river sites. Macroinvertebrate collection methods vary by site type, habitat types, and available substratum. All samples are collected from the surface of the natural substratum in each habitat using a quantitative sampling method. Macroinvertebrate samples are preserved with ethanol in the field and sent to a taxonomy lab for sorting, identification, and enumeration.

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.

Workflow for habitat and sampler selection for macroinvertebrate collection.

Data package contents

inv_persample: Aquatic macroinvertebrate habitat data and QC metrics per sample
inv_identificationHistory: Aquatic macroinvertebrate identification history for records where identifications have changed
inv_fieldData: Aquatic macroinvertebrate field data
inv_pervial: Aquatic macroinvertebrate identified archive data
inv_taxonomyProcessed: Aquatic macroinvertebrate identifications by expert taxonomists - desynonymized
inv_taxonomyRaw: Aquatic macroinvertebrate identifications by expert taxonomists - raw
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

Ten percent of all samples are quality checked for taxonomic difference and difference in enumeration between two taxonomists at the external facility. These records are indicated by the fields qcChecked, qcEnumerationDifference, and qcTaxonomicDifference, and data are corrected if necessary prior to return to NEON.

Please note that quality checks are comprehensive but not exhaustive; therefore, unknown data quality issues may exist. Users are advised to evaluate quality of the data as relevant to the scientific research question being addressed, perform data review and post-processing prior to analysis, and use the data quality information and issue logs included in download packages to aid interpretation.

Standard calculations

For wrapper functions to download data from the API, and functions to merge tabular data files across sites and months, NEON provides the neonUtilities package in R and the neonutilities package in Python. See the Download and Explore NEON Data tutorial for introductory instructions in both programming languages.

Standard calculations for benthic invertebrate data include standardizing the 'estimatedTotalCount' per sample, which takes subsampling into account, reported in the inv_taxonomyProcessed table to abundance per benthic area. To calculate quantitative results, divide by 'benthicArea' reported in the inv_fieldData table to get the number of organisms per square meter of 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. For biomass per m2, the estimated abundance calculated above can be used in conjunction with length/mass relationships in published literature.

Table joining

Table 1	Table 2	Join by field(s)
inv_fieldData	inv_persample	sampleID
inv_persample	inv_taxonomyRaw	sampleID
inv_persample	inv_taxonomyProcessed	sampleID
inv_fieldData	inv_taxonomyRaw	sampleID
inv_fieldData	inv_taxonomyProcessed	sampleID
inv_taxonomyRaw	inv_taxonomyProcessed	Join not recommended. If interested in processed NEON vs. raw lab taxonomy, join by sampleID + scientificName + sizeClass.
inv_fieldData	inv_pervial	sampleID
inv_persample	inv_pervial	sampleID
inv_taxonomyRaw	inv_pervial	Join not recommended. Data resolution does not match other tables.
inv_taxonomyProcessed	inv_pervial	Join not recommended. Data resolution does not match other tables.

Documentation

📄 EcoAnalysts Standard Operating Procedures Laboratory Analysis: NEON Benthic Macroinvertebrates Revision 6, 2024
ECOANALYSTS_Macroinvert_ID_Rev6 | 297.7 KiB | PDF

📄 NEON Aquatic Sampling Strategy
NEON.DOC.001152vD | 846.5 KiB | PDF

📄 AOS Protocol and Procedure: INV – Aquatic Macroinvertebrate Sampling
NEON.DOC.003046vG | 2.7 MiB | PDF

📄 NEON User Guide to Aquatic Macroinvertebrate Collection (NEON.DP1.20120)
NEON_macroinvertebrate_userGuide_vE | 574.1 KiB | PDF

📄 Rhithron Associates, Inc. Standard Operating Procedures: (NEON) Benthic Macroinvertebrate Indicator, rev 3
RHITHRON_Macroinvertebrate_ID_rev3 | 1.5 MiB | PDF

For more information on data product documentation, see:
https://data.neonscience.org/data-products/DP1.20120.001

Citation

To cite data from Macroinvertebrate collection (DP1.20120.001), see citation here:
https://data.neonscience.org/data-products/DP1.20120.001
For general guidance in citing NEON data and documentation, see the citation guidelines page:
https://www.neonscience.org/data-samples/guidelines-policies/citing

Contact Us

NEON welcomes discussion with data users! Reach out with any questions or concerns about NEON data:
Contact Us