

BioDataGuide

Darwin Core Marine Example Compendium

Standardizing Marine Biological Data Working Group

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Preface

This book contains a collection of examples and resources related to mobilizing marine biological data to the [Darwin Core standard](#) for sharing through [OBIS](#). This book has been developed by the Standardizing Marine Biological Data Working Group (SMBD). The working group is an open community of practitioners, experts, and scientists looking to learn and educate the community on standardizing and sharing marine biological data.

If you would like to join the SMBD or learn more, checkout this [README](#).

1 Introduction

The world of standardizing marine biological data can seem complex for the naive oceanographer, biologist, scientist, or programmer. This book intends to ease the burden of learning about the [Darwin Core standard](#) by compiling a list of example applications and tools for translating source data into Darwin Core. This collection of resources does not replace the Darwin Core standards documentation (<https://dwc.tdwg.org/>) or the OBIS Manual (<https://manual.obis.org/>), but instead it supplements those resources with examples of real world applications.

In this book we cover:

- [Applications](#) - These are the real world examples of aligning data to Darwin Core.
- [Frequently Asked Questions](#) - A collection of Frequently Asked Questions.
- [Tools](#) - A collection of useful tools, packages, and programs for working with marine biological data.
- [Extras](#) - Some useful extra tidbits about metadata and using GitHub to debug data issues.

If you would like to learn more about standardizing biological data (not only marine), the [Earth Science Information Partners \(ESIP\) Biological Data Standards Cluster](#) developed [this primer](#) for managers of biological data to provide a quick, easy resource for navigating a selection of the standards that exist. The goal of the primer is to spread awareness about existing standards and is intended to be shared online and at conferences to increase the adoption of standards for biological data and make them [FAIR](#).

Part I

Applications

This chapter contains a series of example applications to convert source data to the Darwin Core standard. You can find these examples (and more!) in the GitHub repository under the [datasets/](#) directory.

2 Aligning Data to Darwin Core - Event Core with Extended Measurement or Fact

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January 9, 2022

2.0.1 General information about this notebook

Script to process the Texas Parks and Wildlife Department (TPWD) Aransas Bay bag seine data from the format used by the Houston Advanced Research Center (HARC) for bays in Texas. Taxonomy was processed using a separate script ([TPWD_Taxonomy.R](#)) using a taxa list pulled from the pdf “[2009 Resource Monitoring Operations Manual](#)”. All original data, processed data and scripts are stored on [an item](#) in USGS ScienceBase.

```
# Load some of the libraries
library(reshape2)
library(tidyverse)
library(readr)
```

```
# Load the data
BagSeine <- read.csv("https://www.sciencebase.gov/catalog/file/get/53a887f4e4b075096c60cfdd?")
```

Note that if not already done you’ll need to run the [TPWD_Taxonomy.R](#) script to get the taxaList file squared away or load the taxonomy file to the World Register of Marine Species Taxon Match Tool <https://www.marinespecies.org/aphia.php?p=match>

2.0.2 Event file

To start we will create the Darwin Core **Event** file. This is the file that will have all the information about the sampling event such as date, location, depth, sampling protocol. Basically anything about the cruise or the way the sampling was done will go in this file. You can see all the Darwin Core terms that are part of the event file here <http://tools.gbif.org/dwca-validator/extension.do?id=dbc:Event>.

The original format for these TPWD HARC files has all of the information associated as the event in the first approximately 50 columns and then all of the information about the occurrence (species) as columns for each species. We will need to start by limiting to the event information only.

```
event <- BagSeine[,1:47]
```

Next there are several pieces of information that need 1) to be added like the geodeticDatum 2) to be pieced together from multiple columns like datasetID or 3) minor changes like the minimum and maximum depth.

```
event <- event %>%
  mutate(type = "Event",
         modified = lubridate::today(),
         language = "en",
         license = "http://creativecommons.org/publicdomain/zero/1.0/legalcode",
         institutionCode = "TPWD",
         ownerInstitutionCode = "HARC",
         coordinateUncertaintyInMeters = "100",
         geodeticDatum = "WGS84",
         georeferenceProtocol = "Handheld GPS",
         country = "United States",
         countryCode = "US",
         stateProvince = "Texas",
         datasetID = gsub(" ", "_", paste("TPWD_HARC_Texas", event$Bay, event$Gear_Type)),
         eventID = paste("Station", event$station_code, "Date", event$completion_dttm, sep =
         sampleSizeUnit = "hectares",
         CompDate = lubridate::mdy_hms(event$CompDate, tz="America/Chicago"),
         StartDate = lubridate::mdy_hms(event$StartDate, tz="America/Chicago"),
         minimumDepthInMeters = ifelse(start_shallow_water_depth_num < start_deep_water_depth_num,
                                         start_shallow_water_depth_num, start_deep_water_depth_num),
         maximumDepthInMeters = ifelse(start_deep_water_depth_num > start_shallow_water_depth_num,
                                         start_deep_water_depth_num, start_shallow_water_depth_num))
```

```
head(event[,48:64], n = 10)
```

	type	modified	language	license	inst.
1	Event	2022-01-09	en	http://creativecommons.org/publicdomain/zero/1.0/legalcode	
2	Event	2022-01-09	en	http://creativecommons.org/publicdomain/zero/1.0/legalcode	
3	Event	2022-01-09	en	http://creativecommons.org/publicdomain/zero/1.0/legalcode	
4	Event	2022-01-09	en	http://creativecommons.org/publicdomain/zero/1.0/legalcode	
5	Event	2022-01-09	en	http://creativecommons.org/publicdomain/zero/1.0/legalcode	
6	Event	2022-01-09	en	http://creativecommons.org/publicdomain/zero/1.0/legalcode	


```
## Calculate duration of bag seine event
event$samplingEffort <- ""
for (i in 1:nrow(event)){
  event[i,]$samplingEffort <- abs(lubridate::as.duration(event[i,]$CompDate - event[i,]$StartDate))
}
event$samplingEffort <- paste(event$samplingEffort, "seconds", sep = " ")
```

Finally there were a few columns that were a direct match to a Darwin Core term and therefore just need to be renamed to follow the standard.

```
event <- event %>%
  rename(samplingProtocol = Gear_Type,
         locality = Estuary,
         waterBody = SubBay,
         decimalLatitude = Latitude,
         decimalLongitude = Longitude,
         sampleSizeValue = surface_area_num,
         eventDate = CompDate)
```

2.0.3 Occurrence file

The next file we need to create is the **Occurrence** file. This file includes all the information about the species that were observed. An occurrence in Darwin Core is the intersection of an organism at a time and a place. We have already done the work to identify the time and place in the event file so we don't need to do that again here. What we do need to is identify all the information about the organisms. Another piece of information that goes in here is `basisOfRecord` which is a required field and has a controlled vocabulary. For the data we work with you'll usually put `HumanObservation` or `MachineObservation`. If it's eDNA data you'll use `MaterialSample`. If your data are part of a museum collection you'll use `PreservedSpecimen`.

Important to note that there is overlap in the Darwin Core terms that “allowed” to be in the event file and in the occurrence file. This is because data can be submitted as “Occurrence Only” where you don't have a separate event file. In that case, the location and date information will need to be included in the occurrence file. Since we are formatting this dataset as a sampling event we will not include location and date information in the occurrence file. To see all the Darwin Core terms that can go in the occurrence file go here <https://tools.gbif.org/dwca-validator/extension.do?id=dwc:occurrence>.

This dataset in its original format is in “wide format”. All that means is that data that we would expect to be encoded as values in the rows are instead column headers. We have to

pull all the scientific names out of the column headers and turn them into actual values in the data.

```
occurrence <- melt(BagSeine, id=1:47, measure=48:109, variable.name="vernacularName", value.name="scientificNameID")
```

You'll notice when we did that step we went from 5481 obs (or rows) in the data to 334341 obs. We went from wide to long.

```
dim(BagSeine)
[1] 5481 109
dim(occurrence)
[1] 334341 49
```

Now as with the event file we have several pieces of information that need to be added or changed to make sure the data are following Darwin Core. We always want to include as much information as possible to make the data as reusable as possible.

```
occurrence <- occurrence %>%
  mutate(vernacularName = gsub("\\\\.", ' ', vernacularName),
         eventID = paste("Station", station_code, "Date", completion_dttm, sep = "_"),
         occurrenceStatus = ifelse(relativeAbundance == 0, "Absent", "Present"),
         basisOfRecord = "HumanObservation",
         organismQuantityType = "Relative Abundance",
         collectionCode = paste(Bay, Gear_Type, sep = " "))
```

We will match the taxa list with our occurrence file data to bring in the taxonomic information that we pulled from WoRMS. To save time you'll just import the processed taxa list which includes the taxonomic hierarchy and the required term scientificNameID which is one of the most important pieces of information to include for OBIS.

```
taxaList <- read.csv("https://www.sciencebase.gov/catalog/file/get/53a887f4e4b075096c60cfdd?")
## Merge taxaList with occurrence
occurrence <- merge(occurrence, taxaList, by = "vernacularName", all.x = T)
## Test that all the vernacularNames found a match in taxaList_updated
Hmisc::describe(occurrence$scientificNameID)
      n missing distinct
334341      0         61

lowest : urn:lsid:marinespecies.org:taxname:105792 urn:lsid:marinespecies.org:taxname:107034
highest: urn:lsid:marinespecies.org:taxname:367528 urn:lsid:marinespecies.org:taxname:396707
```

For that last line of code we are expecting to see no missing values for scientificNameID. Every row in the file should have a value in scientificNameID which should be a WoRMS LSID that look like this `urn:lsid:marinespecies.org:taxname:144531`

We need to create a unique ID for each row in the occurrence file. This is known as the `occurrenceID` and is a required term. The `occurrenceID` needs to be globally unique and needs to be permanent and kept in place if any updates to the dataset are made. You should not create brand new `occurrenceID`s when you update a dataset. To facilitate this I like to build the `occurrenceID` from pieces of information available in the dataset to create a unique ID for each row in the occurrence file. For this dataset I used the `eventID` (Station + Date) plus the scientific name. This only works if there is only one scientific name per station per date so if you have different ages or sexes of species at the same station and date this method of creating the `occurrenceID` won't work for you.

```
occurrence$occurrenceID <- paste(occurrence$eventID, gsub(" ", "_", occurrence$scientificName),
occurrence[1,]$occurrenceID
[1] "Station_95_Date_09JAN1997:14:35:00.000_Atractosteus_spatula"
```

For the occurrence file we only have one column to rename. We could have avoided this step if we had named it `organismQuantity` up above but I kept this to remind me what the data providers had called this.

```
occurrence <- occurrence %>%
  rename(organismQuantity = relativeAbundance)
```

2.0.4 Extended Measurement or Fact extension file

The final file we are going to create is the **Extended Measurement or Fact extension (emof)**. This is a bit like a catch all for any measurements or facts that are not captured in Darwin Core. Darwin Core does not have terms for things like temperature, salinity, gear type, cruise number, length, weight, etc. We are going to create a long format file where each of these is a set of rows in the extended measurement or fact file. You can find all the terms in this extension here <https://tools.gbif.org/dwca-validator/extension.do?id=%3Chttp://rs.iobis.org/obis/terms/ExtendedMeasurementOrFact.>>

OBIS uses the BODC NERC Vocabulary Server to provide explicit definitions for each of the measurements https://vocab.nerc.ac.uk/search_nvs/.

For this dataset I was only able to find code definitions provided by the data providers for some of the measurements. I included the ones that I was able to find code definitions and left out any that I couldn't find those for. The ones I was able to find code definitions for were `Total.Of.Samples_Count`, `gear_size`, `start_wind_speed_num`,

start_barometric_pressure_num, start_temperature_num, start_salinity_num,
start_dissolved_oxygen_num. All the others I left out.

```
totalOfSamples <- event[c("Total.Of.Samples_Count", "eventID")]
totalOfSamples <- totalOfSamples[which(!is.na(totalOfSamples$Total.Of.Samples_Count)),]
totalOfSamples <- totalOfSamples %>%
  mutate(measurementType = "Total number of samples used to calculate relative abundance",
         measurementUnit = "",
         measurementTypeID = "",
         measurementUnitID = "",
         occurrenceID = "") %>%
  rename(measurementValue = Total.Of.Samples_Count)

gear_size <- event[c("gear_size", "eventID")]
gear_size <- gear_size[which(!is.na(gear_size$gear_size)),]
gear_size <- gear_size %>%
  mutate(measurementType = "gear size",
         measurementUnit = "meters",
         measurementTypeID = "http://vocab.nerc.ac.uk/collection/P01/current/MTHAREA1/",
         measurementUnitID = "http://vocab.nerc.ac.uk/collection/P06/current/ULAA/",
         occurrenceID = "") %>%
  rename(measurementValue = gear_size)

start_wind_speed_num <- event[c("start_wind_speed_num", "eventID")]
start_wind_speed_num <- start_wind_speed_num[which(!is.na(start_wind_speed_num$start_wind_sp)],]
start_wind_speed_num <- start_wind_speed_num %>%
  mutate(measurementType = "wind speed",
         measurementUnit = "not provided",
         measurementTypeID = "http://vocab.nerc.ac.uk/collection/P01/current/EWSBZZ01/",
         measurementUnitID = "",
         occurrenceID = "") %>%
  rename(measurementValue = start_wind_speed_num)

start_barometric_pressure_num <- event[c("start_barometric_pressure_num", "eventID")]
start_barometric_pressure_num <- start_barometric_pressure_num[which(!is.na(start_barometric_pressure_num$start_barometric_pressure_num)],]
start_barometric_pressure_num <- start_barometric_pressure_num %>%
  mutate(measurementType = "barometric pressure",
         measurementUnit = "not provided",
         measurementTypeID = "http://vocab.nerc.ac.uk/collection/P07/current/CFSN0015/",
         measurementUnitID = "",
         occurrenceID = "") %>%
  rename(measurementValue = start_barometric_pressure_num)
```

```

start_temperature_num <- event[c("start_temperature_num", "eventID")]
start_temperature_num <- start_temperature_num[which(!is.na(start_temperature_num$start_temperature_num))]
start_temperature_num <- start_temperature_num %>%
  mutate(measurementType = "water temperature",
         measurementUnit = "Celsius",
         measurementTypeID = "http://vocab.nerc.ac.uk/collection/P01/current/TEMPPR01/",
         measurementUnitID = "http://vocab.nerc.ac.uk/collection/P06/current/UPAA/",
         occurrenceID = "") %>%
  rename(measurementValue = start_temperature_num)

start_salinity_num <- event[c("start_salinity_num", "eventID")]
start_salinity_num <- start_salinity_num[which(!is.na(start_salinity_num$start_salinity_num))]
start_salinity_num <- start_salinity_num %>%
  mutate(measurementType = "salinity",
         measurementUnit = "ppt",
         measurementTypeID = "http://vocab.nerc.ac.uk/collection/P01/current/ODSDM021/",
         measurementUnitID = "http://vocab.nerc.ac.uk/collection/P06/current/UPPT/",
         occurrenceID = "") %>%
  rename(measurementValue = start_salinity_num)

start_dissolved_oxygen_num <- event[c("start_dissolved_oxygen_num", "eventID")]
start_dissolved_oxygen_num <- start_dissolved_oxygen_num[which(!is.na(start_dissolved_oxygen_num$start_dissolved_oxygen_num))]
start_dissolved_oxygen_num <- start_dissolved_oxygen_num %>%
  mutate(measurementType = "dissolved oxygen",
         measurementUnit = "ppm",
         measurementTypeID = "http://vocab.nerc.ac.uk/collection/P09/current/DOX2/",
         measurementUnitID = "http://vocab.nerc.ac.uk/collection/P06/current/UPPM/",
         occurrenceID = "") %>%
  rename(measurementValue = start_dissolved_oxygen_num)

alternate_station_code <- event[c("alternate_station_code", "eventID")]
alternate_station_code <- alternate_station_code[which(!is.na(alternate_station_code$alternate_station_code))]
alternate_station_code <- alternate_station_code %>%
  mutate(measurementType = "alternate station code",
         measurementUnit = "",
         measurementTypeID = "",
         measurementUnitID = "",
         occurrenceID = "") %>%
  rename(measurementValue = alternate_station_code)

organismQuantity <- occurrence[c("organismQuantity", "eventID", "occurrenceID")]
organismQuantity <- organismQuantity[which(!is.na(organismQuantity$organismQuantity)),]

```

```

organismQuantity <- organismQuantity %>%
  mutate(measurementType = "relative abundance",
         measurementUnit = "",
         measurementTypeID = "http://vocab.nerc.ac.uk/collection/S06/current/S0600020/",
         measurementUnitID = "") %>%
  rename(measurementValue = organismQuantity)

# Bind the separate measurements together into one file
mof <- rbind(totalOfSamples, start_barometric_pressure_num, start_dissolved_oxygen_num,
             start_salinity_num, start_temperature_num, start_wind_speed_num, gear_size,
             alternate_station_code, organismQuantity)

head(mof)
  measurementValue                                     eventID
1              18 Station_95_Date_09JAN1997:14:35:00.000
2             103 Station_95_Date_18AUG2000:11:02:00.000
3             401 Station_96_Date_28JUN2005:08:41:00.000
4              35 Station_96_Date_23AUG2006:11:47:00.000
5              57 Station_96_Date_17OCT2006:14:23:00.000
6               5 Station_96_Date_19FEB1996:10:27:00.000

                                     measurementType measurementUnit measurementType
1 Total number of samples used to calculate relative abundance
2 Total number of samples used to calculate relative abundance
3 Total number of samples used to calculate relative abundance
4 Total number of samples used to calculate relative abundance
5 Total number of samples used to calculate relative abundance
6 Total number of samples used to calculate relative abundance
  measurementUnitID occurrenceID
1
2
3
4
5
6
tail(mof)
  measurementValue                                     eventID   measurementType measurementUnitID
334336      0.0000000 Station_217_Date_03APR2003:13:28:00.000 relative abundance
334337      0.0000000 Station_217_Date_24FEB2006:10:12:00.000 relative abundance
334338      0.1428571 Station_217_Date_23JUN2001:12:28:00.000 relative abundance
334339      0.0000000 Station_212_Date_23MAY1990:10:43:00.000 relative abundance
334340      0.1224490 Station_212_Date_24JUL1990:09:34:00.000 relative abundance
334341      0.0000000 Station_212_Date_21MAR2001:11:52:00.000 relative abundance
                                     measurementTypeID measurementUnitID

```



```

334336 http://vocab.nerc.ac.uk/collection/S06/current/S0600020/
334337 http://vocab.nerc.ac.uk/collection/S06/current/S0600020/
334338 http://vocab.nerc.ac.uk/collection/S06/current/S0600020/
334339 http://vocab.nerc.ac.uk/collection/S06/current/S0600020/
334340 http://vocab.nerc.ac.uk/collection/S06/current/S0600020/
334341 http://vocab.nerc.ac.uk/collection/S06/current/S0600020/
                                occurrenceID
334336 Station_217_Date_03APR2003:13:28:00.000_Litopenaeus_setiferus
334337 Station_217_Date_24FEB2006:10:12:00.000_Litopenaeus_setiferus
334338 Station_217_Date_23JUN2001:12:28:00.000_Litopenaeus_setiferus
334339 Station_212_Date_23MAY1990:10:43:00.000_Litopenaeus_setiferus
334340 Station_212_Date_24JUL1990:09:34:00.000_Litopenaeus_setiferus
334341 Station_212_Date_21MAR2001:11:52:00.000_Litopenaeus_setiferus

# Write out the file
write.csv(mof, file = (paste0(event[1,]$datasetID, "_mof_", lubridate::today(), ".csv")), file

```

2.0.5 Cleaning up Event and Occurrence files

Now that we have all of our files created we can clean up the **Event** and **Occurrence** files to remove the columns that are not following Darwin Core. We had to leave the extra bits in before because we needed them to create the **emof** file above.

```

event <- event[c("samplingProtocol", "locality", "waterBody", "decimalLatitude", "decimalLongitude",
                 "eventDate", "sampleSizeValue", "minimumDepthInMeters",
                 "maximumDepthInMeters", "type", "modified", "language", "license", "institutionCode",
                 "ownerInstitutionCode", "coordinateUncertaintyInMeters",
                 "geodeticDatum", "georeferenceProtocol", "country", "countryCode", "stateProvince",
                 "datasetID", "eventID", "sampleSizeUnit", "samplingEffort")]

head(event)

