

Standardizing-Marine-Biological-Data

Standardizing Marine Biological Data Working Group

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Preface

Biological data structures, definitions, measurements, and linkages are necessarily as diverse as the systems they represent. This presents a real challenge when integrating data across biological research domains such as ecology, oceanography, fisheries, and climate sciences.

Chapter 1

Introduction

The world of standardizing marine biological data can seem complex for the naive oceanographer, biologist, scientist, or programmer. Transforming and integrating data is about combining the right standards for your desired interoperability with other data types. For example, interoperating fish biology measurements with climate level variables. There are a few concepts necessary to make this possible such as standard data structures, controlled vocabularies and knowledge representations, along with metadata standards to facilitate data discovery. This will permit the inclusion of more data and broader access to better ecosystem based models. Many scientific domains data handling practices are currently being reshaped in light of recent advances in computing power, technology, and data science.

1.1 Data Structures

The OBIS-ENV Darwin Core Archive Data Structure.

OBIS manual

1.2 Ontologies

An ontology is a classification system for establishing a hierarchically related set of concepts. Concepts are often terms from controlled vocabularies.

From Marine Metadata: # TODO: add link

“Ontologies can include all of the following, but are not required to include them, depending on which perspective from above you adhere to:

Classes (general things, types of things) Instances (individual things) Relationships among things Properties of things Functions, processes, constraints, and rules relating to things”

TODO: Research Unified Modelling Language?

Environment Ontology (EnvO) EnvO is a community ontology for the concise, controlled description of environments.

1.3 Controlled Vocabularies

There are a number of controlled vocabularies that are used to describe parameters commonly used in specific research domains. This allows for greater interoperability of data sets within the domain, and ideally between domains. Here, we strive to document a number of relevant examples.

- Climate and Format (CF) Standard Names The purpose of the `standard_name` attribute is to provide a succinct and distinguishing description of a variable, in a way that encourages interoperability. These terms are typically for physical observations, however, there have been advancements in aligning biological taxa into the CF standard names (see here).
- NERC Vocabulary Server The NVS gives access to standardised and hierarchically-organized vocabularies.
 - Device categories using the SeaDataNet device categories
 - Device make/model using the SeaVoX Device Catalogue
 - Platform categories using SeaVoX Platform Categories
 - Platform instances using the ICES Platform Codes
 - Unit of measure
- GCMD Keywords (NASA)
- Geographic Domain/Features of Interest
- GeoLink base ontology was part of the EarthCube GeoLink Project

Note: To describe a measurement or fact of a biological specimen that conforms to Darwin Core standards, it’s necessary to use the ‘Biological entity described elsewhere’ method rather than taxon specific.

1.3.1 Taxonomy

- The World Registry of Marine Species (WoRMS) The aim of a World Register of Marine Species (WoRMS) is to provide an authoritative and comprehensive list of names of marine organisms, including information on synonymy. While the highest priority goes to valid names, other names in use are included so that this register can serve as a guide to interpret taxonomic literature.

1.3.2 Resources

1.3.3 Oceanography

Biological and Chemical Oceanography Data Management Office

Marine metadata interoperability vocab resources

1.3.4 Biology

BioPortal Ecosystem Ontology

1.3.5 NERC Search Interfaces

- SeaDataNet Common Vocab Search Interface:
- SeaDataNet Common Vocabularies:
- SeaDataNet Vocab Library
- Measurement Types in OBIS

1.3.6 Geosciences

UDUNITS are more common unit measurements in geosciences

1.3.7 Eco/EnvO

Environment Ontology including genomics.

1.3.8 Wild Cards

Question: Not sure use case for this.

P01 Biological Entity Parameter Code Builder

1.4 Technologies

1.4.1 ERDDAP

ERDDAP can be thought of as a data server. It provides ‘easier access to scientific data’ by providing a consistent interface that aggregates many disparate data sources. It does this by providing translation services between many common file types for gridded arrays (‘net CDF’ files) and tabular data (spreadsheets). Data access is also made easier because it unifies different types of data servers and access protocols. Here is a basic erddap installation that walks you through how to load a data set.

