PITcleanr\_lite: Workflow Documentation

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Overview

This is a step-by-step process guide for the draft version of PITcleanr\_lite (2022) to import and combine fish mark and recapture histories from PTAGIS and Biologic. The process requires:

1. A PTAGIS account to create and execute queries (<https://www.ptagis.org/>)
2. Access to Biomark’s Biologic database
3. A recent version of R software installed
4. A local copy of the PITcleanr\_lite Github repo (<https://github.com/Mount-Hood-Environmental/PITcleanr_lite>)

Three PTAGIS queries are required. The first two queries construct the list of PIT tags to be pulled in query 3, which is downloaded locally.

1. Tagging detail query: All fish marked at Lemhi RSTs
2. Recapture query: All recaptures at Lemhi RSTs
3. Tag history query: All tagged fish listed in queries 1. *or* 2. This report will contain all of the records to be downloaded from PTAGIS.

To create these queries, you will need to:

1. Navigate to <https://www.ptagis.org/>
2. Login
3. Navigate to Advanced Reporting Home Page
4. Create Query Builder2 Report

PTAGIS

Mark Query

1. Report type: Tagging Detail
2. Select Attributes
   1. ~~Add Length & Weight~~
3. Filters
   1. **4** Capture Method = Screw Trap
   2. **9** Mark Site Subbasin = 17060204:Lemhi
   3. **10** Mark Year = 2020 – Present
   4. **16** Species = Chinook, Steelhead
4. Save query
   1. Give the query a descriptive name, such as “MarkDat\_Lemhi”
   2. **Important:** The query must be saved as “static”. Be sure to check the box as in the highlighted image below



1. Run Report

Recapture Query

1. Report type: Recapture Detail
2. Select Attributes
   1. ~~Add Recap Length & Recap Weight~~
3. Filters
   1. **10** Mark Site Subbasin = 17060204:Lemhi
   2. **19** Recap Capture Method = Screw Trap
   3. **27** Recap Year = 2020 – Present
   4. **32** Recap Species = Chinook, Steelhead
4. Save query
   1. Give the query a descriptive name, such as “RecapDat\_Lemhi”
   2. **Important:** The query must be saved as “static”. Be sure to check the box as in the highlighted image below

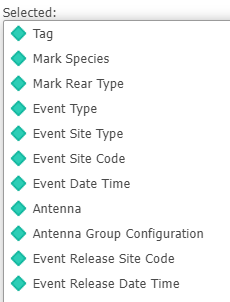


1. Run Report

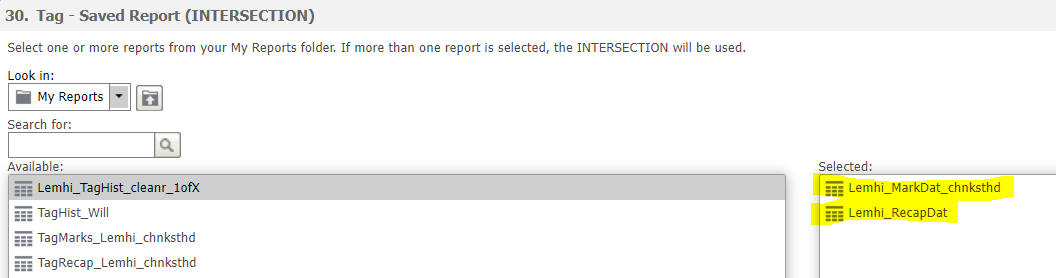
Tag History Query

This query filters the entire PTAGIS database to tags that are recorded in queries 1 or 2 and returns the associated complete tag histories to be downloaded.

1. Report type: Complete Tag History
2. Attributes: Select the attributes listed below



1. Filters
   1. **6** Event Site = HYC, LRW, EVU, S2I, S2O, BHC, S3B, S3A, EVL, LLRTP, LLR
   2. **31** Tag – Saved Report (UNION)
      1. In this window, navigate to “My Reports” and select the 1. Mark query and 2. Recapture tag history query created above. See image below for details.