```

	samplingProtocol	locality	waterBody	decimalLatitude	decimalLongitude
1	Bag Seine Mission-Aransas	Estuary	Aransas Bay	28.13472	-97.00833
2	Bag Seine Mission-Aransas	Estuary	Aransas Bay	28.13528	-97.00722
3	Bag Seine Mission-Aransas	Estuary	Aransas Bay	28.13444	-96.99611
4	Bag Seine Mission-Aransas	Estuary	Aransas Bay	28.13444	-96.99611
5	Bag Seine Mission-Aransas	Estuary	Aransas Bay	28.13444	-96.99611
6	Bag Seine Mission-Aransas	Estuary	Aransas Bay	28.13472	-96.99583

```

                                eventDate sampleSizeValue minimumDepthInMeters maximumDepthInMeters type modified
1 1997-01-09 14:35:00                0.03                0.0                0.6 Event 2022-01-01
2 2000-08-18 11:02:00                0.03                0.1                0.5 Event 2022-01-01
3 2005-06-28 08:41:00                0.03                0.4                0.6 Event 2022-01-01

```

```

4 2006-08-23 11:47:00      0.03      0.2      0.4 Event 2022-0
5 2006-10-17 14:23:00      0.03      0.7      0.8 Event 2022-0
6 1996-02-19 10:27:00      0.03      0.1      0.3 Event 2022-0

      license institutionCode ownerInstitution
1 http://creativecommons.org/publicdomain/zero/1.0/legalcode TPWD
2 http://creativecommons.org/publicdomain/zero/1.0/legalcode TPWD
3 http://creativecommons.org/publicdomain/zero/1.0/legalcode TPWD
4 http://creativecommons.org/publicdomain/zero/1.0/legalcode TPWD
5 http://creativecommons.org/publicdomain/zero/1.0/legalcode TPWD
6 http://creativecommons.org/publicdomain/zero/1.0/legalcode TPWD
coordinateUncertaintyInMeters geodeticDatum georeferenceProtocol country countryCode
1      100      WGS84      Handheld GPS United States      US
2      100      WGS84      Handheld GPS United States      US
3      100      WGS84      Handheld GPS United States      US
4      100      WGS84      Handheld GPS United States      US
5      100      WGS84      Handheld GPS United States      US
6      100      WGS84      Handheld GPS United States      US
      datasetID      eventID sampleSizeUnit
1 TPWD_HARC_Texas_Aransas_Bay_Bag_Seine Station_95_Date_09JAN1997:14:35:00.000      hectares
2 TPWD_HARC_Texas_Aransas_Bay_Bag_Seine Station_95_Date_18AUG2000:11:02:00.000      hectares
3 TPWD_HARC_Texas_Aransas_Bay_Bag_Seine Station_96_Date_28JUN2005:08:41:00.000      hectares
4 TPWD_HARC_Texas_Aransas_Bay_Bag_Seine Station_96_Date_23AUG2006:11:47:00.000      hectares
5 TPWD_HARC_Texas_Aransas_Bay_Bag_Seine Station_96_Date_17OCT2006:14:23:00.000      hectares
6 TPWD_HARC_Texas_Aransas_Bay_Bag_Seine Station_96_Date_19FEB1996:10:27:00.000      hectares
samplingEffort
1      120 seconds
2      120 seconds
3      120 seconds
4      120 seconds
5      120 seconds
6      120 seconds

write.csv(event, file = paste0(event[1,]$datasetID, "_event_", lubridate::today(), ".csv"), f

occurrence <- occurrence[c("vernacularName", "eventID", "occurrenceStatus", "basisOfRecord",
      "scientificName", "scientificNameID", "kingdom", "phylum", "class",
      "order", "family", "genus",
      "scientificNameAuthorship", "taxonRank", "organismQuantity",
      "organismQuantityType", "occurrenceID", "collectionCode")]

head(occurrence)
      vernacularName      eventID occurrenceStatus      basisOfRecord
1 Alligator gar Station_95_Date_09JAN1997:14:35:00.000      Absent HumanObservation

```

```

2 Alligator gar Station_95_Date_18AUG2000:11:02:00.000 Absent HumanObservation
3 Alligator gar Station_96_Date_28JUN2005:08:41:00.000 Absent HumanObservation
4 Alligator gar Station_96_Date_23AUG2006:11:47:00.000 Absent HumanObservation
5 Alligator gar Station_96_Date_17OCT2006:14:23:00.000 Absent HumanObservation
6 Alligator gar Station_96_Date_19FEB1996:10:27:00.000 Absent HumanObservation
      scientificName      scientificNameID kingdom phylum clas
1 Atractosteus spatula urn:lsid:marinespecies.org:taxname:279822 Animalia Chordata Actinopter
2 Atractosteus spatula urn:lsid:marinespecies.org:taxname:279822 Animalia Chordata Actinopter
3 Atractosteus spatula urn:lsid:marinespecies.org:taxname:279822 Animalia Chordata Actinopter
4 Atractosteus spatula urn:lsid:marinespecies.org:taxname:279822 Animalia Chordata Actinopter
5 Atractosteus spatula urn:lsid:marinespecies.org:taxname:279822 Animalia Chordata Actinopter
6 Atractosteus spatula urn:lsid:marinespecies.org:taxname:279822 Animalia Chordata Actinopter
      order      family      genus scientificNameAuthorship taxonRank organismQuan
1 Lepisosteiformes Lepisosteidae Atractosteus (Lacepède, 1803) Species
2 Lepisosteiformes Lepisosteidae Atractosteus (Lacepède, 1803) Species
3 Lepisosteiformes Lepisosteidae Atractosteus (Lacepède, 1803) Species
4 Lepisosteiformes Lepisosteidae Atractosteus (Lacepède, 1803) Species
5 Lepisosteiformes Lepisosteidae Atractosteus (Lacepède, 1803) Species
6 Lepisosteiformes Lepisosteidae Atractosteus (Lacepède, 1803) Species
      organismQuantityType      occurrenceID      co
1 Relative Abundance Station_95_Date_09JAN1997:14:35:00.000_Atractosteus_spatula Aransas Ba
2 Relative Abundance Station_95_Date_18AUG2000:11:02:00.000_Atractosteus_spatula Aransas Ba
3 Relative Abundance Station_96_Date_28JUN2005:08:41:00.000_Atractosteus_spatula Aransas Ba
4 Relative Abundance Station_96_Date_23AUG2006:11:47:00.000_Atractosteus_spatula Aransas Ba
5 Relative Abundance Station_96_Date_17OCT2006:14:23:00.000_Atractosteus_spatula Aransas Ba
6 Relative Abundance Station_96_Date_19FEB1996:10:27:00.000_Atractosteus_spatula Aransas Ba

write.csv(occurrence, file = paste0(event[1,]$datasetID, "_occurrence_",lubridate::today(),"

```

3 Darwin Core Salmon Data Remap

3.1 Salmon Ocean Ecology Data

3.1.1 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.

3.1.2 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.

```

event <- tibble(eventID = survey_seines$seine_id,
               eventData = date(survey_seines$survey_date),
               decimalLatitude = survey_seines$lat,
               decimalLongitude = survey_seines$long,
               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 DOI f
             )

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

```

3.1.3 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.

```

#TODO: Include bycatch data as well

## 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 = "Once")

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 = "Once")

## remove records that have already been assigned an ID
seines_long <- full_join(seines_total_long, seines_taken_long, by = c("seine_id", "scientificName"))
drop_na() %>%

```

```

mutate(n_not_taken = n - n_taken) %>% #so_total includes the number taken so I subtract n_1
select(-n_taken, -n) %>%
filter(n_not_taken > 0)

all_fish_caught <-
  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"
  as.character())

fish_retained_data <- fish_data %>%
  mutate(scientificName = latin) %>%
  select(-species) %>%
  mutate(prefix = "hakai-jsp-",
         occurrenceID = paste0(prefix, ufn)) %>%
  select(-semsp_id, -prefix, -ufn, -fork_length_field, -fork_length, -weight, -weight_field)

occurrence <- bind_rows(all_fish_caught, fish_retained_data) %>%
  mutate(basisOfRecord = "HumanObservation",
         occurrenceStatus = "present") %>%
  rename(eventID = seine_id)

```

For each occurrence of the six different fish species that I caught I need to match the species name that I provide with the official `scientificName` that is part of the World Register of Marine Species database <http://www.marinespecies.org/>

```

# I went directly to the WoRMS website (http://www.marinespecies.org/) to download the full t

species_matched <- readxl::read_excel(here::here("datasets", "hakai_salmon_data", "raw_data"

occurrence <- left_join(occurrence, species_matched, by = c("scientificName" = "ScientificName",
  select(occurrenceID, basisOfRecord, scientificName, eventID, occurrenceStatus = occurrenceStatus)

```

```
write_csv(occurrence, here::here("datasets", "hakai_salmon_data", "occurrence.csv"))
```

3.1.4 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`.

```
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_length <- fish_data %>%
  mutate(occurrenceID = paste0("hakai-jsp-", ufn)) %>%
  select(occurrenceID, eventID = seine_id, fork_length, weight) %>%
  mutate(measurementType = "fork length", measurementValue = fork_length) %>%
  select(eventID, occurrenceID, measurementType, measurementValue) %>%
  mutate(measurementUnit = "millimeters",
         measurementUnitID = "http://vocab.nerc.ac.uk/collection/P06/current/UXMM/")

fish_weight <- fish_data %>%
  mutate(occurrenceID = paste0("hakai-jsp-", ufn)) %>%
  select(occurrenceID, eventID = seine_id, fork_length, weight) %>%
  mutate(measurementType = "mass", measurementValue = weight) %>%
  select(eventID, occurrenceID, measurementType, measurementValue) %>%
  mutate(measurementUnit = "grams",
         measurementUnitID = "http://vocab.nerc.ac.uk/collection/P06/current/UGRM/")

measurementOrFact <- bind_rows(fish_length, fish_weight) %>%
  drop_na(measurementValue)

rm(fish_length, fish_weight)

write_csv(measurementOrFact, here::here("datasets", "hakai_salmon_data", "measurementOrFact.csv"))
```

4 Seagrass Density to DWC eMoF format

4.1 Hakai Seagrass

4.1.1 Setup

This section clears the workspace, checks the working directory, and installs packages (if required) and loads packages, and loads necessary datasets

```
library("knitr")
# Knitr global chunk options
opts_chunk$set(message = FALSE,
                warning = FALSE,
                error = FALSE)
```

4.1.1.1 Load Data

First load the seagrass density survey data, set variable classes, and have a quick look

```
# Load density data
seagrassDensity <-
  read.csv(seagrassDensity_csv,
           colClass = "character") %>%
  mutate(date = ymd(date),
         depth = as.numeric(depth),
         transect_dist = factor(transect_dist),
         collected_start = ymd_hms(collected_start),
         collected_end = ymd_hms(collected_end),
         density = as.numeric(density),
         density_msq = as.numeric(density_msq),
         canopy_height_cm = as.numeric(canopy_height_cm),
         flowering_shoots = as.numeric(flowering_shoots)) %T>%
  glimpse()
```


Rows: 3,031

Columns: 22

```
$ X          <chr> "1", "2", "3", "4", "5", "6", "7", "8", "9", "10", "1~
$ organization <chr> "HAKAI", "HAKAI", "HAKAI", "HAKAI", "HAKAI", "HAKAI",~
$ work_area   <chr> "CALVERT", "CALVERT", "CALVERT", "CALVERT", "CALVERT"~
$ project     <chr> "MARINEGEO", "MARINEGEO", "MARINEGEO", "MARINEGEO", "~
$ survey      <chr> "PRUTH_BAY", "PRUTH_BAY", "PRUTH_BAY", "PRUTH_BAY", "~
$ site_id     <chr> "PRUTH_BAY_INTERIOR4", "PRUTH_BAY_INTERIOR4", "PRUTH~
$ date        <date> 2016-05-13, 2016-05-13, 2016-05-13, 2016-05-13, 2016~
$ sampling_bout <chr> "4", "4", "4", "4", "4", "4", "4", "6", "6", "6", "6"~
$ dive_supervisor <chr> "Zach", "Zach", "Zach", "Zach", "Zach", "Zach", "Zach",~
$ collector    <chr> "Derek", "Derek", "Derek", "Derek", "Derek", "Derek",~
$ hakai_id     <chr> "2016-05-13_PRUTH_BAY_INTERIOR4_0", "2016-05-13_PRUTH~
$ sample_type  <chr> "seagrass_density", "seagrass_density", "seagrass_den~
$ depth        <dbl> 6.0, 6.0, 6.0, 6.0, 5.0, 6.0, 6.0, 9.1, 9.0, 8.9, 9.0~
$ transect_dist <fct> 0, 5, 10, 15, 20, 25, 30, 10, 15, 20, 25, 30, 0, 5, 1~
$ collected_start <dtm> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, ~
$ collected_end  <dtm> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, ~
$ density       <dbl> 13, 10, 18, 22, 16, 31, 9, 5, 6, 6, 6, 3, 13, 30, 23,~
$ density_msq   <dbl> 208, 160, 288, 352, 256, 496, 144, 80, 96, 96, 96, 48~
$ canopy_height_cm <dbl> 60, 63, 80, 54, 55, 50, 63, 85, 80, 90, 95, 75, 60, 6~
$ flowering_shoots <dbl> NA, NA, NA, NA, NA, NA, NA, NA, 0, 0, 0, 0, 0, NA, NA, NA~
$ comments      <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, N~
$ quality_log    <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, N~
```

Next, load the habitat survey data, and same as above, set variable classes as necessary, and have a quick look.

```
# load habitat data, set variable classes, have a quick look
seagrassHabitat <-
  read.csv(seagrassHabitat_csv,
           colClasses = "character") %>%
  mutate(date       = ymd(date),
         depth      = as.numeric(depth),
         hakai_id   = str_pad(hakai_id, 5, pad = "0"),
         transect_dist = factor(transect_dist),
         collected_start = ymd_hms(collected_start),
         collected_end   = ymd_hms(collected_end)) %>%
  glimpse()
```

Rows: 2,052

Columns: 28

```

$ X <chr> "1", "2", "3", "4", "5", "6", "7", "8", "9", "10", "1~
$ organization <chr> "HAKAI", "HAKAI", "HAKAI", "HAKAI", "HAKAI", "HAKAI", ~
$ work_area <chr> "CALVERT", "CALVERT", "CALVERT", "CALVERT", "CALVERT"~
$ project <chr> "MARINEGEO", "MARINEGEO", "MARINEGEO", "MARINEGEO", "~
$ survey <chr> "CHOKED_PASS", "CHOKED_PASS", "CHOKED_PASS", "CHOKED_~
$ site_id <chr> "CHOKED_PASS_INTERIOR6", "CHOKED_PASS_INTERIOR6", "CH~
$ date <date> 2017-11-22, 2017-11-22, 2017-11-22, 2017-11-22, 2017~
$ sampling_bout <chr> "6", "6", "6", "6", "6", "6", "1", "1", "1", "1", "1"~
$ dive_supervisor <chr> "gillian", "gillian", "gillian", "gillian", "gillian"~
$ collector <chr> "zach", "zach", "zach", "zach", "zach", "zach", "zach", "kyle~
$ hakai_id <chr> "10883", "2017-11-22_CHOKED_PASS_INTERIOR6_5 - 10", "~
$ sample_type <chr> "seagrass_habitat", "seagrass_habitat", "seagrass_hab~
$ depth <dbl> 9.2, 9.4, 9.3, 9.0, 9.2, 9.2, 3.4, 3.4, 3.4, 3.4, 3.4~
$ transect_dist <fct> 0 - 5, 10-May, 15-Oct, 15 - 20, 20 - 25, 25 - 30, 0 ~
$ collected_start <dtm> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, ~
$ collected_end <dtm> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, ~
$ bag_uid <chr> "10883", NA, NA, "11094", NA, "11182", "7119", NA, "7~
$ bag_number <chr> "3557", NA, NA, "3520", NA, "903", "800", NA, "318", ~
$ density_range <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, N~
$ substrate <chr> "sand,shell hash", "sand,shell hash", "sand,shell has~
$ patchiness <chr> "< 1", "< 1", "02-Jan", "< 1", "< 1", "< 1", "< 1", "~
$ adj_habitat_1 <chr> "seagrass", "seagrass", "seagrass", "seagrass", "seag~
$ adj_habitat_2 <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, N~
$ sample_collected <chr> "TRUE", "FALSE", "FALSE", "TRUE", "FALSE", "TRUE", "T~
$ vegetation_1 <chr> NA, NA, NA, NA, NA, NA, "des", NA, "des", NA, NA, NA,~
$ vegetation_2 <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, N~
$ comments <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, N~
$ quality_log <chr> "1: Flowering shoots 0 for entire transects", NA, NA,~

```

Finally, load coordinate data for surveys, and subset necessary variables

```

coordinates <-
  read.csv(coordinate_csv,
           colClass = c("Point.Name" = "character")) %>%
  select(Point.Name, Decimal.Lat, Decimal.Long) %T>%
  glimpse()

```

Rows: 70

Columns: 3

```

$ Point.Name <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, N~
$ Decimal.Lat <dbl> 52.06200, 52.05200, 51.92270, 51.92500, 51.80900, 51.8090~
$ Decimal.Long <dbl> -128.4120, -128.4030, -128.4648, -128.4540, -128.2360, -1~

```

4.1.1.2 Merge Datasets

Now all the datasets have been loaded, and briefly formatted, we'll join together the habitat and density surveys, and the coordinates for these.

The seagrass density surveys collect data at discrete points (ie. 5 metres) along the transects, while the habitat surveys collect data over sections (ie. 0 - 5 metres) along the transects. In order to fit these two surveys together, we'll narrow the habitat surveys from a range to a point so the locations will match. Based on how the habitat data is collected, the point the habitat survey is applied to will be the distance at the end of the swath (ie. 10-15m will become 15m). To account for no preceding distance, the 0m distance will use the 0-5m section of the survey.

