A unified dataset of co-located sewage pollution, periphyton, and benthic macroinvertebrate community and food web structure from Lake Baikal (Siberia)

Overview

Authors

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Abstract

Sewage released from lakeside development can introduce nutrients and micropollutants that can restructure aquatic ecosystems. Lake Baikal, the world's most ancient, biodiverse, and voluminous lake, has been experiencing localized sewage pollution from lakeside settlements. Nearby increasing filamentous algal abundance suggests benthic communities are responding to this localized pollution. We surveyed 40-km of Lake Baikal's southwestern shoreline 19-23 August 2015 for sewage indicators, including pharmaceuticals, personal care products, and microplastics with co-located periphyton, macroinvertebrate, stable isotope, and fatty acid samplings. Unique identifiers corresponding to sampling locations are retained throughout all data files to facilitate interoperability among the dataset's 150+ variables. The data are structured in a tidy format (a tabular arrangement familiar to limnologists) to encourage reuse. For Lake Baikal studies, these data can support continued monitoring and research efforts. For global studies of lakes, these data can help characterize

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sewage prevalence and ecological consequences of anthropogenic disturbance across spatial scales.

The data product can be cited as:

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Directory information and structure

This main directory contains three subdirectories, each with their own version of the dataset.

- original_data: Raw, unaggregated data that may have misspellings, some taxa that were poorly preserved, and some misidentified taxa. These data are cleaned and aggregated by script <code>00_disaggregated_data_cleaning.R</code>.
- clean_disaggregated_data: Data are cleaned, standardized, and aggregated
 to the replicate-level. These are available on the Environmental Data
 Initiative (DOI) portal.
- 3. cleaned_data: Site-level aggregated data that have been cleaned and aggregated with script 01_data_cleaning.R.

Scripts and workflow

Scripts in this repository

Scripts that are central to the linear workflow of the dataset's build process are numbered consecutively.

- 1. <code>00_disaggregated_data_cleaning.R</code> : Aggregate datasets to replicate-level, remove poorly preserved or misidentified taxa, and correct spelling
 - Inputs: Disaggregated, replicate level raw CSVs
 - Outputs: Replicate-level CSVs for each type of data collected within a new directory
- 2. 01_data_cleaning.R: Aggregate datasets to site-level for analyses
 - Inputs: Disaggregated, replicate level CSVs and KML file derived from Google Earth project
 - Outputs: Site-level CSVs for each type of data collected within a new directory
- ${\tt 3. \ 02_sewage_indicator_analysis.R: Performs\ sewage\ indicator\ analyses}$
 - $\bullet \quad \text{Inputs: Site-level aggregated data from } \texttt{01_data_cleaning.R} \\$
 - Outputs: Individual and combined plots for each regression analysis.
- 4. 03_community_composition_analysis.R: Performs univariate and multivariate periphyton and benthic macroinvertebrate community composition analyses
 - Inputs: Site-level aggregated data from 01_data_cleaning.R
 - Outputs: Individual and combined univariate and multivariate plots
- 5. 04_fatty_acid_analysis.R: Performs univariate and multivariate analyses pertaining to primary producer and benthic macroinvertebrate fatty acid data
 - $\circ~$ Inputs: Site and species-level aggregated data from $\,$ 01_data_cleaning.R $\,$

- Outputs: CSV tables for particular fatty acid analyses as well as plots resulting from various univariate and multivariate analyses
- 6. 05_table_formatting.R: Aggregate metadata and sewage indicators for accompanying manuscripts
 - Inputs: Site-level aggregated data from 01_data_cleaning.R
 - Outputs: Metadata and sewage indicator tables for accompanying manuscripts
- 7. @6_map_making.R: Create map of study site based on metadata and inverse distance weighted population
 - Inputs: Site-level aggregated data from <code>01_data_cleaning.R</code>
 - Outputs: Map of study region
- 8. 07_stable_isotope_biplot.R: Make biplot based of stable isotope values
 - Inputs: Site-level aggregated data from 01 data cleaning.R
 - Outputs: Biplot of stable isotope data, aggregated by site and grouped IDW population values
- panel_cor_function.R: Sourced script that performs pairwise correlations between variables and calculates R² as well as p-values.

R session info:

The following R packages are essential to produce the dataset:

- tidyverse
- lubridate
- stringr
- janitor
- sf
- spdplyr

Detailed R session info is below:

```
- Session info -
 setting value
 version R version 3.6.2 (2019-12-12)
           Windows 10 x64
 os
 system x86_64, mingw32
 ui
              RStudio
 language (EN)
 collate English_United States.1252
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               America/Los_Angeles
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- Packages -----
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