1. Save report. Unlike the first two, this report can be saved as “prompted”
2. Run Report
   1. **Important: Running this query for all event sites will likely cause PTAGIS to error out due to too many records. Recommend running the report once with event site set to “HYC” only, then again for all other sites. HYC has nearly 1 million records from 2020-2022 alone.**
3. Export
   1. Whole report
   2. CSV file format
   3. Remaining as default
   4. Export
4. Name the downloaded file using the following naming convention: “TagHist\_basin\_sitenames\_year.csv” e.g., “TagHist\_Lemhi\_HYC\_20-22.csv”
5. Save the downloaded file within the “input/PTAGIS\_data” folder in PITcleanr\_lite.

Biologic

Observation data

PIT tag detection data downloaded from the biologic database should consist of 5 columns: site, tag, detected, reader, and antenna. Biologic data downloads are saved to the “input/biologic\_data” folder and must include the string “biologic” in the filename (e.g., “0LL\_tagobs\_biologic\_07302022.csv”).

Site metadata

Site metadata information is contained in “input/site/site\_metadata.csv”. Any modifications or additions must be made within this file.

Configuration

Filtering out Tags

If any tags need to be filtered out from results (e.g., test tags), then they need to be entered into the “input/metadata/filter\_tags.csv” file. List all tags that will be filtered out in the “tag\_num” column.

Node Configuration

A node configuration file is required to convert Biologic reader numbers to array names. The file is located at “input/metadata/node\_config.csv”. Modify the file as necessary to assign reader numbers to nodes.

Directionality

A directionality component can be added to the cleaned and compressed tag observation data. To do so, the directionality file (“input/metadata/node\_direction.csv”) must be configured. The configuration file includes the following columns:

* **parent:** A node directly downstream of the corresponding node in the “child” column
* **child:** A node directly upstream of the node listed in the “parent” column
* **parentOrder:** Describes the hierarchy of nodes, ascending in upstream order
* **parent\_group:** Parent argument used to group together individual nodes in complex systems (e.g., Henry’s reach)
* **child\_group:** Child argument used to group together individual nodes in complex systems (e.g., Henry’s reach)

Running the Scripts

1. In the PITcleanr\_lite parent folder, open the “PITcleanr\_lite” R project file using R or Rstudio.
2. Within R, open the “Workflow.r” script located within the “scripts” folder. This can be done by navigating to “File → Open File”, ctrl+o, or using the “Files” tab in the files and help pane.
3. Highlight the entire script and click the “run” button.
   1. Packages listed under the “load packages” will automatically be downloaded from the CRAN repository if they have not been installed. These are required for the script to run.
   2. **Note:** Some function arguments can be modified for different types of outputs
      1. **AddDirection2()**
         1. group\_nodes = T will use the “parent\_group” and “child\_group” columns from “node\_direction.csv” instead of individual nodes
         2. build\_diagram = T will output a directionality diagram located in “output/figures”
         3. generate\_map = T will generate a map of detection nodes using downloaded NHD flowlines
         4. downstream\_site states the furthest downstream site to map when “generate\_map = T”
         5. The “direction” argument states the direction of fish movement. direction = ‘d’ is for downstream fish movement (i.e. outmigration) and direction = ‘u’ is for upstream migration (i.e. adult returns)
4. This will output three .csv files with cleaned tag observation data. These are located in the “output” folder.
   1. “TagObs\_Compressed\_YY-MM-DD.csv” contains cleaned and compressed tag observation data. Each row describes the number and duration of observations for a single tag at one array.
   2. “TagObs\_Wide\_YY-MM-DD.csv” summarizes compressed tag observation data and pivots it wide. Each row is a unique tag and the associated number of detections at all observation sites.
   3. “TagObs\_Directionality\_YY-MM-DD.csv” contains tag records with associated movement direction. Observations are limited to arrays/nodes are listed in the “input/metadata/node\_direction.csv” configuration file.
5. There is a code chunk following the primary workflow that subsets the “TagObs\_Directionality” dataset to the final detections for each tag and writes it to “TagObs\_FinalPaths\_YY-MM-DD.csv”. This provides the complete detection path for each fish through nodes specified in the “node\_direction” file.