First, we'll make the necessary transformations to the habitat dataset.

```
# Reformat seagrassHabitat to merge with seagrassDensity
## replicate 0 - 5m transect dist to match with 0m in density survey;
## rest of habitat bins can map one to one with density (ie. 5 - 10m -> 10m)
seagrass0tmp <-
  seagrassHabitat %>%
  filter(transect_dist %in% c("0 - 5", "0 - 2.5")) %>%
  mutate(transect_dist = factor(0))

## collapse various levels to match with seagrassDensity transect_dist
seagrassHabitat$transect_dist <-
  fct_collapse(seagrassHabitat$transect_dist,
    "5" = c("0 - 5", "2.5 - 7.5"),
    "10" = c("5 - 10", "7.5 - 12.5"),
    "15" = c("10 - 15", "12.5 - 17.5"),
    "20" = c("15 - 20", "17.5 - 22.5"),
    "25" = c("20 - 25", "22.5 - 27.5"),
    "30" = c("25 - 30", "27.5 - 30"))

## merge seagrass0tmp into seagrassHabitat to account for 0m samples,
## set class for date, datetime variables
seagrassHabitatFull <-
  rbind(seagrass0tmp, seagrassHabitat) %>%
  filter(transect_dist != "0 - 2.5") %>% # already captured in seagrass0tmp
  droplevels(.) # remove now unused factor levels
```

With the distances of habitat and density surveys now corresponding, we can now merge these two datasets plus their coordinates together, combine redundant fields, and remove unnecessary fields.

```

# Merge seagrassHabitatFull with seagrassDensity, then coordinates
seagrass <-
  full_join(seagrassHabitatFull, seagrassDensity,
            by = c("organization",
                  "work_area",
                  "project",
                  "survey",
                  "site_id",
                  "date",
                  "transect_dist")) %>%
# merge hakai_id.x and hakai_id.y into single variable field;
# use combination of date, site_id, transect_dist, and field uid (hakai_id
# when present)
mutate(field_uid = ifelse(sample_collected == TRUE, hakai_id.x, "NA"),
       hakai_id = paste(date, "HAKAI:CALVERT", site_id, transect_dist, sep = ":"),
       # below, aggregate metadata that didn't merge naturally (ie. due to minor
       # differences in watch time or depth gauges)
       dive_supervisor = dive_supervisor.x,
       collected_start = ymd_hms(ifelse(is.na(collected_start.x),
                                       collected_start.y,
                                       collected_start.x)),
       collected_end   = ymd_hms(ifelse(is.na(collected_start.x),
                                       collected_start.y,
                                       collected_start.x)),
       depth_m         = ifelse(is.na(depth.x), depth.y, depth.x),
       sampling_bout   = sampling_bout.x) %>%
left_join(., coordinates, # add coordinates
          by = c("site_id" = "Point.Name")) %>%
select( - c(X.x, X.y, hakai_id.x, hakai_id.y, # remove unnecessary variables
            dive_supervisor.x, dive_supervisor.y,
            collected_start.x, collected_start.y,
            collected_end.x, collected_end.y,
            depth.x, depth.y,
            sampling_bout.x, sampling_bout.y)) %>%
mutate(density_msq = as.character(density_msq),
       canopy_height_cm = as.character(canopy_height_cm),
       flowering_shoots = as.character(flowering_shoots),
       depth_m = as.character(depth_m)) %T>%
glimpse()

```

Rows: 3,743

Columns: 38

```

$ organization      <chr> "HAKAI", "HAKAI", "HAKAI", "HAKAI", "HAKAI", "HAKAI", ~
$ work_area         <chr> "CALVERT", "CALVERT", "CALVERT", "CALVERT", "CALVERT"~
$ project           <chr> "MARINEGEO", "MARINEGEO", "MARINEGEO", "MARINEGEO", "~
$ survey            <chr> "CHOKED_PASS", "CHOKED_PASS", "CHOKED_PASS", "PRUTH_B~
$ site_id           <chr> "CHOKED_PASS_INTERIOR6", "CHOKED_PASS_EDGE1", "CHOKED~
$ date              <date> 2017-11-22, 2017-05-19, 2017-05-19, 2017-07-03, 2017~
$ collector.x       <chr> "zach", "kyle", NA, "tanya", "zach", "zach", "zach", ~
$ sample_type.x     <chr> "seagrass_habitat", "seagrass_habitat", "seagrass_hab~
$ transect_dist     <fct> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, ~
$ bag_uid           <chr> "10883", "7119", "7031", "2352", "10255", "10023", "1~
$ bag_number        <chr> "3557", "800", "301", "324", "3506", "3555", "3534", ~
$ density_range     <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, N~
$ substrate         <chr> "sand,shell hash", "sand,shell hash", "sand,shell has~
$ patchiness        <chr> "< 1", "< 1", "< 1", "< 1", "< 1", "05-Apr", "04-Mar"~
$ adj_habitat_1     <chr> "seagrass", "sand", "standing kelp", "seagrass", "sea~
$ adj_habitat_2     <chr> NA, NA, NA, NA, NA, NA, "standing kelp", NA, NA, NA, ~
$ sample_collected <chr> "TRUE", "TRUE", "TRUE", "TRUE", "TRUE", "TRUE", "TRUE~
$ vegetation_1      <chr> NA, "des", "des", "zm", "des", NA, NA, NA, NA, NA, NA, NA~
$ vegetation_2      <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, "~
$ comments.x        <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, N~
$ quality_log.x     <chr> "1: Flowering shoots 0 for entire transects", NA, NA,~
$ collector.y       <chr> "derek", "ondine", "ondine", "derek", "derek", "derek~
$ sample_type.y     <chr> "seagrass_density", "seagrass_density", "seagrass_den~
$ density           <dbl> 4, 10, 6, 13, 6, 1, 2, 6, 21, 3, 7, 4, 3, 14, 17, 11,~
$ density_msq       <chr> "64", "160", "96", "208", "96", "16", "32", "96", "33~
$ canopy_height_cm  <chr> "80", "80", "110", "60", "125", "100", "100", "125", ~
$ flowering_shoots  <chr> "0", NA, NA, NA, NA, NA, NA, "0", NA, NA, NA, "0", NA~
$ comments.y        <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, N~
$ quality_log.y     <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, "~
$ field_uid         <chr> "10883", "07119", "07031", "02352", "10255", "10023",~
$ hakai_id          <chr> "2017-11-22:HAKAI:CALVERT:CHOKED_PASS_INTERIOR6:0", "~
$ dive_supervisor   <chr> "gillian", "gillian,gillian.sadlierbrown", "gillian,g~
$ collected_start   <dtm> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, ~
$ collected_end     <dtm> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, ~
$ depth_m           <chr> "9.2", "3.4", "4.8", "2.4", "5.3", "5.6", "4.4", "2.5~
$ sampling_bout     <chr> "6", "1", "3", "5", "5", "3", "5", "2", "1", "2", "6"~
$ Decimal.Lat       <dbl> 51.67482, 51.67882, 51.67493, 51.64532, 51.67349, 51.~
$ Decimal.Long      <dbl> -128.1195, -128.1148, -128.1237, -128.1193, -128.1180~

```

4.1.2 Convert Data to Darwin Core - Extended Measurement or Fact format

The Darwin Core ExtendedMeasurementOrFact (eMoF) extension bases records around a core event (rather than occurrence as in standard Darwin Core), allowing for additional measurement variables to be associated with occurrence data.

4.1.2.1 Add Event ID and Occurrence ID variables to dataset

As this dataset will be annually updated, rather than using natural keys (ie. using `package::uuid` to autogenerate) for event and occurrence IDs, here we will use surrogate keys made up of a concatenation of date survey, transect location, observation distance, and sample ID (for occurrenceID, when a sample is present).

```
# create and populate eventID variable
## currently only event is used, but additional surveys and abiotic data
## are associated with parent events that may be included at a later date
seagrass$eventID <- seagrass$hakai_id

# create and populate occurrenceID; combine eventID with transect_dist
# and field_uid
## in the event of <NA> field_uid, no sample was collected, but
## measurements and occurrence are still taken; no further subsamples
## are associated with <NA> field_uids
seagrass$occurrenceID <-
  with(seagrass,
    paste(eventID, transect_dist, field_uid, sep = ":"))
```

4.1.2.2 Create Event, Occurrence, and eMoF tables

Now that we've created eventIDs and occurrenceIDs to connect all the variables together, we can begin to create the Event, Occurrence, and extended Measurement or Fact table necessary for DarwinCore compliant datasets

4.1.2.2.1 Event Table

```
# subset seagrass to create event table
seagrassEvent <-
  seagrass %>%
  distinct %>% # some duplicates in data stemming from database conflicts
  select(date,
```

```

    Decimal.Lat, Decimal.Long, transect_dist,
    depth_m, eventID) %>%
  rename(eventDate      = date,
    decimalLatitude     = Decimal.Lat,
    decimalLongitude    = Decimal.Long,
    coordinateUncertaintyInMeters = transect_dist,
    minimumDepthInMeters = depth_m,
    maximumDepthInMeters = depth_m) %>%
  mutate(geodeticDatum = "WGS84",
    samplingEffort = "30 metre transect") %T>% glimpse

```

Rows: 3,659

Columns: 8

```

$ eventDate      <date> 2017-11-22, 2017-05-19, 2017-05-19, 201~
$ decimalLatitude <dbl> 51.67482, 51.67882, 51.67493, 51.64532, ~
$ decimalLongitude <dbl> -128.1195, -128.1148, -128.1237, -128.11~
$ coordinateUncertaintyInMeters <fct> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0~
$ maximumDepthInMeters <chr> "9.2", "3.4", "4.8", "2.4", "5.3", "5.6"~
$ eventID        <chr> "2017-11-22:HAKAI:CALVERT:CHOKED_PASS_IN~
$ geodeticDatum  <chr> "WGS84", "WGS84", "WGS84", "WGS84", "WGS~
$ samplingEffort <chr> "30 metre transect", "30 metre transect"~

```

```

# save event table to csv
write.csv(seagrassEvent, seagrassEvent_csv)

```

4.1.2.2.2 Occurrence Table

```

# subset seagrass to create occurrence table
seagrassOccurrence <-
  seagrass %>%
  distinct %>% # some duplicates in data stemming from database conflicts
  select(eventID, occurrenceID) %>%
  mutate(basisOfRecord = "HumanObservation",
    scientificName = "Zostera subg. Zostera marina",
    occurrenceStatus = "present")

# Taxonomic name matching
# in addition to the above metadata, DarwinCore format requires further
# taxonomic data that can be acquired through the WoRMS register.
## Load taxonomic info, downloaded via WoRMS tool

```

```

# zmWorms <-
#   read.delim("raw_data/zmworms_matched.txt",
#             header = TRUE,
#             nrows = 1)

zmWorms <- wm_record(id = 145795)

# join WoRMS name with seagrassOccurrence create above
seagrassOccurrence <-
  full_join(seagrassOccurrence, zmWorms,
            by = c("scientificName" = "scientificname")) %>%
  select(eventID, occurrenceID, basisOfRecord, scientificName, occurrenceStatus, AphiaID,
         url, authority, status, unacceptreason, taxonRankID, rank,
         valid_AphiaID, valid_name, valid_authority, parentNameUsageID,
         kingdom, phylum, class, order, family, genus, citation, lsid,
         isMarine, match_type, modified) %T>%
glimpse

```

Rows: 3,660

Columns: 27

```

$ eventID      <chr> "2017-11-22:HAKAI:CALVERT:CHOKED_PASS_INTERIOR6:0", ~
$ occurrenceID <chr> "2017-11-22:HAKAI:CALVERT:CHOKED_PASS_INTERIOR6:0:0:~
$ basisOfRecord <chr> "HumanObservation", "HumanObservation", "HumanObserv~
$ scientificName <chr> "Zostera subg. Zostera marina", "Zostera subg. Zoste~
$ occurrenceStatus <chr> "present", "present", "present", "present", "present~
$ AphiaID       <int> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, ~
$ url           <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, ~
$ authority     <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, ~
$ status       <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, ~
$ unacceptreason <lgl> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, ~
$ taxonRankID   <int> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, ~
$ rank         <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, ~
$ valid_AphiaID <int> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, ~
$ valid_name    <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, ~
$ valid_authority <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, ~
$ parentNameUsageID <int> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, ~
$ kingdom       <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, ~
$ phylum      <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, ~
$ class        <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, ~
$ order        <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, ~
$ family       <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, ~
$ genus        <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, ~

```



```

$ citation      <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, ~
$ lsid         <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, ~
$ isMarine     <int> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, ~
$ match_type   <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, ~
$ modified     <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, ~

```

```

# save occurrence table to csv
write.csv(seagrassOccurrence, seagrassOccurrence_csv)

```

4.1.2.2.3 Extended MeasurementOrFact table

```

seagrassMof <-
  seagrass %>%
  # select variables for eMoF table
  select(date,
    eventID, survey, site_id, transect_dist,
    substrate, patchiness, adj_habitat_1, adj_habitat_2,
    vegetation_1, vegetation_2,
    density_msq, canopy_height_cm, flowering_shoots) %>%
  # split substrate into two variables (currently holds two substrate type in same variable)
  separate(substrate, sep = ",", into = c("substrate_1", "substrate_2")) %>%
  # change variables names to match NERC database (or to be more descriptive where none exists)
  rename(measurementDeterminedDate = date,
    SubstrateTypeA = substrate_1,
    SubstrateTypeB = substrate_2,
    BarePatchLengthWithinSeagrass = patchiness,
    PrimaryAdjacentHabitat = adj_habitat_1,
    SecondaryAdjacentHabitat = adj_habitat_2,
    PrimaryAlgaeSp = vegetation_1,
    SecondaryAlgaeSp = vegetation_2,
    BedAbund = density_msq,
    CanopyHeight = canopy_height_cm,
    FloweringBedAbund = flowering_shoots) %>%
  # reformat variables into DwC MeasurementOrFact format
  # (single values variable, with measurement type, unit, etc. variables)
  pivot_longer( - c(measurementDeterminedDate, eventID, survey, site_id, transect_dist),
    names_to = "measurementType",
    values_to = "measurementValue",
    values_ptypes = list(measurementValue = "character")) %>%
  # use measurement type to fill in remainder of variables relating to
  # NERC vocabulary and metadata fields

```

```

mutate(
  measurementTypeID = case_when(
    measurementType == "BedAbund" ~ "http://vocab.nerc.ac.uk/collection/P01/current/SDBIOL",
    measurementType == "CanopyHeight" ~ "http://vocab.nerc.ac.uk/collection/P01/current/OBS",
    # measurementType == "BarePatchWithinSeagrass" ~ "",
    measurementType == "FloweringBedAbund" ~ "http://vocab.nerc.ac.uk/collection/P01/current/OBS",
  ),
  measurementUnit = case_when(
    measurementType == "BedAbund" ~ "Number per square metre",
    measurementType == "CanopyHeight" ~ "Centimetres",
    measurementType == "BarePatchhhLengthWithinSeagrass" ~ "Metres",
    measurementType == "FloweringBedAbund" ~ "Number per square metre"),
  measurementUnitID = case_when(
    measurementType == "BedAbund" ~ "http://vocab.nerc.ac.uk/collection/P06/current/UPMS/",
    measurementType == "CanopyHeight" ~ "http://vocab.nerc.ac.uk/collection/P06/current/UL",
    measurementType == "BarePatchhhLengthWithinSeagrass" ~ "http://vocab.nerc.ac.uk/collect",
    measurementType == "FloweringBedAbund" ~ "http://vocab.nerc.ac.uk/collection/P06/current/OBS",
  ),
  measurementAccuracy = case_when(
    measurementType == "CanopyHeight" ~ 5),
  measurementMethod = case_when(
    measurementType == "BedAbund" ~ "25cmx25cm quadrat count",
    measurementType == "CanopyHeight" ~ "in situ with ruler",
    measurementType == "BarePatchhhLengthWithinSeagrass" ~ "estimated along transect line",
    measurementType == "FloweringBedAbund" ~ "25cmx25cm quadrat count")) %>%
select(eventID, measurementDeterminedDate, measurementType, measurementValue,
       measurementTypeID, measurementUnit, measurementUnitID, measurementAccuracy,
       measurementMethod) %T>%
# select(!c(survey, site_id, transect_dist)) %T>%
glimpse()

```

Rows: 37,430

Columns: 9

```

$ eventID          <chr> "2017-11-22:HAKAI:CALVERT:CHOKED_PASS_INTERI~
$ measurementDeterminedDate <date> 2017-11-22, 2017-11-22, 2017-11-22, 2017-11-~
$ measurementType   <chr> "SubstrateTypeA", "SubstrateTypeB", "BarePat~
$ measurementValue  <chr> "sand", "shell hash", "< 1", "seagrass", NA,~
$ measurementTypeID <chr> NA, NA, NA, NA, NA, NA, NA, "http://vocab.ne~
$ measurementUnit   <chr> NA, NA, NA, NA, NA, NA, NA, "Number per squa~
$ measurementUnitID <chr> NA, NA, NA, NA, NA, NA, NA, "http://vocab.ne~
$ measurementAccuracy <dbl> NA, NA, NA, NA, NA, NA, NA, NA, 5, NA, NA, N~
$ measurementMethod <chr> NA, NA, NA, NA, NA, NA, NA, "25cmx25cm quadr~

```

```
# save eMoF table to csv
write.csv(seagrassMof, seagrassMof_csv)
```

4.1.3 Session Info

Print session information below in case necessary for future reference

```
# Print Session Info for future reference
sessionInfo()
```

```
R version 4.4.1 (2024-06-14)
Platform: aarch64-apple-darwin20
Running under: macOS Sonoma 14.7.5

Matrix products: default
BLAS:   /Library/Frameworks/R.framework/Versions/4.4-arm64/Resources/lib/libRblas.0.dylib
LAPACK: /Library/Frameworks/R.framework/Versions/4.4-arm64/Resources/lib/libRlapack.dylib;

locale:
 [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8

time zone: UTC
tzcode source: internal

attached base packages:
[1] stats      graphics  grDevices  utils      datasets  methods   base

other attached packages:
 [1] worrms_0.4.3   magrittr_2.0.3 lubridate_1.9.4 forcats_1.0.0
 [5] stringr_1.5.1  dplyr_1.1.4    purrr_1.0.4    readr_2.1.5
 [9] tidyr_1.3.1    tibble_3.2.1   ggplot2_3.5.2   tidyverse_2.0.0
[13] here_1.0.1     knitr_1.50

loaded via a namespace (and not attached):
 [1] gtable_0.3.6      jsonlite_2.0.0    compiler_4.4.1     Rcpp_1.0.14
 [5] tidyselect_1.2.1  urltools_1.7.3    scales_1.4.0       triebeard_0.4.1
 [9] yaml_2.3.10       fastmap_1.2.0     R6_2.6.1           generics_0.1.4
[13] curl_6.2.2        crul_1.5.0        rprojroot_2.0.4    pillar_1.10.2
[17] RColorBrewer_1.1-3 tzdb_0.5.0        rlang_1.1.6        httpcode_0.3.0
[21] stringi_1.8.7     xfun_0.52         timechange_0.3.0   cli_3.6.5
[25] withr_3.0.2       digest_0.6.37     grid_4.4.1         hms_1.1.3
```

[29]	lifecycle_1.0.4	vctrs_0.6.5	evaluate_1.0.3	glue_1.8.0
[33]	farver_2.1.2	rmarkdown_2.29	tools_4.4.1	pkgconfig_2.0.3
[37]	htmltools_0.5.8.1			

5 trawl_catch_data

5.1 Trawl Data

One of the more common datasets that can be standardized to Darwin Core and integrated within OBIS is catch data from e.g. a trawl sampling event, or a zooplankton net tow. Of special concern here are datasets that include both a total (species-specific) catch weight, in addition to individual measurements (for a subset of the overall data). In this case, through our standardization to Darwin Core, we want to ensure that data users understand that the individual measurements are a part of, or subset of, the overall (species-specific) record, whilst at the same time ensure that data providers are not duplicating occurrence records to OBIS.

The GitHub issue related to application is can be found [here](#)

5.1.1 Workflow Overview

In our current setup, this relationship between the overall catch data and subsetted information is provided in the [resourceRelationship](#) extension. This extension *cannot* currently be harvested by GBIF. The required terms for this extension are **resourceID**, **relatedResourceID**, **resourceRelationshipID** and **relationshipOfResource**. The **relatedResourceID** here refers to the *object* of the relationship, whereas the **resourceID** refers to the *subject* of the relationship:

- **resourceRelationshipID**: a unique identifier for the relationship between one resource (the subject) and another (relatedResource, object).
- **resourceID**: a unique identifier for the resource that is the subject of the relationship.
- **relatedResourceID**: a unique identifier for the resource that is the object of the relationship.
- **relationshipOfResource**: The relationship of the subject (identified by the resourceID) to the object (relatedResourceID). The relationshipOfResource is a free text field.

A few resources have been published to OBIS that contain the resourceRelationship extension (examples). Here, I'll lay out the process and coding used for the [Trawl Catch and Species Abundance from the 2019 Gulf of Alaska International Year of the Salmon Expedition](#). In the following code chunks some details are omitted to improve the readability - the overall code to standardize the catch data can be found [here](#). This dataset includes species-specific total

catch data at multiple stations (sampling events). From each catch, individual measurements were also taken. Depending on the number of individual caught in the trawl, this was either the total number of species individuals caught, or only a subset (in case of large numbers of individuals caught).

In this specific data record, we created a single Event Core with three extensions: an *occurrence* extension, *measurement or fact* extension, and the *resourceRelationship* extension. However, in this walk-through I'll only touch on the Event Core, occurrence extension and resourceRelationship extension.