1.5 Notes on Integrating OBIS, Darwin Core as it relates to OOS’s

1.6 Metadata

OBIS uses the GBIF EML profile (version 1.1). In case data providers use ISO19115/ISO19139, there is a mapping available here: <http://rs.gbif.org/schema/eml-gbif-profile/1.1/eml2iso19139.xsl> This will be important for integrating OBIS datasets to other CIOOS and IOOS metadata profiles.

1.7 Data QC

There are a number of tools available to check the quality of data or check your data format against the expected standard.

OBIS Datatools shows some great R packages for this.

1.7.1 Compliance Checking

LifeWatch Belgium provides a number of tools to check your data against. Specifically you can test OBIS data format and see a map of your sample locations to check if they are on land. See <http://www.lifewatch.be/data-services/>

There’s also the GBIF data validator which allows anyone with a GBIF-relevant dataset to receive a report on the syntactical correctness and the validity of the content contained within the dataset.

1.7.2 Semantic Web and Darwin Core

Lessons learned from adapting the Darwin Core vocabulary standard for use in RDF

1.7.3 Resource Description Framework

Darwin Core Resource Description Framework Guide

Chapter 2

Applications

Some *significant* applications are demonstrated in this chapter.

2.1 Salmon Ocean Ecology Data

2.1.1 Intro

One of the goals of the Hakai Institute and the Canadian Integrated Ocean Observing System (CIOOS) is to facilitate Open Science and FAIR (findable, accessible, interoperable, reusable) ecological and oceanographic data. In a concerted effort to adopt or establish how best to do that, several Hakai and CIOOS staff attended an International Ocean Observing System (IOOS) Code Sprint in Ann Arbor, Michigan between October 7–11, 2019, to discuss how to implement FAIR data principles for biological data collected in the marine environment.

The Darwin Core is a highly structured data format that standardizes data table relations, vocabularies, and defines field names. The Darwin Core defines three table types: **event**, **occurrence**, and **measurementOrFact**. This intuitively captures the way most ecologists conduct their research. Typically, a survey (event) is conducted and measurements, counts, or observations (collectively measurementOrFacts) are made regarding a specific habitat or species (occurrence).

In the following script I demonstrate how I go about converting a subset of the data collected from the Hakai Institute Juvenile Salmon Program and discuss challenges, solutions, pros and cons, and when and what’s worthwhile to convert to Darwin Core.

The conversion of a dataset to Darwin Core is much easier if your data are already tidy (normalized) in which you represent your data in separate tables

that reflect the hierarchical and related nature of your observations. If your data are not already in a consistent and structured format, the conversion would likely be very arduous and not intuitive.

2.1.2 event

The first step is to consider what you will define as an event in your data set. I defined the capture of fish using a purse seine net as the **event**. Therefore, each row in the **event** table is one deployment of a seine net and is assigned a unique **eventID**.

My process for conversion was to make a new table called **event** and map the standard Darwin Core column names to pre-existing columns that serve the same purpose in my original **seine_data** table and populate the other required fields.

#TODO: Include abiotic measurements (YSI temp and salinity from 0 and 1 m) to hang off

```
event <- tibble(datasetName = "Hakai Institute Juvenile Salmon Program",
  eventID = survey_seines$seine_id,
  eventDate = date(survey_seines$survey_date),
  eventTime = paste0(survey_seines$set_time, "-0700"),
  eventRemarks = paste3(survey_seines$survey_comments, survey_seines$seine_id),
  decimalLatitude = survey_seines$lat,
  decimalLongitude = survey_seines$long,
  locationID = survey_seines$site_id,
  coordinatePrecision = 0.00001,
  coordinateUncertaintyInMeters = 10,
  country = "Canada",
  countryCode = "CA",
  stateProvince = "British Columbia",
  habitat = "Nearshore marine",
  geodeticDatum = "EPSG:4326 WGS84",
  minimumDepthInMeters = 0,
  maximumDepthInMeters = 9, # seine depth is 9 m
  samplingProtocol = "http://dx.doi.org/10.21966/1.566666", # This is the protocol used
  language = "en",
  license = "http://creativecommons.org/licenses/by/4.0/legalcode",
  bibliographicCitation = "Johnson, B.T., J.C.L. Gan, S.C. Godwin, M. Krueger",
  references = "https://github.com/HakaiInstitute/jsp-data",
  institutionID = "https://www.gbif.org/publisher/55897143-3f69-42f1-810a-4b8b8b8b8b8b",
  institutionCode = "Hakai"
)
```

