www.planetmicrobe.org

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Toward the integration of oceanographic ‘omics, environmental and physiochemical data layers

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Context

Like a pirate's “buried treasure”, oceanographic data are incredibly valuable allowing us to deepen our knowledge of ocean systems at a higher spatiotemporal resolution. Unfortunately, such heterogeneous data are often separated upon collection and are rarely fully re-united. Despite careful curation, data are sometimes shared only with specific collaborators preventing complete dataset reassembly. Additionally, data are often used only to a address specific questions, limiting their reuse.

Currently, no unifying systematic framework exists for the integration of newer ‘omics data with traditional physical, geological, geochemical, and biological data sets commonly generated by the broader oceanographic community.

‘omics data → Public repositories (NCBI, EBI…)

Geochemical measures → Public repositories (BCO-DMO, Pangea…)

Study-specific measurements → Published papers

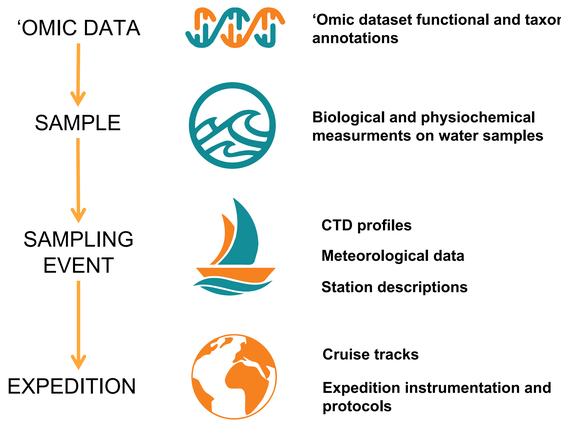
Here, we present here a new web-based cyberinfrastructure platform, **Planet Microbe**, tailored for the reintegration of marine ‘omics datasets with their environmental context.

Our aims

- Reintegration of ‘omics data with their environmental context
- Standardization of semantics for increased data interoperability
- Providing community driven analysis and visualizations tools

Reintegrating ‘omics data in their environmental context

Planet Microbe aims to re-unite taxonomic and functional microbial information from historic ‘omics datasets with their environmental context.



Environmental context can be provided by biological and physio-chemical measurements performed directly on a water sample. At a larger scale, environmental context can be provided by metadata from the sampling event and the sampling station.
Finally, cruise protocols and instrumentation can provide users with a better understanding of the metadata.

Historic datasets

We aim to integrate major historical oceanographic datasets for which abundant environmental metadata were collected.

BATS · TARA OCEANS · OSD (Ocean Sampling Day)

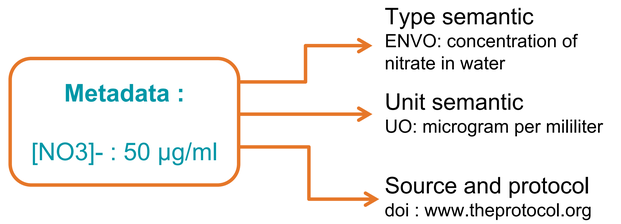
The project includes time-series such as HOT and BATS, as well as large-scale projects such as Tara oceans expeditions and OSD.

Metadata stored in public repositories like BCO-DMO, Rolling Deck repository, CCHDO, Pangea, … or published in research papers will be reintegrated with their respective publicly available ‘omics datasets.

Semantic standardization for data interoperability

Planet Microbe makes use of and extends standardized semantics provided by the Open Biological and Biomedical Ontology (OBO) Foundry and Library.

In order to ensure for well-represented, interoperable metadata **Planet Microbe** combines semantics from a variety of OBO Foundry ontologies including the Environment Ontology (ENVO) to represent metadata types, as well as the Ontology of Units (UO) to represent units.

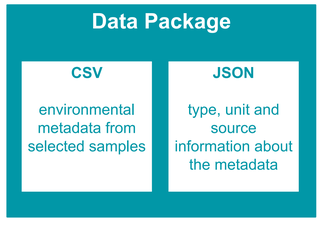


Additionally, a link to the metadata's source protocol is also provided, allowing users to access a detailed description of the instrumentation and protocol used to perform measurements and circumvent measurement bias and error.

Data containers for dataset interoperability

Planet Microbe makes use of frictionless data packages to make datasets interoperable, as well as shareable between systems.

A Data Package is a simple **container** format used to describe and package a dataset. The frictionless data format serves as a convenient wrapper by which to manage and share interoperable data.

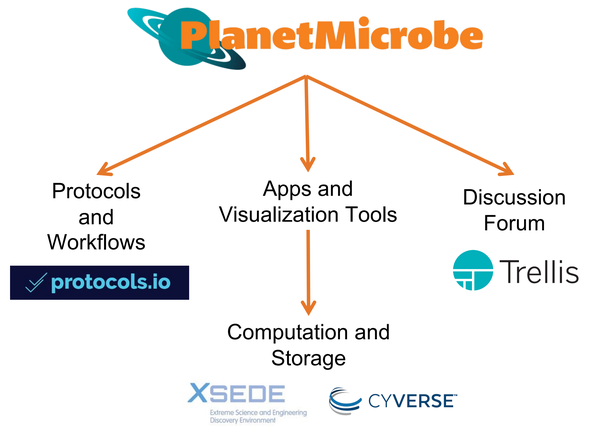


Data Packages can be used to package any tabular data by providing important additional descriptive information. Here, the Data Package allows for the association of each column in the csv metadata file to its OBO type and unit semantics, as well as source description.

Community-driven tools and visualizations

Planet Microbe is not an isolated data platform but operates in a larger cyberinfrastructure system which provide users with the capability to analyze and visualize datasets.

Links to protocol.io and Trellis provides the community with means to share and discuss protocols and workflows.



Planet Microbe provides users with a set of tools and apps for metagenomic analysis and visualization. Compute time and storage is available freely for **Planet Microbe** users through CyVerse and XSEDE resources.

Tool containers for reproducibility

Apps and tools deployed in Planet microbe rely on community-developed docker/singularity containers.

Containers ensure the reproducibility of tools and analytical results in **Planet Microbe** by preserving the code, configurations, and dependencies.

Project timeline

SPRING 2019	SUMMER 2019	FALL 2019
Search interface	Data visualization	Integration of C-DEBI
Integration of HOT, Tara and OSD	Data integration of BATS	Functional/taxonomic annotation
Planet Microbe Ontology	Standard tools	Community tools
Prototype	Beta - release	Release

Future directions

- **Integration of continuous data**
- **Machine Learning approaches for data quality checking and data pattern discovery**

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