The trawl data is part of a larger project collecting various data types related to salmon ocean ecology. Therefore, in our Event Core we nested information related to the sampling event in the specific layer. (include a visual representation of the schema). Prior to creating the Event Core, we ensured that e.g. dates and times followed the correct ISO-8601 standards, and converted to the correct time zone.

```
# Time is recorded numerically (1037 instead of 10:37), so need to change these columns:
trawl2019$END_DEPLOYMENT_TIME <- substr(as.POSIXct(sprintf("%04.0f", trawl2019$END_DEPLOYMENT_TIME)), 0, 10)
trawl2019$BEGIN_RETRIEVAL_TIME <- substr(as.POSIXct(sprintf("%04.0f", trawl2019$BEGIN_RETRIEVAL_TIME)), 0, 10)
# Additionally, the vessel time is recorded in 'Vladivostok' according to the metadata tab.
trawl2019 <- trawl2019 %>%
  mutate(eventDate_start = format_iso_8601(as.POSIXct(paste(EVENT_DATE_START, END_DEPLOYMENT_TIME, sep = "T",
                                                             tz = "Asia/Vladivostok"))),
         eventDate_start = str_replace(eventDate_start, "\\+00:00", "Z"),
         eventDate_finish = format_iso_8601(as.POSIXct(paste(EVENT_DATE_FINISH, BEGIN_RETRIEVAL_TIME, sep = "T",
                                                             tz = "Asia/Vladivostok"))),
         eventDate_finish = str_replace(eventDate_finish, "\\+00:00", "Z"),
         eventDate = paste(eventDate_start, eventDate_finish, sep = "/"),
         project = "IYS",
         cruise = paste(project, "GoA2019", sep = ":"),
         station = paste(cruise, TOW_NUMBER, sep = ":Stn"),
         trawl = paste(station, "trawl", sep = ":"))
```

Then we created the various layers of our Event Core. We created these layers/data frames from two separate datasets that data are pulled from - one dataset that contains the *overall* catch data, and one dataset that contains the *specimen* data:

```
trawl2019_allCatch <- read_excel(here("Trawl", "2019", "raw_data",
                                     "2019_GoA_Fish_Trawl_catchdata.xlsx"), sheet = "CATCH_1")
mutate(project = "IYS",
       cruise = paste(project, "GoA2019", sep = ":"),
       station = paste(cruise, `TOW_NUMBER (number)`, sep = ":Stn"),
       trawl = paste(station, "trawl", sep = ":"))
```

```

trawl2019_specimen <- read_excel(here("Trawl", "2019", "raw_data", "2019_GoA_Fish_Specimen_data.xlsx"),
                                sheet = "SPECIMEN_FINAL") %>%
  mutate(project = "IYS",
         cruise = paste(project, "GoA2019", sep = ":"),
         station = paste(cruise, TOW_NUMBER, sep = ":Stn"),
         trawl = paste(station, "trawl", sep = ":"),
         sample = paste(trawl, "sample", sep = ":"),
         sample = paste(sample, row_number(), sep = ""))

```

Next we created the Event Core, ensuring that we connect the data to the right layer (i.e. date and time should be connected to the layer associated with the sampling event). Please note that because we are creating multiple layers and nesting information, and then at a later stage combining different tables, this results in cells being populated with NA. These have to be removed prior to publishing the Event Core through the IPT.

```

trawl2019_project <- trawl2019 %>%
  select(eventID = project) %>%
  distinct(eventID) %>%
  mutate(type = "project")

trawl2019_cruise <- trawl2019 %>%
  select(eventID = cruise,
         parentEventID = project) %>%
  distinct(eventID, .keep_all = TRUE) %>%
  mutate(type = "cruise")

trawl2019_station <- trawl2019 %>%
  select(eventID = station,
         parentEventID = cruise) %>%
  distinct(eventID, .keep_all = TRUE) %>%
  mutate(type = "station")

# The coordinates associated to the trawl need to be presented in a LINESTRING.
# END_LONGITUDE_DD needs to be inverted (has to be between -180 and 180, inclusive).
trawl2019_coordinates <- trawl2019 %>%
  select(eventID = trawl,
         START_LATITUDE_DD,
         longitude,
         END_LATITUDE_DD,
         END_LONGITUDE_DD) %>%
  mutate(END_LONGITUDE_DD = END_LONGITUDE_DD * -1,

```

```

        footprintWKT = paste("LINESTRING (", longitude, START_LATITUDE_DD, ",",
                              END_LONGITUDE_DD, END_LATITUDE_DD, ")")
    trawl2019_linestring <- obistools::calculate_centroid(trawl2019_coordinates$footprintWKT)
    trawl2019_linestring <- cbind(trawl2019_coordinates, trawl2019_linestring) %>%
        select(eventID, footprintWKT, decimalLatitude, decimalLongitude, coordinateUncertaintyInMe

    trawl2019_trawl <- trawl2019 %>%
        select(eventID = trawl,
               parentEventID = station,
               eventDate,
               year,
               month,
               day) %>%
        mutate(minimumDepthInMeters = 0, # headrope was at the surface
               maximumDepthInMeters = trawl2019$MOUTH_OPENING_HEIGHT,
               samplingProtocol = "midwater trawl", # when available add DOI to paper here
               locality = case_when(
                   trawl2019$EVENT_SUB_TYPE == "Can EEZ" ~ "Canadian EEZ"),
               locationID = case_when(
                   trawl2019$EVENT_SUB_TYPE == "Can EEZ" ~ "http://marineregions.org/mrgid/8493")) %>%
        left_join(trawl2019_linestring, by = "eventID") %>%
        distinct(eventID, .keep_all = TRUE) %>%
        mutate(type = "midwater trawl")

    trawl2019_sample <- trawl2019_specimen %>%
        select(eventID = sample,
               parentEventID = trawl) %>%
        distinct(eventID, .keep_all = TRUE) %>%
        mutate(type = "individual sample")

    trawl2019_event <- bind_rows(trawl2019_project,
                                trawl2019_cruise,
                                trawl2019_station,
                                trawl2019_trawl,
                                trawl2019_sample)

    # Remove NAs from the Event Core:
    trawl2019_event <- sapply(trawl2019_event, as.character)
    trawl2019_event[is.na(trawl2019_event)] <- ""
    trawl2019_event <- as.data.frame(trawl2019_event)

```

TO DO: Add visual of e.g. the top 10 rows of the Event Core.

Now that we created the Event Core, we create the occurrence extension. To do this, we create two separate occurrence data tables: one that includes the occurrence data for the *total* catch, and one data table for the *specimen* data. Finally, the Occurrence extension is created by combining these two data frames. Personally, I prefer to re-order it so it makes visual sense to me (nest the specimen occurrence records under their respective overall catch data).

```

trawl2019_allCatch_worms <- worrms::wm_records_names(unique(trawl2019_allCatch$scientificname))
trawl2019_occ <- left_join(trawl2019_allCatch, trawl2019_allCatch_worms, by = "scientificname")
  rename(eventID = trawl,
         specificEpithet = species,
         scientificNameAuthorship = authority,
         taxonomicStatus = status,
         taxonRank = rank,
         scientificName = scientificname,
         scientificNameID = lsid,
         individualCount = `CATCH_COUNT (pieces)(**includes Russian expansion for some species)`,
         occurrenceRemarks = COMMENTS) %>%
  mutate(occurrenceID = paste(eventID, "occ", sep = ":"),
         occurrenceID = paste(occurrenceID, row_number(), sep = ":"),
         occurrenceStatus = "present",
         sex = "")

trawl2019_catch_ind_worms <- worrms::wm_records_names(unique(trawl2019_catch_ind$scientificname))
trawl2019_catch_ind_occ <- left_join(trawl2019_catch_ind, trawl2019_catch_ind_worms, by = "scientificname")
  rename(scientificNameAuthorship = authority,
         taxonomicStatus = status,
         taxonRank = rank,
         scientificName = scientificname,
         scientificNameID = lsid) %>%
  mutate(occurrenceID = paste(eventID, "occ", sep = ":"),
         occurrenceStatus = "present",
         individualCount = 1)

# Combine the two occurrence data frames:
trawl2019_occ_ext <- dplyr::bind_rows(trawl2019_occ_fnl, trawl2019_catch_ind_fnl)

# To re-order the occurrenceID, use following code:
order <- stringr::str_sort(trawl2019_occ_ext$occurrenceID, numeric=TRUE)
trawl2019_occ_ext <- trawl2019_occ_ext[match(order, trawl2019_occ_ext$occurrenceID),] %>%
  mutate(basisOfRecord = "HumanObservation")

```

TO DO: Add visual of e.g. the top 10 rows of the Occurrence extension.

Please note that in the *overall* species-specific occurrence data frame, *individualCount* was not included. This term should not be used for abundance studies, but to avoid confusion and the appearance that the specimen records are an additional observation on top of the overall catch record, the *individualCount* term was left blank for the overall catch data.

A resource relationship extension is created to further highlight that the individual samples in the occurrence extension are part of a larger overall catch that was also listed in the occurrence extension. In this extension, we wanted to make sure to highlight that the *specimen* occurrence records are *a subset of* the *overall* catch data through the field `relationshipOfResource1`. Each of these relationships gets a unique `resourceRelationshipID`.

```
trawl_resourceRelationship <- trawl2019_occ_ext %>%
  select(eventID, occurrenceID, scientificName) %>%
  mutate(resourceID = ifelse(grepl("sample", trawl2019_occ_ext$occurrenceID), trawl2019_occ_ext$occurrenceID, trawl2019_occ_ext$eventID)) %>%
  mutate(eventID = gsub(":sample.*", "", trawl2019_occ_ext$eventID)) %>%
  group_by(eventID, scientificName) %>%
  filter(n() != 1) %>%
  ungroup()

trawl_resourceRelationship <- trawl_resourceRelationship %>%
  mutate(relatedResourceID = ifelse(grepl("sample", trawl_resourceRelationship$occurrenceID), trawl_resourceRelationship$occurrenceID, trawl_resourceRelationship$eventID)) %>%
  mutate(relationshipOfResource = ifelse(!is.na(resourceID), "is a subset of", NA)) %>%
  dplyr::arrange(eventID, scientificName) %>%
  fill(relatedResourceID) %>%
  filter(!is.na(resourceID))

order <- stringr::str_sort(trawl_resourceRelationship$resourceID, numeric = TRUE)
trawl_resourceRelationship <- trawl_resourceRelationship[match(order, trawl_resourceRelationship$resourceID), ]

trawl_resourceRelationship <- trawl_resourceRelationship %>%
  mutate(resourceRelationshipID = paste(relatedResourceID, "rr", sep = ":"),
         ID = sprintf("%03d", row_number()),
         resourceRelationshipID = paste(resourceRelationshipID, ID, sep = ":")) %>%
  select(eventID, resourceRelationshipID, resourceID, relationshipOfResource, relatedResourceID)
```

TO DO: Add visual of e.g. the top 10 rows of the `ResourceRelationship` extension.

5.1.2 FAQ

Q1. Why not use the terms *associatedOccurrence* or *associatedTaxa*? **A.** There seems to be a movement away from the term *associatedOccurrence* as the `resourceRelationship` extension

has a much broader use case. Some issues that were raised on GitHub exemplify this, see e.g. [here](#). *associatedTaxa* is used to provide identifiers or names of taxa and the associations of an Occurrence with them. This term is not apt for establishing relationships between taxa, only between specific Occurrences of an organism with other taxa. As noted on the [TDWG website](#), [...] *Note that the ResourceRelationship class is an alternative means of representing associations, and with more detail.* See also e.g. [this issue](#).

6 dataset-edna

By [Diana LaScala-Gruenewald](#)



Figure 6.1: Binder

6.1 Introduction

Rationale:

DNA derived data are increasingly being used to document taxon occurrences. To ensure these data are useful to the broadest possible community, [GBIF](#) published a guide entitled “[Publishing DNA-derived data through biodiversity data platforms](#).” This guide is supported by the [DNA derived data extension](#) for [Darwin Core](#), which incorporates [MIXS](#) terms into the Darwin Core standard.

This use case draws on both the guide and the extension to illustrate how to incorporate a DNA derived data extension file into a Darwin Core archive.

For further information on this use case and the DNA Derived data extension in general, see the recording of the [OBIS Webinar on Genetic Data](#).

Project abstract:

The example data employed in this use case are from marine filtered seawater samples collected at a nearshore station in Monterey Bay, California, USA. They were collected by CTD rosette and filtered by a peristaltic pump system. Subsequently, they underwent metabarcoding for the 18S V9 region. The resulting ASVs, their assigned taxonomy, and the metadata associated with their collection are the input data for the conversion scripts presented here.

A selection of samples from this collection were included in the publication “[Environmental DNA reveals seasonal shifts and potential interactions in a marine community](#)” which was published with open access in *Nature Communications* in 2020.

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6.2 Published data

- [GBIF](#)
- [OBIS](#)

6.3 Repo structure

```
.
+-- README.md           :Description of this repository
+-- LICENSE             :Repository license
+-- .gitignore          :Files and directories to be ignored by git
+-- environment.yml      :Conda environment configuration file for Binder
|
+-- raw
|   +-- asv_table.csv    :Source data containing ASV sequences and number of reads
|   +-- taxa_table.csv   :Source data containing taxon matches for each ASV
|   +-- metadata_table.csv :Source data containing metadata about samples (e.g. collect
|
+-- src
|   +-- conversion_code.py :Darwin Core mapping script
|   +-- conversion_code.ipynb :Darwin Core mapping Jupyter Notebook
|   +-- WoRMS.py          :Functions for querying the World Register of Marine Species
|
+-- processed
|   +-- occurrence.csv    :Occurrence file, generated by conversion_code
|   +-- dna_extension.csv :DNA Derived Data Extension file, generated by conversion_co
```

7 Converting ATN netCDF file to Darwin Core

An R Markdown document converted from “atn_satellite_telemetry_netCDF2DwC.ipynb”

Created: 2022-03-23 Updated: 2023-11-16

Credit: Stephen Formel, Mathew Biddle

This notebook walks through downloading an example netCDF file from the an Archive package at NCEI and translating it to a Darwin Core Archive compliant package for easy loading and publishing via the Integrated Publishing Toolkit (IPT). The example file follows a specific specification for ATN satellite trajectory observations as documented [here](#). More information about the ATN netCDF specification can be found in the repository <https://github.com/ioos/ioos-atn-data>.

This example uses the [tidync](#) package to work with netCDF data.

Data used in this notebook are available from NCEI at the following link <https://www.ncei.noaa.gov/archive/accession/0282699>.

```
#Load libraries
```

```
library(tidync)
library(obistools)
library(ncdf4)
library(tidyverse) #includes stringr
```

```
-- Attaching core tidyverse packages ----- tidyverse 2.0.0 --
```

```
v dplyr      1.1.4      v readr      2.1.5
v forcats    1.0.0      v stringr    1.5.1
v ggplot2    3.5.2      v tibble     3.2.1
v lubridate  1.9.4      v tidyr      1.3.1
v purrr      1.0.4
```

```
-- Conflicts ----- tidyverse_conflicts() --
```

```
x dplyr::filter() masks stats::filter()
x dplyr::lag()     masks stats::lag()
```

```
i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become
```

```
library(lubridate)
library(maps)
```

Attaching package: 'maps'

The following object is masked from 'package:purrr':

map

```
library(mapdata)
```

7.1 Downloading and preprocessing the source data

See <https://www.ncei.noaa.gov/archive/accession/0282699>

```
# paths ----
url_nc = 'https://www.nodc.noaa.gov/archive/arc0217/0282699/1.1/data/0-data/atn_45866_great-
dir_data <- here::here("datasets/atn_satellite_telemetry/data")
file_nc <- file.path(dir_data, "src", basename(url_nc))
stopifnot(dir.exists(dir_data))

if (!file.exists(file_nc))
  download.file(url_nc, file_nc, mode = "wb")
```

7.1.1 Open the netCDF file

Once the file is opened, we print out the details of what the netCDF file contains.

```
atn <- nc_open(file_nc)
atn
```

File /Users/runner/work/bio_data_guide/bio_data_guide/datasets/atn_satellite_telemetry/data/

```
36 variables (excluding dimension variables):
  string deploy_id[]    (Contiguous storage)
    long_name: id for this deployment. This is typically the tag ptt
    comment: Friendly name given to the tag by the user. If no specific friendly name
```

```

coordinates: time z lon lat
instrument: instrument_location
platform: animal
coverage_content_type: referenceInformation
_FillValue: -9999
double time[obs]    (Contiguous storage)
units: seconds since 1990-01-01 00:00:00Z
standard_name: time
axis: T
_CoordinateAxisType: Time
calendar: standard
long_name: Time of the measurement, in seconds since 1990-01-01
actual_min: 2009-09-23T00:00:00Z
actual_max: 2009-11-23T05:12:00Z
ancillary_variables: qartod_time_flag qartod_rollup_flag qartod_speed_flag
instrument: instrument_location
platform: animal
coverage_content_type: coordinate
_FillValue: NaN
int z[obs]    (Contiguous storage)
_FillValue: -9999
axis: Z
long_name: depth of measurement
positive: down
standard_name: depth
units: m
actual_min: 0
actual_max: 0
instrument:
platform: animal
comment: This variable is synthetically generated to represent the depth of observation
coverage_content_type: coordinate
double lat[obs]    (Contiguous storage)
axis: Y
_CoordinateAxisType: Lat
long_name: Latitude portion of location in decimal degrees North
standard_name: latitude
units: degrees_north
valid_max: 90
valid_min: -90
actual_min: 23.59
actual_max: 34.045
ancillary_variables: qartod_location_flag qartod_rollup_flag qartod_speed_flag etc

```



```

    instrument: instrument_location
    platform: animal
    coverage_content_type: coordinate
    _FillValue: NaN
double lon[obs]    (Contiguous storage)
    axis: X
    _CoordinateAxisType: Lon
    long_name: Longitude portion of location in decimal degrees East
    standard_name: longitude
    units: degrees_east
    valid_max: 180
    valid_min: -180
    actual_min: -166.18
    actual_max: -118.504
    ancillary_variables: qartod_location_flag qartod_rollup_flag qartod_speed_flag et
    instrument: instrument_location
    platform: animal
    coverage_content_type: coordinate
    _FillValue: NaN
int ptt[obs]    (Chunking: [29]) (Compression: shuffle,level 1)
    _FillValue: -9999
    coordinates: time z lon lat
    long_name: Platform Transmitter Terminal (PTT) id used for Argos transmissions
    comment: PTT id for this deployment. PTT ids may be used on multiple deployments
    coverage_content_type: referenceInformation
    instrument: instrument_location
    platform: animal
string instrument[obs]    (Contiguous storage)
    coordinates: time z lon lat
    comment: Wildlife Computers instrument family. Variable may report manufacturer
    long_name: Instrument family
    instrument: instrument_location
    platform: animal
    coverage_content_type: referenceInformation
string type[obs]    (Contiguous storage)
    coordinates: time z lon lat
    comment: Type of location: Argos, FastGPS or User
    long_name: Type of location information - Argos, GPS satellite or user provided
    instrument: instrument_location
    platform: animal
    coverage_content_type: referenceInformation
string location_class[obs]    (Contiguous storage)
    coordinates: time z lon lat

```

```

standard_name: quality_flag
comment: Quality codes from the ARGOS satellite (in meters): G,3,2,1,0,A,B,Z. See
long_name: Location Quality Code from ARGOS satellite system
code_values: G,3,2,1,0,A,B,Z
code_meanings: estimated error less than 100m and 1+ messages received per satellite
instrument: instrument_location
platform: animal
ancillary_variables: lat lon
coverage_content_type: qualityInformation
int error_radius[obs] (Chunking: [29]) (Compression: shuffle,level 1)
  _FillValue: -9999
  coordinates: time z lon lat
  long_name: Error radius
  units: m
  comment: If the position is best represented as a circle, this field gives the radius
  instrument: instrument_location
  platform: animal
  ancillary_variables: lat lon offset offset_orientation
  coverage_content_type: qualityInformation
int semi_major_axis[obs] (Chunking: [29]) (Compression: shuffle,level 1)
  _FillValue: -9999
  coordinates: time z lon lat
  long_name: Error - ellipse semi-major axis
  units: m
  comment: If the estimated position error is best expressed as an ellipse, this field gives the semi-major axis
  instrument: instrument_location
  platform: animal
  ancillary_variables: lat lon ellipse_orientation offset offset_orientation
  coverage_content_type: qualityInformation
int semi_minor_axis[obs] (Chunking: [29]) (Compression: shuffle,level 1)
  _FillValue: -9999
  coordinates: time z lon lat
  long_name: Error - ellipse semi-minor axis
  units: m
  comment: If the estimated position error is best expressed as an ellipse, this field gives the semi-minor axis
  instrument: instrument_location
  platform: animal
  ancillary_variables: lat lon ellipse_orientation offset offset_orientation
  coverage_content_type: qualityInformation
int ellipse_orientation[obs] (Chunking: [29]) (Compression: shuffle,level 1)
  _FillValue: -9999
  coordinates: time z lon lat
  long_name: Error - ellipse orientation in degrees clockwise from true north

```

```

units: degrees
comment: The angle in degrees of the ellipse from true north, proceeding clockwise
instrument: instrument_location
platform: animal
ancillary_variables: lat lon semi_major_axis semi_minor_axis offset offset_orient
coverage_content_type: qualityInformation
int offset[obs]    (Chunking: [29]) (Compression: shuffle,level 1)
  _FillValue: -9999
coordinates: time z lon lat
long_name: Error - offset in meters to center of error ellipse or circle
units: m
comment: This field is non-zero if the circle or ellipse are not centered on the
instrument: instrument_location
platform: animal
ancillary_variables: lat lon error_radius semi_major_axis semi_minor_axis offset
coverage_content_type: qualityInformation
int offset_orientation[obs]  (Chunking: [29]) (Compression: shuffle,level 1)
  _FillValue: -9999
coordinates: time z lon lat
long_name: Error - offset orientation angle to ellipse center
units: degrees
comment: If the "Offset" field is non-zero, this field is the angle in degrees from
instrument: instrument_location
platform: animal
ancillary_variables: lat lon error_radius semi_major_axis semi_minor_axis offset
coverage_content_type: qualityInformation
double gpe_msd[obs]  (Chunking: [29]) (Compression: shuffle,level 1)
coordinates: time z lon lat
comment: Historical. No longer applicable.
long_name:
units:
instrument: instrument_location
platform: animal
coverage_content_type: auxiliaryInformation
_FillValue: NaN
double gpe_u[obs]    (Chunking: [29]) (Compression: shuffle,level 1)
coordinates: time z lon lat
comment: Historical. No longer applicable.
long_name:
units:
instrument: instrument_location
platform: animal
coverage_content_type: auxiliaryInformation