2.1.3 occurrence

Next you'll want to determine what constitutes an occurrence for your data set. Because each event captures fish, I consider each fish to be an occurrence. Therefore, the unit of observation (each row) in the occurrence table is a fish. To link each occurrence to an event you need to include the `eventID` column for every occurrence so that you know what seine (event) each fish (occurrence) came from. You must also provide a globally unique identifier for each occurrence. I already have a locally unique identifier for each fish in the original `fish_data` table called `ufn`. To make it globally unique I pre-pend the organization and research program metadata to the `ufn` column.

Not every fish is actually collected and given a Universal Fish Number (UFN) in our fish data tables, so in our field data sheets we record the total number of fish captured and the total number retained. So to get an occurrence row for every fish captured I create a row for every fish caught (minus the number taken) and create a generic numeric id (ie hakai-jsp-1) in one table and then join that to the fish table that includes a row for every fish retained that already has a UFN.

```
## make table long first
seines_total_long <- survey_seines %>%
  select(seine_id, so_total, pi_total, cu_total, co_total, he_total, ck_total) %>%
  pivot_longer(-seine_id, names_to = "scientificName", values_to = "n")

seines_total_long$scientificName <- recode(seines_total_long$scientificName, so_total = "Oncorhynchus")

seines_taken_long <- survey_seines %>%
  select(seine_id, so_taken, pi_taken, cu_taken, co_taken, he_taken, ck_taken) %>%
  pivot_longer(-seine_id, names_to = "scientificName", values_to = "n_taken")

seines_taken_long$scientificName <- recode(seines_taken_long$scientificName, so_taken = "Oncorhynchus")

## remove records that have already been assigned an ID because they were actually retained
seines_long <- full_join(seines_total_long, seines_taken_long, by = c("seine_id", "scientificName"))
seines_long <- drop_na() %>%
  mutate(n_not_taken = n - n_taken) %>% #so_total includes the number taken so I subtract n_taken
  select(-n_taken, -n) %>%
  filter(n_not_taken > 0)

all_fish_not_retained <-
  seines_long[rep(seq.int(1, nrow(seines_long)), seines_long$n_not_taken), 1:3] %>%
  select(-n_not_taken) %>%
  mutate(prefix = "hakai-jsp-",
         suffix = 1:nrow(.),
         occurrenceID = paste0(prefix, suffix))
```

```

) %>%
  select(-prefix, -suffix)

#

# Change species names to full Scientific names
latin <- fct_recode(fish_data$species, "Oncorhynchus nerka" = "SO", "Oncorhynchus gorbuscha" = "GO",
  as.character())

fish_retained_data <- fish_data %>%
  mutate(scientificName = latin) %>%
  select(-species) %>%
  mutate(prefix = "hakai-jsp-",
    occurrenceID = paste0(prefix, ufn)) %>%
  select(seine_id, scientificName, occurrenceID)

occurrence <- bind_rows(all_fish_not_retained, fish_retained_data) %>%
  rename(eventID = seine_id) %>% # rename = dplyr::rename; vs plyr::rename
  mutate(`Life stage` = "juvenile")

unique_taxa <- unique(occurrence$scientificName)
worms_names <- wm_records_names(unique_taxa) # library(worms)
df_worms_names <- bind_rows(worms_names) %>%
  select(scientificName = scientificname,
    scientificNameAuthorship = authority,
    taxonRank = rank,
    scientificNameID = lsid
  )

#include bycatch species

unique_bycatch <- unique(bycatch$scientificName) %>% glimpse()

## chr [1:29] "Oncorhynchus nerka" "Oncorhynchus tshawytscha" ...

by_worms_names <- wm_records_names(unique_bycatch) %>%
  bind_rows() %>%
  select(scientificName = scientificname,
    scientificNameAuthorship = authority,
    taxonRank = rank,
    scientificNameID = lsid
  )

bycatch_occurrence <- bycatch %>%
  select(eventID = seine_id, occurrenceID, scientificName, `Life stage` = bm_ageclass)

