NOAA's Acropora cervicornis Data Coordination Hub Database Import Guide Patrick Kiel

Overview

The goal of this guide is to direct you through importing data into the database using the observationImport.csv and the metadata_template.rtf file you downloaded. Please follow every step carefully to ensure your data are correctly ingested into the database. If you have any questions, please contact Nathan Formel: nathan.formel@noaa.gov.

The dataset follows an observation-measurement ontology where a single observation groups together all measurements taken at a discrete time point. To submit data in this format, place each unique observation in its own row and create a new column for each corresponding measurement. For individual observations that do not have a corresponding measurement, place a missing identifier such as NA. Ensure the trait names in the csv match the trait names in the metadata form. Traits must match the naming convention of the database. A list of applicable traits is available in the downloaded zip folder. Traits are inclusive of contextual and organismal data.

Monitoring Data Example

blue indicates contextual trait; grey indicates observational data; green indicates organismal trait

tag	geno_name	study_location	TLE	temperature	date
H34	Struggle Bus	Rainbow Reef	8.7	25.6	1/6/2019
H34	Struggle Bus	Rainbow Reef	19.7	29.8	8/29/2019
H36	CRF-13	Tortuga Reef	14.3	29.8	8/29/2019
H39	ML40	Rainbow Reef	18.2	29.8	8/29/2019

Observation level data

"tag" unique tag or identifier of the specific ramet. Necessary to group ramets for repeated measurements design

{trait.name} replace with actual name of trait, inclusive of organismal & environmental or contextual traits (e.g. TLE, date, lipids, skeletal density)

*Make sure the metadata trait names match the trait names in the csv e.g. for the above example

Name	Description	Units	Method	Missing Data Identifier
TLE	Total linear extension	cm	ruler	NA
temperature	Water temperature	Degree Celsius	data logger	NA
date	Calendar date of observation	MM/DD/YYYY	date	NA
tag	Unique identifier	Character	tag	NA

[&]quot;geno_name" name of the genotype

[&]quot;study_location" setting of the observation