```

```

    _FillValue: NaN
int count[obs]    (Chunking: [29]) (Compression: shuffle,level 1)
    _FillValue: -9999
    coordinates: time z lon lat
    comment: Total number of times a particular data item was received, verified, and
    long_name: Count
    units: count
    instrument: instrument_location
    platform: animal
    coverage_content_type: auxillaryInformation
unsigned byte qartod_time_flag[obs]    (Chunking: [29]) (Compression: shuffle,level 1)
    _FillValue: 241
    coordinates: time z lon lat
    standard_name: gross_range_test_quality_flag
    long_name: Time QC test - gross range test
    implementation: https://github.com/ioos/ioos_qc/
    flag_meanings: PASS NOT_EVALUATED SUSPECT FAIL MISSING
    flag_values: 1
        flag_values: 2
        flag_values: 3
        flag_values: 4
        flag_values: 9
    references: https://cdn.ioos.noaa.gov/media/2020/03/QARTOD_TS_Manual_Update2_2003
    coverage_content_type: qualityInformation
unsigned byte qartod_speed_flag[obs]    (Chunking: [29]) (Compression: shuffle,level 1)
    _FillValue: 241
    coordinates: time z lon lat
    standard_name: gross_range_test_quality_flag
    long_name: Speed QC test - gross range test
    references: https://cdn.ioos.noaa.gov/media/2020/03/QARTOD_TS_Manual_Update2_2003
    implementation: https://github.com/ioos/ioos_qc/
    flag_meanings: PASS NOT_EVALUATED SUSPECT FAIL MISSING
    flag_values: 1
        flag_values: 2
        flag_values: 3
        flag_values: 4
        flag_values: 9
    coverage_content_type: qualityInformation
unsigned byte qartod_location_flag[obs]    (Chunking: [29]) (Compression: shuffle,level 1)
    _FillValue: 241
    coordinates: time z lon lat
    standard_name: location_test_quality_flag
    long_name: Location QC test - Location test

```

```

implementation: https://github.com/ioos/ioos_qc/
flag_meanings: PASS NOT_EVALUATED SUSPECT FAIL MISSING
flag_values: 1
             flag_values: 2
             flag_values: 3
             flag_values: 4
             flag_values: 9
references: https://cdn.ioos.noaa.gov/media/2020/03/QARTOD_TS_Manual_Update2_2003
coverage_content_type: qualityInformation
unsigned byte qartod_rollup_flag[obs]    (Chunking: [29]) (Compression: shuffle,level=1)
    _FillValue: 241
    coordinates: time z lon lat
    standard_name: aggregate_quality_flag
    long_name: Aggregate QC value
    implementation: https://github.com/ioos/ioos_qc/
    flag_meanings: PASS NOT_EVALUATED SUSPECT FAIL MISSING
    flag_values: 1
                flag_values: 2
                flag_values: 3
                flag_values: 4
                flag_values: 9
    references: https://cdn.ioos.noaa.gov/media/2020/03/QARTOD_TS_Manual_Update2_2003
    coverage_content_type: qualityInformation
int crs[]    (Contiguous storage)
    epsg_code: EPSG:4326
    grid_mapping_name: latitude_longitude
    inverse_flattening: 298.257223563
    long_name: Coordinate Reference System - http://www.opengis.net/def/crs/EPSSG/0/4326
    semi_major_axis: 6378137
    coverage_content_type: referenceInformation
string trajectory[]    (Contiguous storage)
    cf_role: trajectory_id
    long_name: trajectory identifier
int animal_age[]    (Contiguous storage)
    _FillValue: -9999
    units:
        long_name: age of the animal as measured or estimated at deployment
        coverage_content_type: referenceInformation
        animal_age: Not provided
string animal_life_stage[]    (Contiguous storage)
    animal_life_stage: juvenile
    long_name: Lifestage of the animal at time of deployment
    coverage_content_type: referenceInformation

```

```

string animal_sex[]    (Contiguous storage)
    animal_sex: male
    long_name: sex of the animal at time of tag deployment
    coverage_content_type: referenceInformation
float animal_weight[]  (Contiguous storage)
    _FillValue: NaN
    units: kg
    long_name: mass of the animal as measured or estimated at deployment
    animal_weight: Not provided
    coverage_content_type: referenceInformation
float animal_length[]  (Contiguous storage)
    _FillValue: NaN
    animal_length_type: total length
    units: cm
    animal_length: 213.0 (cm) total length
    long_name: length of the animal as measured or estimated at deployment
    coverage_content_type: referenceInformation
float animal_length_2[] (Contiguous storage)
    _FillValue: NaN
    animal_length_2_type: Not provided
    units:
    animal_length_2: Not provided
    long_name: length of the animal as measured or estimated at deployment
    coverage_content_type: referenceInformation
string animal[]        (Contiguous storage)
    rank: Species
    infraorder:
    scientificname: Carcharodon carcharias
    long_name: tagged animal id
    superdomain: Biota
    order: Lamniformes
    authority: (Linnaeus, 1758)
    kingdom: Animalia
    species: Carcharodon carcharias
    genus: Carcharodon
    megaclass:
    family: Lamnidae
    taxonRankID: 220
    class: Elasmobranchii
    cf_role: trajectory_id
    coverage_content_type: referenceInformation
    subphylum: Vertebrata
    phylum: Chordata

```

```

AphiaID: 105838
valid_name: Carcharodon carcharias
infraphylum: Gnathostomata
subclass: Neoselachii
suborder:
string instrument_tag[] (Contiguous storage)
  manufacturer: Wildlife Computers
  make_model: SPOT5
  serial_number: 07S0230
  long_name: telemetry tag applied to animal
  coverage_content_type: referenceInformation
  calibration_date: Not Provided
string instrument_location[] (Contiguous storage)
  manufacturer: Wildlife Computers
  make_model: SPOT5
  serial_number: 07S0230
  long_name: Wildlife Computers SPOT5
  location_type: argos / modeled
  comment: Location
  coverage_content_type: referenceInformation
  calibration_date: Not Provided
string taxon_name[] (Contiguous storage)
  standard_name: biological_taxon_name
  long_name: most precise taxonomic classification for the tagged animal
  coverage_content_type: referenceInformation
  source: Froese, R. and D. Pauly. Editors. (2023). FishBase. Carcharodon carcharias
  url: https://www.marinespecies.org/aphia.php?p=taxdetails&id=105838
string taxon_lsid[] (Contiguous storage)
  standard_name: biological_taxon_lsid
  long_name: Namespaced Taxon Identifier for the tagged animal
  coverage_content_type: referenceInformation
  source: Froese, R. and D. Pauly. Editors. (2023). FishBase. Carcharodon carcharias
  url: https://www.marinespecies.org/aphia.php?p=taxdetails&id=105838
string comment[obs] (Contiguous storage)
  long_name: Comment
  comment: Optional text field
  coordinates: time z lon lat
  instrument: instrument_location
  platform: animal
  coverage_content_type: auxillaryInformation

```

```

1 dimensions:
  obs Size:29 (no dimvar)

```

```

89 global attributes:
  date_created: 2023-08-16T20:00:00Z
  featureType: trajectory
  cdm_data_type: Trajectory
  Conventions: CF-1.10, ACDD-1.3, IOOS-1.2
  argos_program_number: 2414
  creator_email: chris.lowe@csulb.edu
  id: 5f0668a86321be13bc7ef628
  tag_type: SPOT5
  source: Service Argos
  acknowledgement: NOAA IOOS, Axiom Data Science, Navy ONR, NOAA NMFS, Wildlife Comput
  creator_name: Chris G. Lowe
  creator_url:
  geospatial_lat_units: degrees_north
  geospatial_lon_units: degrees_east
  infoUrl: https://portal.atn.ioos.us/#metadata/6e2ba85c-2f61-4bc5-8c2b-34d6734155ed/p
  institution: California State University Long Beach
  keywords: EARTH SCIENCE > AGRICULTURE > ANIMAL SCIENCE > ANIMAL ECOLOGY AND BEHAVIOR
  license: These data may be used and redistributed for free, but are not intended for
  metadata_link:
  naming_authority: com.wildlifecomputers
  platform_category: animal
  platform: fish
  platform_vocabulary: https://vocab.nerc.ac.uk/collection/L06/current/
  processing_level: NetCDF file created from position data obtained from Wildlife Comput
  project: Project White Shark: Juvenile Satellite Biotelemetry, 2001-2020
  publisher_email: atndata@ioos.us
  publisher_institution: US Integrated Ocean Observing System Office
  publisher_name: US Integrated Ocean Observing System (IOOS) Animal Telemetry Network
  publisher_url: https://atn.ioos.us
  publisher_country: USA
  standard_name_vocabulary: CF-v78
  vendor: Wildlife Computers
  geospatial_lat_min: 23.59
  geospatial_lat_max: 34.045
  geospatial_lon_min: -166.18
  geospatial_lon_max: -118.504
  geospatial_bbox: POLYGON ((-118.504 23.59, -118.504 34.045, -166.18 34.045, -166.18 2
  geospatial_bounds: POLYGON ((-166.18 23.59, -118.581 34.038, -118.53 34.045, -118.50
  geospatial_bounds_crs: EPSG:4326
  time_coverage_start: 2009-09-23T00:00:00Z
  time_coverage_end: 2009-11-23T05:12:00Z

```


time_coverage_duration: P61DT5H12M0S
time_coverage_resolution: P2DT2H39M43S
date_issued: 2023-08-16T20:00:00Z
date_modified: 2023-08-16T20:00:00Z
history: 2023-08-07T20:24:04Z - Created by the IOOS ATN DAC from the Wildlife Comput
summary: Wildlife Computers SPOT5 tag (ptt id 45866) deployed on a great white shark
title: Great white shark (Carcharodon carcharias) location data from a satellite tel
uuid: ff554ebf-bf4b-5a82-8a90-9c0ceb799d96
platform_name: Carcharodon carcharias
platform_id: 105838
vendor_id: 5f0668a86321be13bc7ef628
sea_name: North Pacific Ocean
arbitrary_keywords: ATN, Animal Telemetry Network, IOOS, Integrated Ocean Observing S
contributor_role_vocabulary: <https://vocab.nerc.ac.uk/collection/G04/current/>
creator_role_vocabulary: <https://vocab.nerc.ac.uk/collection/G04/current/>
creator_sector_vocabulary: <https://mmisw.org/ont/ioos/sector>
creator_type: person
date_metadata_modified: 20230816
instrument: Satellite telemetry tag
instrument_vocabulary:
keywords_vocabulary: GCMD Science Keywords v15.1
ncei_template_version: NCEI_NetCDF_Trajectory_Template_v2.0
product_version:
program: IOOS Animal Telemetry Network
publisher_type: institution
references:
animal_common_name: great white shark
animal_id: 09_13
animal_scientific_name: Carcharodon carcharias
deployment_id: 5f0668a86321be13bc7ef628
deployment_start_datetime: 2009-09-23T00:00:00Z
deployment_end_datetime: 2009-11-23T00:00:00Z
wmo_platform_code:
comment: 09_13-45866
ptt_id: 45866
deployment_start_lat: 34.03
deployment_start_lon: -118.56
contributor_name: Thomas Farrugia
contributor_email: tjfarrugia@alaska.edu
contributor_role: collaborator
contributor_institution: California State University Long Beach
contributor_url:
creator_role: principalInvestigator

```

creator_sector: academic
creator_country: USA
creator_institution: California State University Long Beach
creator_institution_url: https://www.csulb.edu/shark-lab
citation: Lowe, Chris G.; Farrugia, Thomas. (2023) great white shark (Carcharodon c

```

7.1.2 Collect all the metadata from the netCDF file.

This gathers not only the global attributes, but the variable level attributes as well. As you can see in the **variable** column the term NC_GLOBAL refers to global attributes.

```

metadata <- ncmeta::nc_atts(file_nc)
metadata

# A tibble: 381 x 4
   id name                variable value
  <int> <chr>              <chr>    <named list>
1     0 long_name        deploy_id <chr [1]>
2     1 comment          deploy_id <chr [1]>
3     2 coordinates      deploy_id <chr [1]>
4     3 instrument       deploy_id <chr [1]>
5     4 platform         deploy_id <chr [1]>
6     5 coverage_content_type deploy_id <chr [1]>
7     6 _FillValue       deploy_id <dbl [1]>
8     0 units            time      <chr [1]>
9     1 standard_name    time      <chr [1]>
10    2 axis             time      <chr [1]>
# i 371 more rows

```

7.1.3 Store the data as a tibble

Collect the data dimensioned by **time** from the netCDF file as a tibble. Then, print the first ten rows.

```

atn <- tidync(file_nc)

atn_tbl <- atn %>% hyper_tibble(force=TRUE)

head(atn_tbl, n=4)

```

```
# A tibble: 4 x 23
      time      z  lat  lon  ptt instrument type location_class error_radius
  <dbl> <int> <dbl> <dbl> <int> <chr>      <chr> <chr>          <int>
1 622512000      0 34.0 -119. 45866 SPOT      User   nan            NA
2 622708920      0 23.6 -166. 45866 SPOT      Argos   A            NA
3 622724940      0 34.0 -119. 45866 SPOT      Argos   1            NA
4 622725060      0 34.0 -119. 45866 SPOT      Argos   0            NA
# i 14 more variables: semi_major_axis <int>, semi_minor_axis <int>,
#   ellipse_orientation <int>, offset <int>, offset_orientation <int>,
#   gpe_msd <dbl>, gpe_u <dbl>, count <int>, qartod_time_flag <int>,
#   qartod_speed_flag <int>, qartod_location_flag <int>,
#   qartod_rollup_flag <int>, comment <chr>, obs <chr>
```

7.1.4 Dealing with time

Notice the data in the **time** column aren't formatted as times. We need to read the metadata associated with the time variable to understand what the units are. Below, we print a tibble of all the attributes from the **time** variable.

Notice the *units* attribute and it's value of **seconds** since 1990-01-01 00:00:00Z. We need to use that information to convert the time variable to something useful that **ggplot** can handle.

```
time_attrs <- metadata %>% dplyr::filter(variable == "time")
time_attrs
```

```
# A tibble: 13 x 4
      id name                variable value
  <int> <chr>                <chr>   <named list>
1     0 units              time     <chr [1]>
2     1 standard_name      time     <chr [1]>
3     2 axis                time     <chr [1]>
4     3 _CoordinateAxisType time     <chr [1]>
5     4 calendar            time     <chr [1]>
6     5 long_name           time     <chr [1]>
7     6 actual_min          time     <chr [1]>
8     7 actual_max          time     <chr [1]>
9     8 ancillary_variables time     <chr [1]>
10    9 instrument          time     <chr [1]>
11   10 platform            time     <chr [1]>
12   11 coverage_content_type time     <chr [1]>
13   12 _FillValue           time     <dbl [1]>
```

So, we grab the value from the `units` attribute, split the string to collect the date information, and apply that to a time conversion function `as.POSIXct`.

```
#library(stringr) - loaded with tidyverse
# grab origin date from time variable units attribute
tunit <- time_attrs %>% dplyr::filter(name == "units")
lunit <- str_split(tunit$value, ' ')[[1]]
atn_tbl$time <- as.POSIXct(atn_tbl$time, origin=lunit[3], tz="GMT")

str(atn_tbl)
```

```
tibble [29 x 23] (S3: tbl_df/tbl/data.frame)
 $ time          : POSIXct[1:29], format: "2009-09-23 00:00:00" "2009-09-25 06:42:00"
 $ z             : int [1:29] 0 0 0 0 0 0 0 0 0 0 ...
 $ lat          : num [1:29] 34 23.6 34 34 34 ...
 $ lon          : num [1:29] -119 -166 -119 -119 -119 ...
 $ ptt          : int [1:29] 45866 45866 45866 45866 45866 45866 45866 45866 45866 45866 45866 ...
 $ instrument    : chr [1:29] "SPOT" "SPOT" "SPOT" "SPOT" ...
 $ type         : chr [1:29] "User" "Argos" "Argos" "Argos" ...
 $ location_class : chr [1:29] "nan" "A" "1" "0" ...
 $ error_radius  : int [1:29] NA NA NA NA NA NA NA NA NA NA ...
 $ semi_major_axis : int [1:29] NA NA NA NA NA NA NA NA NA NA ...
 $ semi_minor_axis : int [1:29] NA NA NA NA NA NA NA NA NA NA ...
 $ ellipse_orientation : int [1:29] NA NA NA NA NA NA NA NA NA NA ...
 $ offset        : int [1:29] NA NA NA NA NA NA NA NA NA NA ...
 $ offset_orientation : int [1:29] NA NA NA NA NA NA NA NA NA NA ...
 $ gpe_msd       : num [1:29] NaN NaN NaN NaN NaN NaN NaN NaN NaN NaN ...
 $ gpe_u         : num [1:29] NaN NaN NaN NaN NaN NaN NaN NaN NaN NaN ...
 $ count         : int [1:29] NA NA NA NA NA NA NA NA NA NA ...
 $ qartod_time_flag : int [1:29] 1 1 1 1 1 1 1 1 1 1 ...
 $ qartod_speed_flag : int [1:29] 2 4 4 4 1 1 1 1 1 1 ...
 $ qartod_location_flag : int [1:29] 1 1 1 1 1 1 1 1 1 1 ...
 $ qartod_rollup_flag : int [1:29] 1 4 4 4 1 1 1 1 1 1 ...
 $ comment       : chr [1:29] "" "" "" "" ...
 $ obs           : chr [1:29] "1" "2" "3" "4" ...
```

7.2 Converting to Darwin Core

Now let's work through converting this netCDF file to Darwin Core. Following the guidance published at <https://github.com/tdwg/dwc-for-biologging/wiki/Data-guidelines>

and https://github.com/ocean-tracking-network/biologging_standardization/tree/master/examples/braun-blueshark/darwincore-example

7.2.1 Occurrence Core

Below is the mapping table from DarwinCore to the netCDF file.

DarwinCore Term	Status	netCDF source
occurrenceStatus	Required	hardcoded to present .
basisOfRecord	Required	data contained in the type variable where type of User = HumanObservation and Argos = MachineObservation .
occurrenceID	Required	eventDate , plus data contained in z variable, plus animal_common_name global attribute.
organismID	Required	platform_id global attribute plus the animal_common_name global attribute.
eventDate	Required	data contained in time variable. Converted to ISO8601.
decimalLatitude & decimalLongitude	Required	data in lat and lon variable, respectively.
geodeticDatum	Required	attribute epsg_code in the crs variable.
scientificName	Required	data from the variable taxon_name .
scientificNameID		data from the variable taxon_lsid .
eventID	Strongly recommended	animal_common_name global attribute plus the eventDate .
samplingProtocol	Strongly recommended	
kingdom	Strongly recommended	kingdom attribute in the animal variable.
taxonRank	Strongly recommended	rank attribute in the animal variable.
coordinateUncertaintyInMeters	Share if available	maximum value of the data from the variables error_radius , semi_major_axis , and offset .

DarwinCore Term	Status	netCDF source
lifeStage	Share if available	data from the variable <code>animal_life_stage</code> .
sex	Share if available	data from the variable <code>animal_sex</code> .

