VegCore

< place | occurrence >

vegpath.org/VegCore/ERD.pdf

categories

place | occurrence | source | event | individual | party | method | specimen | community | taxon

relationships

id | HAS-A | base_class (id, referenced_class) | inherits from record | IS-A | derived_class (id)

validatable_place (id, coordinates, path)

place_path (id, continent, country, state_province, county, municipality, ranks)

coordinates (id, latitude_deg, longitude_deg)

geovalidation (id, geovalid, lat_long_domain_valid, lat_long_in_ranks)

place (id, parent, coordinates, path, locality)

event (id, parent, name, date_range, place, method)

plot (id, name, area_m2, bounding_box)

subplot (id, x_m, y_m)

event_participant (event, party, sort_order)

project (id, name, info)

method (id, parent, info)

stratum (id, name, info)

record (id, source, source_id_scope, source_record_id, info)

source (id, parent, name, first_publisher, owner, info)

relationship (id, record, related_record, info)

party (id, info)

organization (id, info)

geological_context (id, name, info)

community (id, name, info)

place_observation (id, place, elevation_m, slope_incline_deg, slope_direction_deg_N, geological_context, community, observations)

soil_observation (id, observations)

taxon_observation (id, taxon_occurrence, collector, collector_number, voucher, growth_form, cultivated, traits)

taxon_occurrence (id, current_determination, original_determination)

taxon_presence (id, taxon_concept, traits)

aggregate_observation (id, taxon_concept, traits)

individual_observation (id, individual, code, traits)

individual (id, tag)

stem_observation (id, individual_observation, stem, traits)

stem (id, individual)

specimen (id, individual, code_in_individual, collection_event, orig_collection, barcode, accession_number, current_collection, owner_collection)

collection (id, institution, name)

specimen_observation (id, specimen, traits)

specimenholder_institution (specimen, institution, sort_order)

taxon_determination (id, taxon_assertion, identified_by, fit_info)

TNRS taxonomic scrubbing steps >

1a. verbatim v

taxon_string (string, parsed_taxon_assertion)

3. parsed v

^ 2. concatenated

taxon_assertion (id, string, taxon, cf_aff, annotations)

1b. verbatim >

taxon_name (id, unique_name, formal_name, taxon_name, author, common_name, rank)

taxon_path (id, family, genus, specific_epithet, ranks)

parsed_taxon_assertion (id, matched_taxon_concept, match_score, match_info)

4. matched >

taxon_concept (id, according_to, parent, accepted_taxon_concept)

< 5. accepted