**National Rivers and Stream Assessment Fish Assemblage Quality Assurance Protocol (Draft)**

**Darin Kopp, Richard Mitchell, Louis Reynolds, and Dave Peck**

Diagram

Description automatically generated

**1) Name Reconciliation**

* Fish are identified in the field. Through the app, crews are given common name options from a drop-down menu or can enter the name manually if the taxon has not been recorded in the NRSA database.
* All names for taxa identified in the field must have a matching name in the NRSA Fish autecology file.
* QA Check: Taxon names assigned in the field could be misspelled or ambiguous.

Procedure:

* Reconcile names - Merge NAME\_COM with FINAL\_NAME from NRSA Taxa List
  + Check "Unknown" or unidentified taxa against UNKNOWNS in FINAL\_NAME using grep
    - **Can these be resolved with voucher specimens?**
  + Check NAME\_COM against most similar taxa listed in FINAL\_NAME using
    - Corrected obvious spelling errors
  + Compare NAME\_COM with taxa previously collected from the state during 1819 NRSA survey. Given an ambiguous taxon (i.e. NAME\_COM could potentially be joined with two names in the NRSA autecology files), if the taxon was collected from the state previously, assume that is the correct name for the ambiguous taxa.
  + Compare NAME\_COM to AFS accepted common names (see: Names-of-Fishes-8-Table1.pdf). If the common name assigned in the field is also accepted by AFS these taxa are added as new records in NRSA autecology
  + Identify instances where NAME\_COM is different from FINAL\_NAME and confirm the name change is appropriate.

R-script: “Reconcile\_Names.R”

Files produced:

Reconciled\_Taxa\_Names.csv – List of record with TAXA\_ID assignments from NRSA Autecology dataset

Check\_Taxa\_NRSA\_Reconciled\_Names\_2023.csv – List of records with different NAME\_COM and FINAL\_NAMES

**2) Range Checks and Nativeness**

* Fish names assigned in the field could misidentified or non-native. Often field crews do not indicate whether a taxon is introduced. Native status is used to calculate MMI and assigned at the HUC8 scale.

* QA Check: Compare fish collected and identified in the field with native range shapefiles provided by NatureServe and the non-indigenous aquatic species (NAS) database from USGS.

Procedure:

* Each site needs to be assigned a HUC8. Some handpicked sites may be missing a HUC8 assignment but this will be fixed with site.info file is finalized.
* For each species, query NatureServe shapefiles stored locally: "L:/Public/dpeck/NRSA 2018-19 FISH DATA CLEANUP/NATURESERVE FISH DISTRIBUTION SHAPEFILES 2020/Shapefiles", non-native records from NAS and previous NRSA surveys to obtain a list of HUC8 where species is either native, non-native, or collected previously.
  + API query stalls on a few taxa which will have to be searched manually. NAS API is also very slow. Consider making a “master list” that contains all HUC8 records for species collected by NRSA.
  + When a HUC was surveyed during a previous cycle, assign the native/non-native designation. This is essentially leveraging expert opinion from previous NRSA (i.e. Dave Peck et al.)
* Compare list of HUC8's with the HUC8 of the 2324 site where the taxon was collected and assign native if HUC8 was included in NatureServe Database or Non-native if HUC8 was included in NAS
  + In some cases, a species can be assigned both native and non-native because of conflicting sources/information or maybe species could be non-native in some streams within the HUC8 but native in others. I think we should handle these as “all or nothing” if it is non-native anywhere in the HUC8 it should be designated as non-native.
* If a HUC8 was not surveyed by a previous survey or included in NatureServe or NAS, aggregate to the HUC6 level, and compare again.
  + This will list all HUC8’s that are nested within a HUC 6 and tally the records. Typically, taxa in neighboring HUC8s are all either Non-native or native but we’ll have to handle conflicting assignments.
* If no records were provided for HUC6 aggregation, then used the INTRODUCED column value given by field crew.
* Manually check taxa that were unmatched and/or have conflicting assignments.
  + Unmatched taxa could be due to a name change between shapefile and scientific name. In the future explore options to harmonize names to most recent accepted name.

R-script: Range\_Check.R

**3) Evaluate Fish Info and Sampling sufficiency (Need to consult with Dave Peck/Gregg Lomnicky**)

* Ensure methods are appropriate for the stream width.
* Determine sampling sufficiency: number of individuals collected, or percent of reach fished.

R-script: In Progress