Now start working through the crosswalk. A few thoughts about some of the functions we use:

1. `case_when` is a [function from dplyr](#) that is essentially a ‘vectorized’ ifelse function. The take-home is that it plays nice with other `tidyverse` functions, like `mutate` and IMO is a bit more readable than a complex ifelse statement.
2. `rename` is another nice `dplyr` function for renaming columns. It works well following `mutate` because you can see the mutation applied to a column and then the column renamed, rather than a complex creation of a new column and dropping of the old column.

```
# Defined to grab attributes in subsequent code
nc <- nc_open(file_nc)

occurrencedf <- atn_tbl %>%
  select( # Select desired columns

    time,
    lat,
    lon,
    type,
    location_class,
    qartod_time_flag,
    qartod_speed_flag,
    qartod_location_flag,
    qartod_rollup_flag

    ) %>%
  mutate( # add and mutate columns.

    type = case_when(type == 'User' ~ 'HumanObservation',
                      type == 'Argos' ~ 'MachineObservation'),

    time = format(time, '%Y-%m-%dT%H:%M:%SZ'),
```

```

kingdom = metadata %>% dplyr::filter(variable == "animal" & name == "kingdom") %>% pull(kingdom)

taxonRank = metadata %>% dplyr::filter(variable == "animal" & name == "rank") %>% pull(taxonRank)

occurrenceStatus = "present",

sex = ncvar_get( nc, 'animal_sex'),

lifeStage = ncvar_get( nc, 'animal_life_stage'),

scientificName = ncvar_get( nc, 'taxon_name'),

scientificNameID = ncvar_get( nc, "taxon_lsid")

) %>%

rename( # rename columns to Darwin Core terms

  basisOfRecord = type,
  eventDate = time,
  decimalLatitude = lat,
  decimalLongitude = lon) %>%

  arrange(eventDate) #arrange by increasing date

# minimumDepthInMeters = z,
occurrencedf$minimumDepthInMeters = atn_tbl$z

# maximumDepthInMeters = z,
occurrencedf$maximumDepthInMeters = atn_tbl$z

# organismID - {platformID}_{common_name}
common_name_tbl <- metadata %>% dplyr::filter(variable == "NC_GLOBAL") %>% dplyr::filter(name == "common_name")
common_name <- chartr(" ", "_", common_name_tbl$value)
platform_id_tbl <- metadata %>% dplyr::filter(variable == "NC_GLOBAL") %>% dplyr::filter(name == "platform_id")
platform_id <- chartr(" ", "_", platform_id_tbl$value)
occurrencedf$organismID <- paste(platform_id , common_name, sep = "_")

# occurrenceID - {eventDate}_{depth}_{common_name}
occurrencedf$occurrenceID <- sub(" ", "_", paste(occurrencedf$eventDate, atn_tbl$z, common_name))

# geodeticDatum

```

```
gd_tbl <- metadata %>% dplyr::filter(variable == "crs") %>% dplyr::filter(name == "epsg_code")
occurrencedf$geodeticDatum <- paste(gd_tbl$value)

# eventID
#eventID - {common_name}_{dateTime}
cname = metadata %>% dplyr::filter(variable == "NC_GLOBAL") %>% dplyr::filter(name == "animal")
occurrencedf$eventID <- sub(" ", "_", paste0(cname$value, "_", occurrencedf$eventDate))

str(occurrencedf)
```

```
tibble [29 x 22] (S3: tbl_df/tbl/data.frame)
 $ eventDate      : chr [1:29] "2009-09-23T00:00:00Z" "2009-09-25T06:42:00Z" "2009-09-25T06:42:00Z" ...
 $ decimalLatitude : num [1:29] 34 23.6 34 34 34 ...
 $ decimalLongitude : num [1:29] -119 -166 -119 -119 -119 ...
 $ basisOfRecord   : chr [1:29] "HumanObservation" "MachineObservation" "MachineObservation" ...
 $ location_class  : chr [1:29] "nan" "A" "1" "0" ...
 $ qartod_time_flag : int [1:29] 1 1 1 1 1 1 1 1 1 1 ...
 $ qartod_speed_flag : int [1:29] 2 4 4 4 1 1 1 1 1 1 ...
 $ qartod_location_flag : int [1:29] 1 1 1 1 1 1 1 1 1 1 ...
 $ qartod_rollup_flag : int [1:29] 1 4 4 4 1 1 1 1 1 1 ...
 $ kingdom         : chr [1:29] "Animalia" "Animalia" "Animalia" "Animalia" ...
 $ taxonRank       : chr [1:29] "Species" "Species" "Species" "Species" ...
 $ occurrenceStatus : chr [1:29] "present" "present" "present" "present" ...
 $ sex            : chr [1:29] "male" "male" "male" "male" ...
 $ lifeStage       : chr [1:29] "juvenile" "juvenile" "juvenile" "juvenile" ...
 $ scientificName   : chr [1:29] "Carcharodon carcharias" "Carcharodon carcharias" "Carcharodon carcharias" ...
 $ scientificNameID : chr [1:29] "urn:lsid:marinespecies.org:taxname:105838" "urn:lsid:marinespecies.org:taxname:105838" ...
 $ minimumDepthInMeters : int [1:29] 0 0 0 0 0 0 0 0 0 0 ...
 $ maximumDepthInMeters : int [1:29] 0 0 0 0 0 0 0 0 0 0 ...
 $ organismID      : chr [1:29] "105838_great_white_shark" "105838_great_white_shark" "105838_great_white_shark" ...
 $ occurrenceID     : chr [1:29] "2009-09-23T00:00:00Z_0_great_white_shark" "2009-09-25T06:42:00Z_0_great_white_shark" ...
 $ geodeticDatum    : chr [1:29] "EPSG:4326" "EPSG:4326" "EPSG:4326" "EPSG:4326" ...
 $ eventID         : chr [1:29] "great_white shark_2009-09-23T00:00:00Z" "great_white shark_2009-09-25T06:42:00Z" ...
```

7.2.1.1 Add coordinateUncertaintyInMeters AND filter by location_class

When we add coordinateUncertaintyInMeters we are also filtering out where location_class == A,B,or Z.

In these data we also have additional information about the Location Quality Code from ARGOS satellite system. Below are the codes and those meanings.

code_values	code meanings
G	estimated error less than 100m and 1+ messages received per satellite pass
3	estimated error less than 250m and 4+ messages received per satellite pass
2	estimated error between 250m and 500m and 4+ messages per satellite pass
1	estimated error between 500m and 1500m and 4+ messages per satellite pass
0	estimated error greater than 1500m and 4+ messages received per satellite pass
A	no least squares estimated error or unbounded kalman filter estimated error and 3 messages received per satellite pass
B	no least squares estimated error or unbounded kalman filter estimated error and 1 or 2 messages received per satellite pass
Z	invalid location (available for Service Plus or Auxilliary Location Processing)

Since codes A, B, and Z are essentially bad values, I propose that we filter those out.

Also, create a mapping table for `coordinateUncertaintyInMeters` that corresponds to the ARGOS code maximum error as shown in the table below:

code	coordinateUncertaintyInMeters
G	100
3	250
2	500
1	1500
0	10000 (ref)

Below we create a lookup table for the `location_class` values we agree are good, which contains the `coordinateUncertaintyInMeters` for the appropriate location class. When we merge that table with our raw data, the observations that don't match the `location_classes` in our lookup table will not be transferred over (ie. they will be filtered out).

```
occurrencedf <- occurrencedf %>%
  filter(location_class %in% c('nan','G','3','2','1','0')) %>%
  mutate( # This returns NA for any other values than those defined below
```

```

coordinateUncertaintyInMeters = case_when(location_class == 'nan' ~ 0,
                                           location_class == 'G' ~ 200,
                                           location_class == '3' ~ 250,
                                           location_class == '2' ~ 500,
                                           location_class == '1' ~ 1500,
                                           location_class == '0' ~ 10000) # https://
) %>%
arrange(eventDate) # arrange by increasing date

occurrencedf

```

```

# A tibble: 19 x 23
  eventDate      decimalLatitude decimalLongitude basisOfRecord location_class
<chr>          <dbl>          <dbl> <chr>          <chr>
1 2009-09-23T00:~      34.0          -119. HumanObserva~ nan
2 2009-09-25T11:~      34.0          -119. MachineObser~ 1
3 2009-09-25T11:~      34.0          -119. MachineObser~ 0
4 2009-09-27T17:~      34.0          -119. MachineObser~ 1
5 2009-10-08T20:~      34.0          -119. MachineObser~ 2
6 2009-10-15T11:~      34.0          -119. MachineObser~ 0
7 2009-10-17T06:~      34.0          -119. MachineObser~ 0
8 2009-10-17T09:~      34.0          -119. MachineObser~ 2
9 2009-10-17T10:~      34.0          -119. MachineObser~ 3
10 2009-10-18T08:~      34.0          -119. MachineObser~ 1
11 2009-10-18T10:~      34.0          -119. MachineObser~ 2
12 2009-10-18T11:~      34.0          -119. MachineObser~ 0
13 2009-10-23T23:~      34.0          -119. MachineObser~ 2
14 2009-10-24T00:~      34.0          -119. MachineObser~ 0
15 2009-10-26T10:~      34.0          -119. MachineObser~ 3
16 2009-10-27T16:~      34.0          -119. MachineObser~ 1
17 2009-10-27T16:~      34.0          -119. MachineObser~ 2
18 2009-10-29T11:~      34.0          -119. MachineObser~ 2
19 2009-10-31T21:~      34.0          -119. MachineObser~ 0
# i 18 more variables: qartod_time_flag <int>, qartod_speed_flag <int>,
#   qartod_location_flag <int>, qartod_rollup_flag <int>, kingdom <chr>,
#   taxonRank <chr>, occurrenceStatus <chr>, sex <chr>, lifeStage <chr>,
#   scientificName <chr>, scientificNameID <chr>, minimumDepthInMeters <int>,
#   maximumDepthInMeters <int>, organismID <chr>, occurrenceID <chr>,
#   geodeticDatum <chr>, eventID <chr>, coordinateUncertaintyInMeters <dbl>

```

Notice how we went from 29 rows down to 19 rows by only selecting specific the loca-

tion_class.

7.2.2 Create a dataGeneralizations column to describe how many duplicates were found for each deprecation series

Add a dataGeneralizations column containing a string like ‘first of # records’ to indicate there are more records in the raw dataset to be discovered by the super-curious.

The dataGeneralizations string is compiled by counting the number of consecutive duplicates and inserting that into a standard string. That string is “first of [n] records” which will make more sense once we’ve filtered down to keep the first occurrence of the hour.

The next step below this, we filter out only the first observation of the hour.

```
# sort by date
occurrencedf <- occurrencedf %>% arrange(eventDate)

occurrencedf <- occurrencedf %>%
  mutate(eventDateHrs = format(as.POSIXct(eventDate, format="%Y-%m-%dT%H:%M:%SZ"), "%Y-%m-%d %H:%M"),
         ) %>%
  add_count(eventDateHrs) %>%
  mutate(dataGeneralizations = case_when(n == 1 ~ "",
                                         TRUE ~ paste("first of ", n, "records")
                                         )
         ) %>%
  select(-n)

occurrencedf
```

A tibble: 19 x 25

	eventDate	decimallLatitude	decimallLongitude	basisOfRecord	location_class
	<chr>	<dbl>	<dbl>	<chr>	<chr>
1	2009-09-23T00:~	34.0	-119.	HumanObserva~	nan
2	2009-09-25T11:~	34.0	-119.	MachineObser~	1
3	2009-09-25T11:~	34.0	-119.	MachineObser~	0
4	2009-09-27T17:~	34.0	-119.	MachineObser~	1
5	2009-10-08T20:~	34.0	-119.	MachineObser~	2
6	2009-10-15T11:~	34.0	-119.	MachineObser~	0
7	2009-10-17T06:~	34.0	-119.	MachineObser~	0
8	2009-10-17T09:~	34.0	-119.	MachineObser~	2
9	2009-10-17T10:~	34.0	-119.	MachineObser~	3
10	2009-10-18T08:~	34.0	-119.	MachineObser~	1

```

11 2009-10-18T10::~ 34.0 -119. MachineObser~ 2
12 2009-10-18T11::~ 34.0 -119. MachineObser~ 0
13 2009-10-23T23::~ 34.0 -119. MachineObser~ 2
14 2009-10-24T00::~ 34.0 -119. MachineObser~ 0
15 2009-10-26T10::~ 34.0 -119. MachineObser~ 3
16 2009-10-27T16::~ 34.0 -119. MachineObser~ 1
17 2009-10-27T16::~ 34.0 -119. MachineObser~ 2
18 2009-10-29T11::~ 34.0 -119. MachineObser~ 2
19 2009-10-31T21::~ 34.0 -119. MachineObser~ 0
# i 20 more variables: qartod_time_flag <int>, qartod_speed_flag <int>,
# qartod_location_flag <int>, qartod_rollup_flag <int>, kingdom <chr>,
# taxonRank <chr>, occurrenceStatus <chr>, sex <chr>, lifeStage <chr>,
# scientificName <chr>, scientificNameID <chr>, minimumDepthInMeters <int>,
# maximumDepthInMeters <int>, organismID <chr>, occurrenceID <chr>,
# geodeticDatum <chr>, eventID <chr>, coordinateUncertaintyInMeters <dbl>,
# eventDateHrs <chr>, dataGeneralizations <chr>

```

7.2.2.0.1 Decimate occurrences down to the first detection/location per hour

Here we've done the decimation in Python: <https://gist.github.com/MathewBiddle/d434ac2b538b2728aa80c6a7945f94be>

Essentially we build a new column that is the date plus the two digit hour. Then we find where that column has duplicates and keep the first entry.

In R, we do something slightly different as we only keep the distinct (ie. unique) rows and if there are duplicates, pick the first row of the duplicate.

```

# sort by date
occurrencedf_dec <- occurrencedf %>% arrange(eventDate)

# filter table to only unique date + hour and pick the first row.
occurrencedf_dec <- distinct(occurrencedf_dec,eventDateHrs,.keep_all = TRUE) %>%
  select(-eventDateHrs)

occurrencedf_dec

```

```

# A tibble: 17 x 24
  eventDate      decimalLatitude decimalLongitude basisOfRecord location_class
  <chr>          <dbl>          <dbl> <chr>          <chr>
1 2009-09-23T00::~ 34.0          -119. HumanObserva~ nan
2 2009-09-25T11::~ 34.0          -119. MachineObser~ 1
3 2009-09-27T17::~ 34.0          -119. MachineObser~ 1

```

```

4 2009-10-08T20::~ 34.0 -119. MachineObser~ 2
5 2009-10-15T11::~ 34.0 -119. MachineObser~ 0
6 2009-10-17T06::~ 34.0 -119. MachineObser~ 0
7 2009-10-17T09::~ 34.0 -119. MachineObser~ 2
8 2009-10-17T10::~ 34.0 -119. MachineObser~ 3
9 2009-10-18T08::~ 34.0 -119. MachineObser~ 1
10 2009-10-18T10::~ 34.0 -119. MachineObser~ 2
11 2009-10-18T11::~ 34.0 -119. MachineObser~ 0
12 2009-10-23T23::~ 34.0 -119. MachineObser~ 2
13 2009-10-24T00::~ 34.0 -119. MachineObser~ 0
14 2009-10-26T10::~ 34.0 -119. MachineObser~ 3
15 2009-10-27T16::~ 34.0 -119. MachineObser~ 1
16 2009-10-29T11::~ 34.0 -119. MachineObser~ 2
17 2009-10-31T21::~ 34.0 -119. MachineObser~ 0
# i 19 more variables: qartod_time_flag <int>, qartod_speed_flag <int>,
#   qartod_location_flag <int>, qartod_rollup_flag <int>, kingdom <chr>,
#   taxonRank <chr>, occurrenceStatus <chr>, sex <chr>, lifeStage <chr>,
#   scientificName <chr>, scientificNameID <chr>, minimumDepthInMeters <int>,
#   maximumDepthInMeters <int>, organismID <chr>, occurrenceID <chr>,
#   geodeticDatum <chr>, eventID <chr>, coordinateUncertaintyInMeters <dbl>,
#   dataGeneralizations <chr>

```

Notice that we have gone from 19 rows to 17 rows. Removing rows observed on 2009-09-25T11:11:00Z and 2009-10-27T16:22:00Z as they were the second points within that specific hour.

7.2.2.0.2 Filter on QARTOD flags?

We also have QARTOD flags and they are as follows:

value	meaning
1	PASS
2	NOT_EVALUATED
3	SUSPECT
4	FAIL
9	MISSING

The QARTOD tests are:

variable	long_name
qartod_time_flag	Time QC test - gross range test
qartod_speed_flag	Speed QC test - gross range test
qartod_location_flag	Location QC test - Location test
qartod_rollup_flag	Aggregate QC value

I'm not sure what to do here. My preference would be to include all rows where `qartod_rollup_flag == 1` and drop the rest. But I'm open to suggestions.

```
# perform filter but don't save it.
```

```
filter(occurrencedf_dec, qartod_rollup_flag == 1)
```

```
# A tibble: 16 x 24
```

```
  eventDate      decimalLatitude decimalLongitude basisOfRecord location_class
  <chr>          <dbl>             <dbl> <chr>          <chr>
1 2009-09-23T00:~ 34.0             -119. HumanObserva~ nan
2 2009-09-27T17:~ 34.0             -119. MachineObser~ 1
3 2009-10-08T20:~ 34.0             -119. MachineObser~ 2
4 2009-10-15T11:~ 34.0             -119. MachineObser~ 0
5 2009-10-17T06:~ 34.0             -119. MachineObser~ 0
6 2009-10-17T09:~ 34.0             -119. MachineObser~ 2
7 2009-10-17T10:~ 34.0             -119. MachineObser~ 3
8 2009-10-18T08:~ 34.0             -119. MachineObser~ 1
9 2009-10-18T10:~ 34.0             -119. MachineObser~ 2
10 2009-10-18T11:~ 34.0             -119. MachineObser~ 0
11 2009-10-23T23:~ 34.0             -119. MachineObser~ 2
12 2009-10-24T00:~ 34.0             -119. MachineObser~ 0
13 2009-10-26T10:~ 34.0             -119. MachineObser~ 3
14 2009-10-27T16:~ 34.0             -119. MachineObser~ 1
15 2009-10-29T11:~ 34.0             -119. MachineObser~ 2
16 2009-10-31T21:~ 34.0             -119. MachineObser~ 0
```

```
# i 19 more variables: qartod_time_flag <int>, qartod_speed_flag <int>,
#   qartod_location_flag <int>, qartod_rollup_flag <int>, kingdom <chr>,
#   taxonRank <chr>, occurrenceStatus <chr>, sex <chr>, lifeStage <chr>,
#   scientificName <chr>, scientificNameID <chr>, minimumDepthInMeters <int>,
#   maximumDepthInMeters <int>, organismID <chr>, occurrenceID <chr>,
#   geodeticDatum <chr>, eventID <chr>, coordinateUncertaintyInMeters <dbl>,
#   dataGeneralizations <chr>
```

Drop the quality flag columns to align with DarwinCore standard.

```

occurrencedf_dec <- occurrencedf_dec %>%
  select(
    -c(location_class,
        qartod_time_flag,
        qartod_speed_flag,
        qartod_location_flag,
        qartod_rollup_flag
    ))

names(occurrencedf_dec)

```

```

[1] "eventDate"           "decimalLatitude"
[3] "decimalLongitude"    "basisOfRecord"
[5] "kingdom"             "taxonRank"
[7] "occurrenceStatus"    "sex"
[9] "lifeStage"           "scientificName"
[11] "scientificNameID"    "minimumDepthInMeters"
[13] "maximumDepthInMeters" "organismID"
[15] "occurrenceID"        "geodeticDatum"
[17] "eventID"             "coordinateUncertaintyInMeters"
[19] "dataGeneralizations"

```

7.2.2.0.3 Write decimated occurrence file as csv

```

tag_id <- metadata %>% dplyr::filter(variable == "NC_GLOBAL" & name == "ptt_id")

occurrencedf_dec_csv <- glue::glue("{dir_data}/dwc/atn_{tag_id$value}_occurrence.csv")

write.csv(occurrencedf_dec, file=occurrencedf_dec_csv, row.names=FALSE, fileEncoding="UTF-8")

```

7.2.2.1 Measurement or Fact

Since we do have any additional observations, we can create a measurement or fact file to include those data. Might be worthwhile to include tag/device metadata, some of the animal measurements, and the detachment information. Each term should have a definition URI.

The measurementOrFact file will only contain information referencing the `basisOfRecord = HumanObservation` as these observations were made when the animal was directly tagged, in person (ie. when `basisOfRecord == HumanObservation`).

DarwinCore Term	Status	netCDF
organismID		The <code>platform_id</code> global attribute plus the <code>animal_common_name</code> global attribute.
occurrenceID	Required	<code>eventDate</code> , plus data contained in <code>z</code> variable, plus <code>animal_common_name</code> global attribute.
measurementType	Required	<code>long_name</code> attribute of the <code>animal_weight</code> , <code>animal_length</code> , <code>animal_length_2</code> variables.
measurementValue	Required	The data from the <code>animal_weight</code> , <code>animal_length</code> , <code>animal_length_2</code> variables.
eventID	Strongly Recommended	<code>animal_common_name</code> global attribute plus the <code>eventDate</code> .
measurementUnit	Strongly Recommended	<code>unit</code> attribute of the <code>animal_weight</code> , <code>animal_length</code> , <code>animal_length_2</code> variables.
measurementMethod	Strongly Recommended	<code>animal_weight</code> , <code>animal_length</code> , <code>animal_length_2</code> attributes of their respective variables.
measurementTypeID	Strongly Recommended	mapping table somewhere?
measurementMethodID	Strongly Recommended	mapping table somewhere?

