Contribution ID: **2** Type: **Talk**

HARMONise –Enhancing the interoperability of marine biomolecular (meta)data across Helmholtz Centres

Wednesday 11 October 2023 10:50 (20 minutes)

Biomolecules, such as DNA and RNA, provide a wealth of information about the distribution and function of marine organisms, and biomolecular research in the marine realm is pursued across several Helmholtz Centers. Biomolecular metadata, i.e. DNA and RNA sequences and all steps involved in their creation, exhibit great internal diversity and complexity. However, high-quality (meta)data management is not yet well developed and harmonized in environmentally focused Helmholtz Centers. As part of the HMC Project HARMONise, we develop sustainable solutions and digital cultures to enable high-quality, standards-compliant curation and management of marine biomolecular metadata at AWI and GEOMAR to better embed biomolecular science into broader digital ecosystems and research domains. Our approach builds on a relational database that aligns metadata with community standards such as the MIxS (Minimum Information about any (x) sequence) supported by the International Nucleotide Sequence Database Collaboration (INSDC) to promote global interoperability. At the same time, we ensure the harmonization of metadata with existing Helmholtz repositories (e.g. PANGAEA). A web-based hub will enable the standardized export and exchange of core metadata. Alignment with domain-specific standards and relevant data exchange formats (e.g. UNESCO ODIS-Arch specifications) supports connectivity to the Helmholtz knowledge graph as well as global interoperability. Here we will highlight the use of standards and fields in the database scheme that promote interoperability, outline the establishment of a web-based exchange hub for sharing and validating biomolecular metadata across Helmholtz Centers, and present links with high-level international programs such as the Ocean Biomolecular Observing Network (OBON) of the UN Decade of Ocean Science. Enabling sustainable data stewardship, export and publication routines will support researchers in delivering Helmholtz biomolecular data to national European and global repositories in alignment with community standards and the FAIR principles.

Please assign your contribution to one of the following topics

Data interoperability through harmonised metadata and interoperable semantics

Please specify ”other” (stakeholder)

In addition please add keywords.

sequence data management, interoperability, metadata harmonization, FAIR principles

Please assign yourself (presenting author) to one of the stakeholders.

Scientists and technicians who maintain and operate research infrastructure for data generation

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