```



```

  filter(scientificName != "unknown")

  bycatch_occurrence$`Life stage`[bycatch_occurrence$`Life stage` == "J"] <- "juvenile"
  bycatch_occurrence$`Life stage`[bycatch_occurrence$`Life stage` == "A"] <- "adult"
  bycatch_occurrence$`Life stage`[bycatch_occurrence$`Life stage` == "Y"] <- "Young of year"

  combined_worms_names <- bind_rows(by_worms_names, df_worms_names) %>%
    distinct(scientificName, .keep_all = TRUE)

  occurrence <- bind_rows(bycatch_occurrence, occurrence)

  occurrence <- left_join(occurrence, combined_worms_names) %>%
    mutate(basisOfRecord = "HumanObservation",
           occurrenceStatus = "present")

  write_csv(occurrence, "../datasets/hakai_salmon_data/raw_data/occurrence.csv") # here::here("../",

# This removes events that didn't result in any occurrences
  event <- dplyr::semi_join(event, occurrence, by = 'eventID') %>%
    mutate(coordinateUncertaintyInMeters = ifelse(is.na(decimalLatitude), 1852, coordinateUncertaintyInMeters))

  simple_sites <- sites %>%
    select(site_id, ocgy_std_lat, ocgy_std_lon)

  event <- dplyr::left_join(event, simple_sites, by = c("locationID" = "site_id")) %>%
    mutate(decimalLatitude = coalesce(decimalLatitude, ocgy_std_lat),
           decimalLongitude = coalesce(decimalLongitude, ocgy_std_lon)) %>%
    select(-c(ocgy_std_lat, ocgy_std_lon))

  write_csv(event, "../datasets/hakai_salmon_data/raw_data/event.csv") # here::here("../", "datasets/

```

2.1.4 measurementOrFact

To convert all your measurements or facts from your normal format to Darwin Core you essentially need to put all your measurements into one column called `measurementType` and a corresponding column called `MeasurementValue`. This standardizes the column names are in the `measurementOrFact` table. There are a number of predefined `measurementTypes` listed on the NERC database that should be used where possible. I found it difficult to navigate this page to find the correct `measurementType`.

Here I convert length, and weight measurements that relate to an event and an occurrence and call those `measurementTypes` as `length` and `weight`.

```

mof_types <- read_csv("https://raw.githubusercontent.com/HakaiInstitute/jsp-data/master/

fish_data$weight <- coalesce(fish_data$weight, fish_data$weight_field)
fish_data$fork_length <- coalesce(fish_data$fork_length, fish_data$fork_length_field)
fish_data$`Life stage` <- "juvenile"

measurementOrFact <- fish_data %>%
  mutate(occurrenceID = paste0("hakai-jsp-", ufn)) %>%
  select(occurrenceID, eventID = seine_id, "Length (fork length)" = fork_length,
        "Standard length" = standard_length, "Weight" = weight, `Life stage`) %>%
  pivot_longer(`Length (fork length)`:`Life stage`,
               names_to = "measurementType",
               values_to = "measurementValue",
               values_transform = list(measurementValue = as.character)) %>%
  filter(measurementValue != "NA") %>%
  left_join(mof_types, by = c("measurementType")) %>%
  mutate(measurementValueID = case_when(measurementValue == "juvenile" ~ "http://vocab
        measurementID = paste(eventID, measurementType, occurrenceID, sep = "-"))

write_csv(measurementOrFact, "../datasets/hakai_salmon_data/raw_data/extendedMeasurement

#Check that every eventID in Occurrence occurs in event table
no_keys <- dm(event, occurrence, measurementOrFact)
only_pk <- no_keys %>%
  dm_add_pk(event, eventID) %>%
  dm_add_pk(occurrence, occurrenceID) %>%
  dm_add_pk(measurementOrFact, measurementID)
dm_examine_constraints(only_pk)

model <- only_pk %>%
  dm_add_fk(occurrence, eventID, event) %>%
  dm_add_fk(measurementOrFact, occurrenceID, occurrence)
dm_examine_constraints(model)

#TODO: Fix bookdown issues so that dm_draw shows data model html output. Perhaps add
# dm_draw(model, view_type = "all")

```

2.2 Example Two

Add another example here, perhaps zooplankton?