DarwinCore Term	Status	netCDF
measurementUnitID	Strongly Recommended	mapping table somewhere?
measurementAccuracy	Share if available	
measurementDeterminedDate	Share if available	
measurementDeterminedBy	Share if available	
measurementRemarks	Share if available	
measurementValueID	Share if available	

7.2.2.1.1 Extracting variables for Extended Measurement Or Fact (eMOF)

Here there are two approaches to transforming a variable to the eMOF Darwin Core extension. The goal is to collapse the measurement name, value, unit, related identifiers and remarks into a generalized long format that can be linked to occurrences and events. For more info see:

1. [The OBIS manual](#)
2. The [Marine Biological Data Mobilization Workshop 2023](#) (SF:Not sure if it's cool to reference the workshop like this)

The first several lines of the below code show an example of pulling out the variable attributes and individually mapping them to the eMOF terms. However, this can be done more efficiently (although less readable) via this chunk of code:

```
# Supply vector of variable names
c("animal_length",
  "animal_length_2",
  "animal_weight") %>%

  # Create a named list of the variable attributes and convert it into a data frame, for
  purrr::map_df(function(x) {
    0list(measurementValue = ncvar_get( nc, x),
          measurementType = ncatt_get( nc, x)$long_name,
          measurementUnit = ncatt_get( nc, x)$units,
          measurementMethod = ncatt_get( nc, x)[[paste0(x, '_type')]])
  })

# # Measurement or Fact extension
# # Need to find the occurrence where basisOfRecord == HumanObservation, then pull the organ

emof_data <- #var_names %>%
  #filter(str_starts(name, pattern = "animal_[lw]e")) %>% #example using regex to parse name
```

```

#   pull(name) %>%

# Example using vector of variables
c("animal_length",
  "animal_length_2",
  "animal_weight") %>%
purrr::map_df(function(x) {
  list(measurementValue = ncvar_get( nc, x),
        measurementType = ncatt_get( nc, x)$long_name,
        measurementUnit = ncatt_get( nc, x)$units,
        measurementMethod = ncatt_get( nc, x)[[paste0(x, '_type')]])
}) %>%

filter(measurementValue != "NaN")

emofdf <- occurredcdf %>%
  filter(basisOfRecord == 'HumanObservation') %>%
  select(organismID, eventID, occurrenceID) %>%
  cbind(emof_data)

str(emofdf)

```

```

'data.frame':   1 obs. of  7 variables:
 $ organismID      : chr "105838_great_white_shark"
 $ eventID         : chr "great_white_shark_2009-09-23T00:00:00Z"
 $ occurrenceID    : chr "2009-09-23T00:00:00Z_0_great_white_shark"
 $ measurementValue : num 213
 $ measurementType  : chr "length of the animal as measured or estimated at deployment"
 $ measurementUnit  : chr "cm"
 $ measurementMethod: chr "total length"

```

7.2.2.1.2 Write emof file as csv

```

tag_id <- metadata %>% dplyr::filter(variable == "NC_GLOBAL") %>% dplyr::filter(name == "ptt.

emof_csv <- glue::glue("{dir_data}/dwc/atn_{tag_id$value}_emof.csv")

write.csv(emofdf, file=emof_csv, row.names=FALSE, fileEncoding="UTF-8", quote=TRUE, na="")

```

7.2.2.2 Metadata creation

Now that we know our data are aligned to Darwin Core, we can start collecting metadata. Using the R package [EML](#) we can create the EML metadata to associate with the data above.

Some good sources to help identify what requirements we need in the EML metadata can be found at:

- <https://github.com/gbif/ipt/wiki/GMPHowToGuide>
- <https://github.com/gbif/ipt/wiki/GMPHowToGuide#dataset-resource>

```
# library(EML)
```

The first thing we need to do is collect all of the relevant pieces of metadata for our EML record.

```
# me <- list(individualName = list(givenName = "Matt", surName = "Biddle"))

# my_eml <- list(dataset = list(

#           title = "A Minimal Valid EML Dataset",

#           creator = me,

#           contact = me

#         )

#       )
```

```
# geographicDescription <- metadata %>% dplyr::filter(variable == "NC_GLOBAL") %>% dplyr::fi
# west <- metadata %>% dplyr::filter(variable == "NC_GLOBAL") %>% dplyr::filter(name == "geos
# east <- metadata %>% dplyr::filter(variable == "NC_GLOBAL") %>% dplyr::filter(name == "geos
# north <- metadata %>% dplyr::filter(variable == "NC_GLOBAL") %>% dplyr::filter(name == "geos
# south <- metadata %>% dplyr::filter(variable == "NC_GLOBAL") %>% dplyr::filter(name == "geos
# altitudeMin <- metadata %>% dplyr::filter(variable == "NC_GLOBAL") %>% dplyr::filter(name == "geos
```

```

# altitudeMax <- metadata %>% dplyr::filter(variable == "NC_GLOBAL") %>% dplyr::filter(name =
# altitudeUnits <- metadata %>% dplyr::filter(variable == "NC_GLOBAL") %>% dplyr::filter(name

# coverage <-
#   set_coverage(begin = format(min(atn_tbl$time), '%Y-%m-%d'), end = format(max(atn_tbl$time),
#
#       sci_names = RNetCDF::var.get.nc(RNetCDF::open.nc("atn_trajectory_template.nc"),
#
#       geographicDescription = paste(geographicDescription$value),
#
#       west = paste(west$value),
#
#       east = paste(east$value) ,
#
#       north = paste(north$value) ,
#
#       south = paste(south$value) ,
#
#       altitudeMin = paste(altitudeMin$value),
#
#       altitudeMaximum = paste(altitudeMax$value),
#
#       altitudeUnits = ifelse (paste(altitudeUnits$value) == 'm', "meter", "?"))

# creator_name <- metadata %>% dplyr::filter(variable == "NC_GLOBAL") %>% dplyr::filter(name
# creator_email <- metadata %>% dplyr::filter(variable == "NC_GLOBAL") %>% dplyr::filter(name
# creator_sector <- metadata %>% dplyr::filter(variable == "NC_GLOBAL") %>% dplyr::filter(name
# creator <- eml$creator(
#
#   eml$individualName(
#
#       givenName = paste(creator_name$value),
#
#       surName = paste(creator_name$value)
#
#   ),

```

```

#           position = paste(creator_sector$value),
#           electronicMailAddress = paste(creator_email$value)
#       )

# #contact_name = metadata %>% dplyr::filter(variable == "NC_GLOBAL") %>% dplyr::filter(name
# contact <- eml$contact(
#
#     eml$individualName(
#
#         givenName = paste(creator_name$value),
#         surName = paste(creator_name$value)),
#         position = paste(creator_sector$value),
#         electronicMailAddress = paste(creator_email$value)
#     )

# #metadata_name
# metadataProvider <- eml$metadataProvider(
#
#     eml$individualName(
#
#         givenName = paste(creator_name$value),
#         surName = paste(creator_name$value)),
#         position = paste(creator_sector$value),
#         electronicMailAddress = paste(creator_email$value)
#     )

# ## these are the entries in contributor, need to iterate since comma separated list.
# contrib_name <- metadata %>% dplyr::filter(variable == "NC_GLOBAL") %>% dplyr::filter(name

```

```

# contrib_position <- metadata %>% dplyr::filter(variable == "NC_GLOBAL") %>% dplyr::filter(
# contrib_email <- metadata %>% dplyr::filter(variable == "NC_GLOBAL") %>% dplyr::filter(name

# associatedParty <- eml$associatedParty(
#
#     eml$individualName(
#
#         givenName = paste(contrib_name$value),
#
#         surName = paste(contrib_name$value)),
#
#         position = paste(contrib_position$value),
#
#         electronicMailAddress = paste(contrib_email$value)
#
#     )

# abstract <- metadata %>% dplyr::filter(variable == "NC_GLOBAL") %>% dplyr::filter(name ==

# # keywords

# keywords <- metadata %>% dplyr::filter(variable == "NC_GLOBAL") %>% dplyr::filter(name ==
# kw_vocab <- metadata %>% dplyr::filter(variable == "NC_GLOBAL") %>% dplyr::filter(name ==
# keywordSet <- list(
#
#     list(
#
#         keywordThesaurus = kw_vocab$value$keywords_vocabulary,
#
#         keyword = as.list(strsplit(keywords$value$keywords, ", "))
#
#     ))

# title <- metadata %>% dplyr::filter(variable == "NC_GLOBAL") %>% dplyr::filter(name == "ti

# methods <- "NEED TO MAP FROM NCFILE"

```

```
# license <- metadata %>% dplyr::filter(variable == "NC_GLOBAL") %>% dplyr::filter(name == ")
```

Now build the eml file.

```
# library(uuid)

# physical <- set_physical(file_name_occur)

# # attributeList <-
# #   set_attributes(attributes,
# #                 factors,
# #                 col_classes = c("character",
# #                               "Date",
# #                               "Date",
# #                               "Date",
# #                               "factor",
# #                               "factor",
# #                               "factor",
# #                               "numeric"))

# my_eml <- eml$eml(
#   packageId = paste(uuid_tbl$value),
#   system = "uuid",
#   dataset = eml$dataset(
#     alternateIdentifier = UUIDgenerate(use.time = TRUE),
```

```

#         title = title$value,
#
#         creator = creator,
#
#         metadataProvider = metadataProvider,
#
#         #associatedParty = associatedParty,
#
#         contact = contact,
#
#         pubDate = format(Sys.time(), '%Y-%m-%d'),
#
#         language = "English",
#
#         intellectualRights = eml$intellectualRights(
#
#             para = "To the extent possible under law, the publisher
#
#             #para = paste(license$value),
#
#             ),
#
#         abstract = eml$abstract(
#
#             para = abstract$value$summary,
#
#             ),
#
#         keywordSet = keywordSet,
#
#         coverage = coverage,
#
# #         license = eml$license(
#
# #             licenseName = "CC0 1.0",
#
# #             #licenseName = paste(license$value),
#
# #             ),
#
#         #dataTable = eml$dataTable(

```



```
#           #  entityName = file_name_occur,
#           #  entityDescription = "Occurrences",
#           #  physical = physical)
#           ))
```

Validate EML

```
# val <- eml_validate(my_eml)
# attr(val,"errors")
```

Write eml to file.

```
# file_name_eml <- 'eml.xml'
# write_eml(my_eml, file_name_eml)
```

Raw EML

```
# my_eml
```

7.2.2.2.1 Create meta.xml

Below is an example of the contents of meta.xml:

```
<archive xmlns="http://rs.tdwg.org/dwc/text/" metadata="eml.xml">
  <core encoding="UTF-8" fieldsTerminatedBy="\t" linesTerminatedBy="\n" fieldsEnclosedBy="\"
    <files>
      <location>occurrence.txt</location>
    </files>
    <id index="0" />
```

```

<field index="1" term="http://rs.tdwg.org/dwc/terms/datasetID"/>

<field index="2" term="http://rs.tdwg.org/dwc/terms/institutionCode"/>

<field index="3" term="http://rs.tdwg.org/dwc/terms/collectionCode"/>

<field index="4" term="http://rs.tdwg.org/dwc/terms/basisOfRecord"/>

<field index="5" term="http://rs.tdwg.org/dwc/terms/occurrenceID"/>

<field index="6" term="http://rs.tdwg.org/dwc/terms/catalogNumber"/>

<field index="7" term="http://rs.tdwg.org/dwc/terms/occurrenceRemarks"/>

<field index="8" term="http://rs.tdwg.org/dwc/terms/individualCount"/>

<field index="9" term="http://rs.tdwg.org/dwc/terms/sex"/>

<field index="10" term="http://rs.tdwg.org/dwc/terms/occurrenceStatus"/>

<field index="11" term="http://rs.tdwg.org/dwc/terms/eventDate"/>

<field index="12" term="http://rs.tdwg.org/dwc/terms/year"/>

<field index="13" term="http://rs.tdwg.org/dwc/terms/decimalLatitude"/>

<field index="14" term="http://rs.tdwg.org/dwc/terms/decimalLongitude"/>

<field index="15" term="http://rs.tdwg.org/dwc/terms/coordinateUncertaintyInMeters"/>

<field index="16" term="http://rs.tdwg.org/dwc/terms/scientificNameID"/>

<field index="17" term="http://rs.tdwg.org/dwc/terms/scientificName"/>

</core>

<extension encoding="UTF-8" fieldsTerminatedBy="\t" linesTerminatedBy="\n" fieldsEnclosedBy="<br>">

  <files>

    <location>extendedmeasurementorfact.txt</location>

```

```

</files>

<coreid index="0" />

<field index="1" term="http://rs.tdwg.org/dwc/terms/occurrenceID"/>

<field index="2" term="http://rs.tdwg.org/dwc/terms/measurementType"/>

<field index="3" term="http://rs.tdwg.org/dwc/terms/measurementValue"/>

<field index="4" term="http://rs.tdwg.org/dwc/terms/measurementUnit"/>

<field index="5" term="http://rs.iobis.org/obis/terms/measurementUnitID"/>

<field index="6" term="http://rs.tdwg.org/dwc/terms/measurementDeterminedDate"/>

</extension>

</archive>

```

Checkout [XML package for R](#).

```
conda install -c conda-forge r-xml
```

Another example in this [github repository](#).

Or use the [gui here](#) to create meta.xml.

```

# library(XML)

# doc = newXMLDoc()

# archiveNode = newXMLNode("archive", attrs = c(metadata=file_name_eml), namespaceDefinitions

# ## For the core occurrence

# coreNode = newXMLNode("core", attrs = c(encoding="UTF-8", linesTerminatedBy="\r\n", fiel

# filesNode = newXMLNode("files", parent = coreNode)

# locationNode = newXMLNode("location", file_name_occur, parent = filesNode)

```

```

# idnode = newNode("id", attrs = c(index="9"), parent = coreNode)

# # iterate over the columns in occurrence file to create field elements

# i=0

# for (col in colnames(occurrencedf))

#   {

#     termstr = paste("http://rs.tdwg.org/dwc/terms/",col, sep="")

#     i=i+1

#     fieldnode = newNode("field", attrs = c(index=i, term=termstr), parent=coreNode)

#   }


# ## for the extensions

# extensionNode = newNode("extension", attrs = c(encoding="UTF-8", linesTerminatedBy="\r\n"), parent = coreNode)

# filesNode = newNode("files", parent = extensionNode)

# locationNode = newNode("location", file_name_event, parent = filesNode)

# idnode = newNode("id", attrs = c(index="0"), parent = extensionNode)


# # iterate over the columns in occurrence file to create field elements

# i=0

# for (col in colnames(eventdf))

#   {

#     if (col == 'modified'){

```

```

#         termstr = paste("http://purl.org/dc/terms/", col, sep="")
#     } else {
#         termstr = paste("http://rs.tdwg.org/dwc/terms/", col, sep="")
#     }

#     i=i+1

#     fieldnode = newNode("field", attrs = c(index=i, term=termstr), parent=extensionNode)
# }

# print(doc)

# saveXML(doc, file="meta.xml")

```

7.2.2.3 Build the DarwinCore-Archive zip package

```

# library(zip)

# files = c(file_name_occur, file_name_event, file_name_eml, "meta.xml")

# zip::zip(
#     "atn.zip",
#     files,
#     root = ".",
#     mode = "mirror",

```

```
# )
```

```
# zip_list("atn.zip")
```

7.2.3 sessionInfo()

```
sessionInfo()
```

```
R version 4.4.1 (2024-06-14)
```

```
Platform: aarch64-apple-darwin20
```

```
Running under: macOS Sonoma 14.7.5
```

```
Matrix products: default
```

```
BLAS: /Library/Frameworks/R.framework/Versions/4.4-arm64/Resources/lib/libRblas.0.dylib
```

```
LAPACK: /Library/Frameworks/R.framework/Versions/4.4-arm64/Resources/lib/libRlapack.dylib;
```

```
locale:
```

```
[1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
```

```
time zone: UTC
```

```
tzcode source: internal
```

```
attached base packages:
```

```
[1] stats      graphics  grDevices  utils      datasets  methods    base
```

```
other attached packages:
```

```
[1] mapdata_2.3.1  maps_3.4.2.1  lubridate_1.9.4 forcats_1.0.0  
[5] stringr_1.5.1  dplyr_1.1.4   purrr_1.0.4    readr_2.1.5  
[9] tidyr_1.3.1    tibble_3.2.1  ggplot2_3.5.2  tidyverse_2.0.0  
[13] ncd4_1.24      obistools_0.1.0 tidync_0.4.0
```

```
loaded via a namespace (and not attached):
```

```
[1] utf8_1.2.5      rappdirs_0.3.3  generics_0.1.4  xml2_1.3.8  
[5] stringi_1.8.7   hms_1.1.3       digest_0.6.37   magrittr_2.0.3  
[9] evaluate_1.0.3  grid_4.4.1      timechange_0.3.0 RColorBrewer_1.1-3  
[13] fastmap_1.2.0   rprojroot_2.0.4 jsonlite_2.0.0  ncmeta_0.4.0  
[17] crosstalk_1.2.1 scales_1.4.0    cli_3.6.5       RNetCDF_2.11-1  
[21] rlang_1.1.6     withr_3.0.2     yaml_2.3.10     tools_4.4.1
```

[25]	tzdb_0.5.0	here_1.0.1	vctrs_0.6.5	R6_2.6.1
[29]	lifecycle_1.0.4	leaflet_2.2.2	htmlwidgets_1.6.4	pkgconfig_2.0.3
[33]	pillar_1.10.2	gtable_0.3.6	glue_1.8.0	xfun_0.52
[37]	tidyselect_1.2.1	data.tree_1.1.0	knitr_1.50	farver_2.1.2
[41]	htmltools_0.5.8.1	rmarkdown_2.29	compiler_4.4.1	

A FAQ

Frequently Asked Questions

1. **Q.** What data structure does OBIS recommend?
A. The OBIS-ENV Darwin Core Archive Data Structure. [OBIS manual](#)
2. **Q.** What is a controlled vocabulary, why use them?
A. There are a number of controlled vocabularies that are used to describe parameters commonly used in specific research domains. Using terms defined in a controlled vocabulary allows for greater interoperability of data sets within the domain, and ideally between domains by ensuring that variables that are the same can be identified.
3. **Q.** What controlled vocabularies does OBIS rely on?
A. [WoRMS](#), [NERC Vocabulary Server](#) including:
 - [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](#)
4. **Q.** How can I find out which common measurementTypes are used in measurement or facts tables in existing OBIS datasets?
A. See [Measurement Types in OBIS](#)
5. **Q.** What is an ontology?
A. An ontology is a classification system for establishing a hierarchically related set of concepts. Concepts are often terms from controlled vocabularies. Ontologies can include all of the following, but are not required to include them.
 - Classes (general things, types of things)
 - Instances (individual things)
 - Relationships among things

- Properties of things
- Functions, processes, constraints, and rules relating to things

6. **Q.** What is ERDDAP?

A. [ERDDAP](#) is 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 (‘netCDF’ files) and tabular data (spreadsheets). Data access is also made easier because it unifies different types of data servers and access protocols.

7. **Q.** What metadata profile does OBIS use?

A. OBIS uses the [GBIF EML profile](#) (version 1.1)

8. **Q.** Can Darwin Core be used in the Semantic Web/Resource Description Framework?

A. See [Darwin Core Resource Description Framework Guide](#) and [Lessons learned from adapting the Darwin Core vocabulary standard for use in RDF](#)

B Tools

Below are some of the tools and packages used in workflows. R and Python package “Type” is BIO for packages specifically for biological applications, and GEN for generic packages.

B.1 R

Package	Type	Description
bdveRse	BIO	A family of R packages for biodiversity data.
ecocomDP	BIO	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.
EDIorg/EMLasseblyline	BIO	For scientists and data managers to create high quality EML metadata for dataset publication.
finch	BIO	Parse Darwin Core Files
iobis/obistools	BIO	Tools for data enhancement and quality control.
robis	BIO	R client for the OBIS API
ropensci/EML	BIO	Provides support for the serializing and parsing of all low-level EML concepts

Package	Type	Description
taxize	BIO	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.
worms	BIO	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.
Hmisc	GEN	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.

Package	Type	Description
lubridate	GEN	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	GEN	Simple, Consistent Wrappers for Common String Operations
tidyverse	GEN	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.
uuid	GEN	Tools for generating and handling of UUIDs (Universally Unique Identifiers).

B.2 Python

Package	Type	Description
metatype	BIO	A lightweight Python 3 library for generating EML metadata

Package	Type	Description
python-dwca-reader	BIO	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.
pyworms	BIO	Python client for the World Register of Marine Species (WoRMS) REST service.
numpy	GEN	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.
pandas	GEN	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!
uuid	GEN	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. Built in – part of the Python standard library.

