

Database Schema

Future decision: If schema required for Specify DB is different than the columns given to us in the input CSV than we may want to separate completed specimens from input data in order to avoid leaving columns blank.

Domain Class: Specimen - List of all specimens including raw data and combined data.

- id -Integer, unique row identifier (Primary Key)
 - Note: and id is given with the input data. We will most likely trash this one and generate our own. If this id is needed we'll need a separate id field.
- collection - String, Which specimen collection the row belongs to. In our case "crabs"
- subject_id - Integer, **unknown**.
- filename - Integer, numerical value of the images which correspond to this row
- user_name - String, user who translated the specimen data.
- created_at - Date, time which the specimen data was translated
- accessionNumber - Date or Integer, **unknown**
- catalogNumber - String, catalog which specimen belongs to. Multiple formats, includes letters, numbers, '/' and '-' (?)
- centerNumber - String, center which collected the specimen. Similar format with catalogNumber and often mixed up. (?)
- collectors - String, Person or organization responsible for obtaining the specimen
- depth - Integer, depth value the specimen was collected at
- depthUnits - String, units of depth value
- eventDate - Date, date the specimen was collected (?)
- geographicLocality - String, where the specimen was collected
- habitat - String, general habitat the specimen came from
- identifierName - String, Person or Organization who identified the specimen (?)
- identifierName2nd - String, (?)

- latitude - Decimal (?), latitude specimen was collected at
- longitude - Decimal (?), longitude specimen was collected at
- otherText - String, general input for uncategorized text on specimen label
- scientificName - String, Scientific Name of specimen if supplied on label
- scientificName2nd - String, Scientific Name for second specimen (?)
- stationNumber - String, station number the specimen was collected at
- processerId - String, Name of scientist who combined the specified sample into the final sample
- processDate - Date, date at which the specimen was combined using the web app.
- isFinal - Boolean, whether or not this is a final (combined) specimen.