Chapter 3

Final Words

We have finished a nice book.

Chapter 4

Tools

Below are some of the tools and packages used in workflows.

4.1 R

Package	Description
robis	R client for the OBIS API
iobis/obistools	Tools for data enhancement and quality control.
worms	Client for World Register of Marine Species. Includes functions for each of the API methods, including searching for names by name, date and common names, searching using external identifiers, fetching synonyms, as well as fetching taxonomic children and taxonomic classification.
tidyverse	The ‘tidyverse’ is a set of packages that work in harmony because they share common data representations and ‘API’ design. This package is designed to make it easy to install and load multiple ‘tidyverse’ packages in a single step.
lubridate	Functions to work with date-times and time-spans: fast and user friendly parsing of date-time data, extraction and updating of components of a date-time (years, months, days, hours, minutes, and seconds), algebraic manipulation on date-time and time-span objects.
stringr	Simple, Consistent Wrappers for Common String Operations

Package	Description
ecocomDP	Work with the Ecological Community Data Design Pattern. ‘ecocomDP’ is a flexible data model for harmonizing ecological community surveys, in a research question agnostic format, from source data published across repositories, and with methods that keep the derived data up-to-date as the underlying sources change.
finch	Parse Darwin Core Files
taxize	Interacts with a suite of web ‘APIs’ for taxonomic tasks, such as getting database specific taxonomic identifiers, verifying species names, getting taxonomic hierarchies, fetching downstream and upstream taxonomic names, getting taxonomic synonyms, converting scientific to common names and vice versa, and more.
Hmisc	Contains many functions useful for data analysis, high-level graphics, utility operations, functions for computing sample size and power, simulation, importing and annotating datasets, imputing missing values, advanced table making, variable clustering, character string manipulation, conversion of R objects to LaTeX and html code, and recoding variables. Particularly check out the describe() function.
uuid	Tools for generating and handling of UUIDs (Universally Unique Identifiers).
ropensci/EML	Provides support for the serializing and parsing of all low-level EML concepts
EDIorg/EMLasseblyline	For scientists and data managers to create high quality EML metadata for dataset publication.
bdveRse	A family of R packages for biodiversity data.

4.2 Python

Package	Description
pandas	pandas is a fast, powerful, flexible and easy to use open source data analysis and manipulation tool, built on top of the Python programming language. Super helpful when manipulating tabular data!

Package	Description
numpy	NumPy (Numerical Python) is an open source Python library that's used in almost every field of science and engineering. It's the universal standard for working with numerical data in Python, and it's at the core of the scientific Python and PyData ecosystems.
pyworms	Python client for the World Register of Marine Species (WoRMS) REST service.
uuid	This module provides immutable UUID objects (class UUID) and the functions uuid1(), uuid3(), uuid4(), uuid5() for generating version 1, 3, 4, and 5 UUIDs as specified in RFC 4122.
python-dwca-reader	A simple Python package to read and parse Darwin Core Archive (DwC-A) files, as produced by the GBIF website, the IPT and many other biodiversity informatics tools.
metatype	A lightweight Python 3 library for generating EML metadata

4.3 Google Sheets

Package	Description
Google Sheet DarwinCore Archive Assistant add-on	Google Sheet add-on which assists the creation of Darwin Core Archives (DwCA) and publishing to Zenodo. DwCA's are stored into user's Google Drive and can be downloaded for upload into IPT installations or other software which is able to read DwC-archives.

4.4 Validators

Name	Description
Darwin Core Archive Validator	This validator verifies the structural integrity of a Darwin Core Archive. It does not check the data values, such as coordinates, dates or scientific names.

Name	Description
GBIF DATA VALIDATOR	The GBIF data validator is a service that allows anyone with a GBIF-relevant dataset to receive a report on the syntactical correctness and the validity of the content contained within the dataset.
LifeWatch Belgium	Through this interactive section of the LifeWatch.be portal users can upload their own data using a standard data format, and choose from several web services, models and applications to process the data.

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