Package	Type	Description
obis-qc	BIO	Quality checks on occurrence records. Checks <code>occurrenceStatus</code> , <code>individualCount</code> , <code>eventDate</code> , <code>decimalLatitude</code> , <code>decimalLongitude</code> , <code>coordinateUncertaintyInMeters</code> , <code>minimumDepthInMeters</code> , <code>maximumDepthInMeters</code> , <code>scientificName</code> , <code>scientificNameID</code> . Checks from Vandepitte et al. flags not implemented: 3, 9, 14, 15, 16, 10, 17, 21-30.
biopython	BIO	Biopython is a set of freely available tools for biological computation written in Python by an international team of developers. It is a distributed collaborative effort to develop Python libraries and applications which address the needs of current and future work in bioinformatics.

B.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.

B.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.
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.

C Extras

Below is some more in-depth information into specific areas associated with standardizing your data to Darwin Core and uploading it through the IPT.

C.1 Ecological Metadata Language (EML)

The Ecological Metadata Language (EML) is a community developed and maintained metadata standard that is typically associated with ecological-, and earth and environmental data. The purpose of EML is to provide the ecological community with an extensible, flexible, metadata standard used in data analysis and archiving, which will allow automated machine processing, searching and retrieval. EML has been around since 2003, and can be considered a “dialect” or specification to XML to describe tables and other data objects. The XML Schema provides a framework for the metadata, with defined “rules” on how to organize the metadata without any stipulations (another way to put it, *XML is the language that defines the rules that govern the EML syntax*). The XML Schema defines the structure of some information in a document (e.g. elements and attributes names and relationships), but does not provide any specific details the information included within. An EML document or file (eml.xml) is used to provide detailed description of metadata related to data objects, including tables (and other data objects), their columns, typing etc, and how data tables are linked or grouped. EML is widely used for datasets about ecosystem level observations, and can be used to detail data table information to a high granularity, which allows data users to arrange data tables in any way they need to. EML is particularly useful for wide data tables as table level details are entirely contained within the metadata document, meaning that there is not necessarily a need for external definitions such as a code list. However, if you have a long table arrangement, like the Darwin Core Archive (DwC-A), you can define the allowable values for the column in the metadata as well.

EML is excellent at describing the details of a column of data so that the data values in the tables can be read into analysis systems or an analysis environment using the metadata, or even into a relational database. EML allows for tables to be easily reusable, and read into workflows, translated or reformatted. A drawback to EML is that, compared to the ISO standard, EML is a community standard, adopting a more ‘bottom-up’ approach. This is contrary to the ISO standard, which are internationally agreed upon standards by experts (‘top-down’). However, at the time of EML development in the early 2000’s there was a gap in metadata options to describe ecological data tables, with ISO standards typically being

more applicable to geographic data. EML can cover almost anything and is particularly good at tabular data. But at the same time, due to the self-contained nature, there can be little control from outside lists, which means that the description is left to the EML constructor (data provider/manager) and consequently, individual datasets can look quite different from each other, even when they contain similar measurements. As such, it will be important to document best practices and clear mapping of fields between different metadata schemas (e.g. cross-walks between ISO.xml and EML.xml). As of version 2.2, EML can link to external ontologies, and there is capacity for annotation with external terms (e.g. through their URIs). Code lists and external dictionaries can help as they sometimes contain additional information that might not fit into EML (e.g. protocols, or code lists stored in ontologies). Having these external code lists and exporting them as EML snippets could go a long way in reducing that heterogeneity, because the constructors can then select measurements from lists when developing EML documents.

EML is implemented as a series of XML document types (modules) that can be used in an extensible manner to document ecological data. Each EML module is designed to describe one logical part of the total metadata that should be included with any ecological dataset. The architecture of EML was designed to serve the needs of the ecological community, and has benefitted from previous work in other related metadata standards. Using this format can facilitate future growth of the metadata language, and EML supports an active developer community (see e.g. NCEAS EML GitHub). EML adopts much of its syntax from the other metadata standards that have evolved from the expertise of groups in other disciplines. Whenever possible, EML adopted entire trees of information in order to facilitate conversion of EML documents into other metadata languages. The GBIF IPT is a tool used to create a single eml.xml file format inside the DwC-A data package. However, the IPT does not use any of the EML's built-in table description modules, and perhaps primarily uses one EML module (resource module) for high-level metadata.

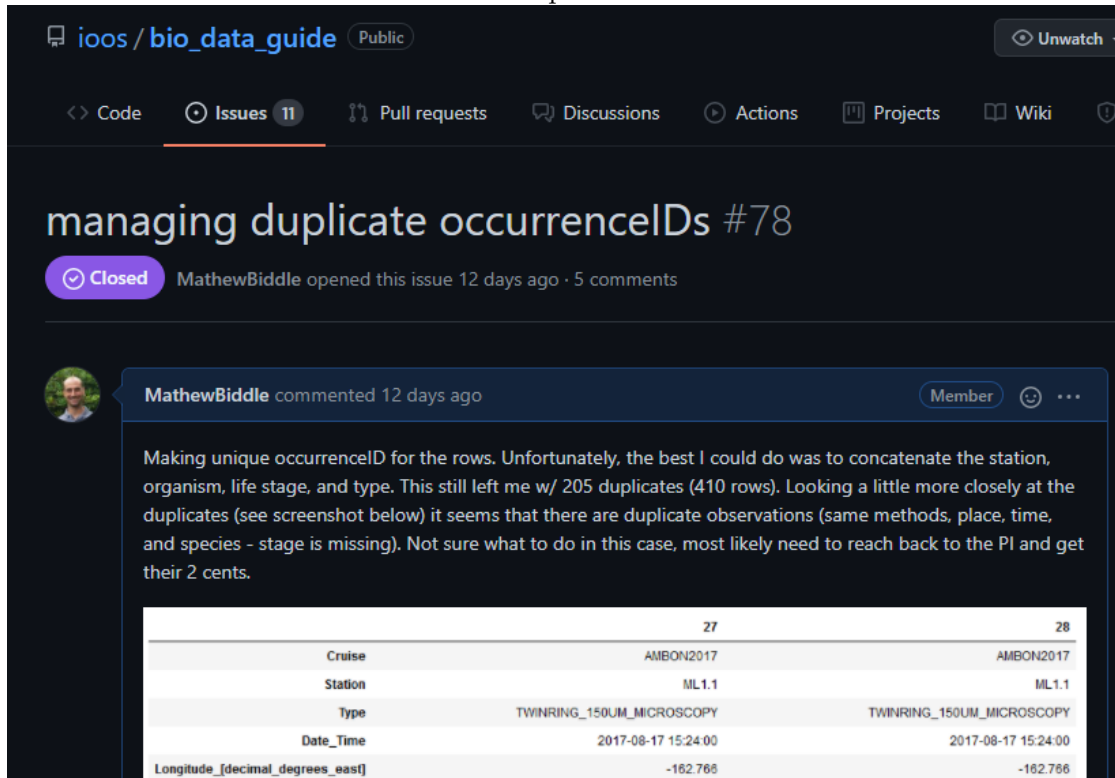
However, it is important to know how both OBIS and GBIF use EML, as often a higher granularity of the metadata can be found in the original data tables. An example of this is spatial coverage. The IPT only allows for either a bounding box to be documented (populating North, South, East, and West coordinates), or a single polygon. The EML document however would be able to capture multiple polygons worth of spatial coverage (i.e. a polygon for each transect surveyed). This more detailed information however is often captured in the data (in an OBIS record). Additionally, not all fields that can be populated in an EML document can be translated to the IPT, or harvested by OBIS and GBIF. The GBIF IPT only produces a select number of fields or attributes available in EML.

Important: When reading the EML section in the [OBIS manual](#), you'll notice that it reads that OBIS uses the GBIF EML profile (version 1.1). However, the current EML version is 2.2.0, as per [EcoInformatics](#). This does not mean that these versions are not compatible, rather, it means that the GBIF IPT currently uses a subset of available EML 2.2.0 fields and attributes, the subset of which they have versioned 1.1.

If you are interested in creating an EML metadata file, it is possible to upload those into the IPT. There are R packages that can help in developing an EML.xml file. These packages are e.g. [EML](#), [emld](#) or [EMLassemblyline](#).

C.2 Example using GitHub to resolve errors

1. Dataset sent to OBIS-USA via email.
2. OBIS-USA uploaded to IPT.
3. Once the data were uploaded, the IPT identified there was an issue with the `occurrenceID` field. The issue was then presented and discussed in a GitHub ticket:



ioos / bio_data_guide Public Unwatch

<> Code Issues 11 Pull requests Discussions Actions Projects Wiki

managing duplicate occurrenceIDs #78

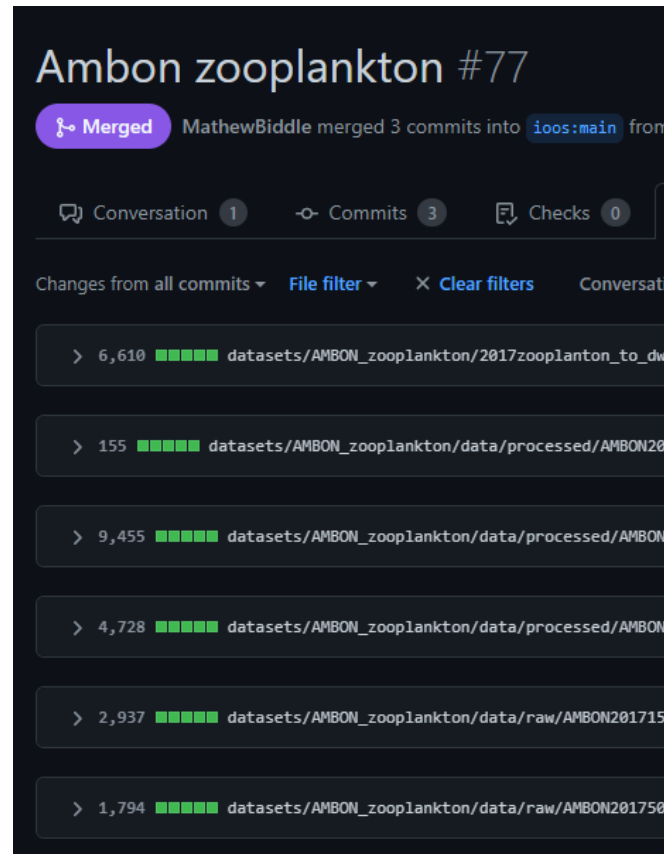
Closed MathewBiddle opened this issue 12 days ago · 5 comments

MathewBiddle commented 12 days ago Member

Making unique occurrenceID for the rows. Unfortunately, the best I could do was to concatenate the station, organism, life stage, and type. This still left me w/ 205 duplicates (410 rows). Looking a little more closely at the duplicates (see screenshot below) it seems that there are duplicate observations (same methods, place, time, and species - stage is missing). Not sure what to do in this case, most likely need to reach back to the PI and get their 2 cents.

	27	28
Cruise	AMBON2017	AMBON2017
Station	ML1.1	ML1.1
Type	TWINRING_150UM_MICROSCOPY	TWINRING_150UM_MICROSCOPY
Date_Time	2017-08-17 15:24:00	2017-08-17 15:24:00
Longitude_[decimal_degrees_east]	-162.766	-162.766

4. The data manager uploaded the raw data and code to GitHub through the pull request



below. This included a fix for the `occurrenceID` issue.

5. The OBIS node manager was notified of the availability of a revised dataset by pointing



directly to the appropriate commit in GitHub:

6. The OBIS node manager downloaded the data from the commit above and uploaded

them to the IPT.

- The IPT returned a summary of the dataset including that 434 records had invalid `scientificNameID` records in the occurrence file.
- After some data sleuthing, the data manager noticed that the code accidentally removed

```
#taxonid needs to not have trailing
taxons = df[['taxonID']].astype('s
t=taxons['taxonID'].convert_dtypes
t=t.str.strip('.0')
t
df['taxonID']=t
df.head()
```

trailing zeros from `scientificNameID` that ended in 0:

- So, the data manager updated the code to resolve the issue and generate a new occurrence

fixing taxonID and aphialID columns #82

Merged MathewBiddle merged 1 commit into ioos:main from MathewBiddle:ambon_patch_sciName 3 days ago

Conversation 2 Commits 1 Checks 0 Files changed 2

Changes from all commits File filter Clear filters Conversations Jump to

> 915 datasets/AMBON_zooplankton/2017zooplankton_to_dwc(2)_mmb.ipynb

> 1,304 datasets/AMBON_zooplankton/data/processed/AMBON2017_zooplankton_Occurrence_DWC_mb.csv

file.

```
1 #OK, rename and then add new columns
2 #rename columns as necessary
3
4 df.rename(columns={'Depth_m': 'minimumDepthInMeters',
5                  'Life_Stage': 'lifeStage',
6                  'Type': 'samplingProtocol',
7                  'Longitude_decimal_degrees_east': 'decimalLongitude',
8                  'Latitude_decimal_degrees_north': 'decimalLatitude',
9                  'Accepted_Organism_Identification': 'scientificName',
10                 'APHIA_ID': 'taxonID' }, inplace=True)
11
12 # add new parameters
13
14 df['scientificNameID'] = 'urn:lsid:marinespecies.org:taxname:' + df['taxonID'].astype(str)
15
16 df['identificationReferences'] = 'WoRMS'
17 df['basalOfRecord'] = 'HumanObservation' #nospace!
18 df['occurrenceStatus'] = 'present'
19 df.head()
```

- Here is fixing the `scientificNameID` generation:

```

1 #finally!
2 #nope it's scientificNameID that needs this
3 sciids = df[['scientificNameID']].astype('string', errors='ignore')
4 s = sciids['scientificNameID'].convert_dtypes()
5 s=s.str.strip('.0')
6 df['scientificNameID']=s

7 df.head()

```

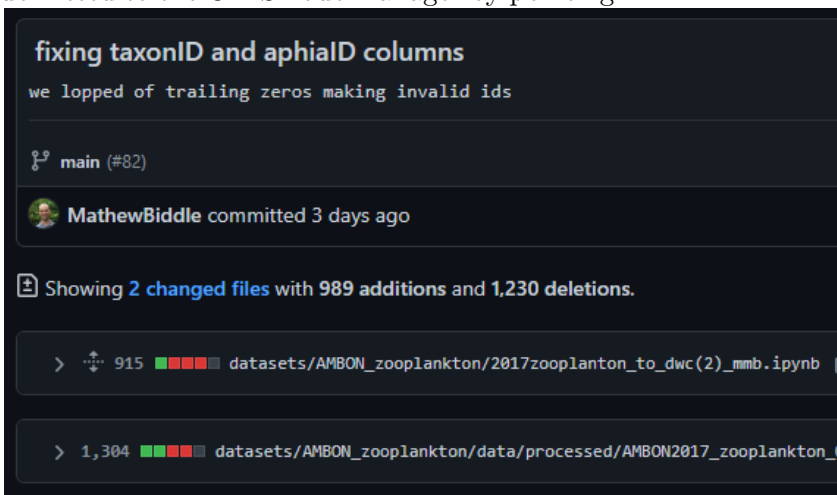
2. Here is removing the problematic code:

```

1 #finally!
2 #nope it's scientificNameID that needs this
3
4 # mmb - Think this was not necessary.
5 # sciids = df[['scientificNameID']].astype('string', errors='ignore')
6 # s = sciids['scientificNameID'].convert_dtypes()
7 # s=s.str.strip('.0')
8 # df['scientificNameID']=s
9 # df.head()

```

10. The revised occurrence file was then resubmitted to the OBIS node manager by pointing



them at the appropriate commit record:

11. The OBIS node manager downloaded the data from the commit above and uploaded them to the IPT.
12. The IPT and OBIS landing page now indicated that no more issues with these data are

Zooplankton Species Distribution and Abundance Data, Arctic Marine Biodiversity Observing Network (AMBON) Chukchi Sea research cruise, August 2017

URL https://www.ebi.ac.uk/odon/species/occurrences?taxon=zooplankton_2017

Repository URL <https://www.ebi.ac.uk/odon/species/>

Node GBIS USA

Published 2025-09-16 10:43

First registered 2025-06-29 21:00

Abstract
This dataset contains zooplankton species distribution and abundance data collected in the Chukchi Sea during the August 2017 Arctic Marine Biodiversity Observing Network (AMBON) research cruise. The dataset is a comma-separate values file (.csv) exported from a Microsoft Excel spreadsheet. The data include the location, date, time, depth, abundance and biomass of zooplankton collected during the 2017 AMBON cruise. Zooplankton were caught with traditional 150µm plankton nets and taxonomically identified. Each data file includes the location, date, time, depth, and identification of zooplankton taxa collected during the 2017 AMBON cruise. The data in the file named AMBON2017_Zooplankton_Abundance_150_100.csv and AMBON2017_150_100_Zooplankton_Abundance_150_100.csv consists of abundance per tow of zooplankton. The data in the file named AMBON2017_Zooplankton_Biomass_150_100.csv and AMBON2017_150_100_Zooplankton_Biomass_150_100.csv consists of biomass per tow of zooplankton. These data files are presented in a table structure using Darwin Core term names as column names. This dataset also contains the file AMBON_station_metadata.csv, describing stations sampled during AMBON cruises. The goal of the Arctic Marine Biodiversity Observing Network (AMBON) project is to demonstrate and build an operational marine biodiversity observing network from microbes to whales, integrating diversity levels from genetic to organismal. AMBON is funded through the National Ocean Partnership Program, with contributions from the National Oceanic and Atmospheric Administration (NOAA), the Bureau of Ocean and Energy Management (BOEM), Shell Exploration and Production Company, and the National Science Foundation (NSF). The AMBON field region is located in the Chukchi Sea, northwest shelf in the US Arctic, an area exposed to climatic changes and anthropogenic influences. AMBON is composed of a team of multi-institutional and multi-sector partners active in a variety of Arctic biodiversity observing programs and covering disciplines ranging from genetic to organismal to ecosystem. Zooplankton are the link between primary production and many other trophic levels. Their incredible numbers and their ability to store large amounts of lipids make them an essential food source for many pelagic feeding fishes, birds and mammals.

Citation

To the extent possible under law, the publisher has waived all rights to these data and has dedicated them to the Public Domain (CC0 1.0)

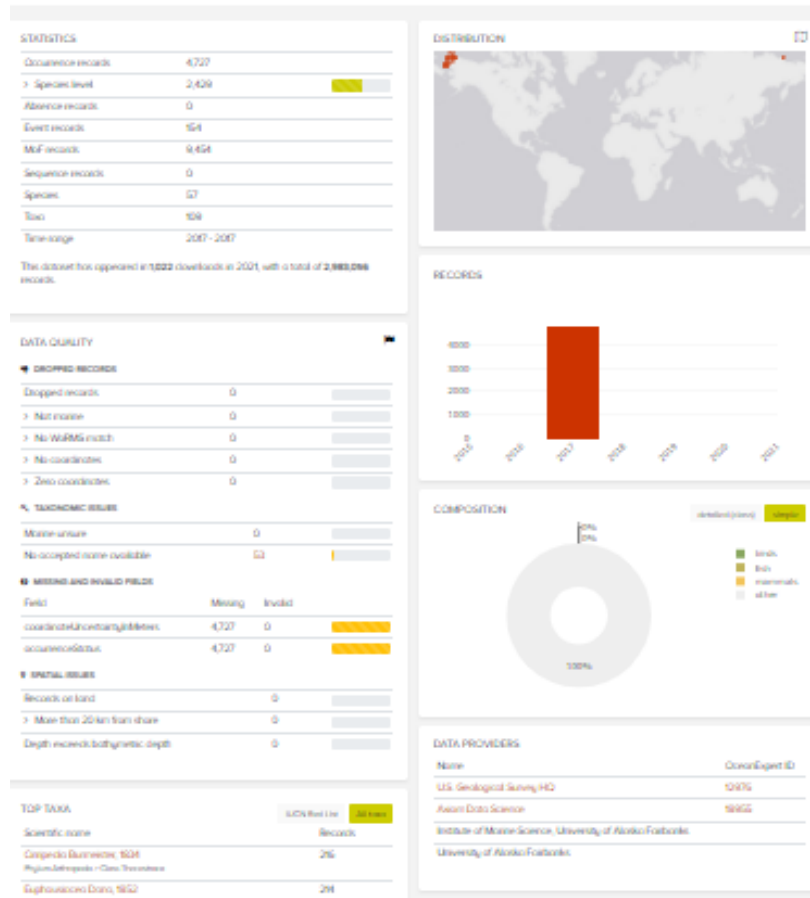
Keywords

Sampling event

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Alaska Data Science

[Report issue](#) [Source GBIF](#) [In progress](#)



present:

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