PITcleanr\_lite: Workflow Documentation

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Modified by: Mark Roes

Overview

The following is a step-by-step guide to compile PIT-tag mark and observation data and process them into capture histories useful for analysis of fish or animal movement, growth, survival, etc. The workflow uses a draft version of the GitHub repository [PITcleanr\_lite](https://github.com/Mount-Hood-Environmental/PITcleanr_lite) which is intended to be a user-friendly, stand-alone group of R functions and scripts that leverages functionality and is a companion to the previously developed [PITcleanr](https://github.com/KevinSee/PITcleanr) R package. PITcleanr\_lite is designed to “compress” large, sometimes unwieldy PIT-tag observation datasets for a given list of PIT-tagged fish into observation records and capture histories that are more manageable to aid in fisheries analyses. PITcleanr\_lite accommodates observation data downloaded from either the Columbia Basin PIT Tag Information System ([PTAGIS](https://www.ptagis.org/)) or from the Biomark, Inc. [BioLogic](https://data3.biomark.com/) web portal. PTAGIS is the centralized database for PIT-tagged fish in the Columbia River basin and houses observation data for many of the more permanent PIT-tag arrays located throughout the region. However, PTAGIS does not contain most observation data from either 1) observation sites outside of the Columbia River basin or 2) temporary or project-specific detection sites (e.g., litz cords). These observations can instead be found in BioLogic™ database and web portal, at least for arrays and infrastructure installed by Biomark, Inc.

In this document, we provide an example of the use of PITcleanr\_lite (2022) to compile a list of unique PIT-tagged fish that are marked and/or released at rotary screw traps (RST) in the Lemhi River watershed. Our focus is on juvenile Chinook salmon *Oncorhynchus tshawystscha* and steelhead *O. mykiss* released at two RSTs located just upstream from the confluence of Hayden Creek and the upper Lemhi River: the Upper Lemhi River Rotary Screw Trap (LEMTRP) and the Hayden Creek Rotary Screw Trap (HYDTRP). Each of these traps are intended to monitor the emigration timing, abundance, and survival from subpopulations spawning upstream; juveniles are then tracked through the lower Lemhi River (downstream from Hayden Creek to the confluence with the Salmon River) including through multiple stream habitat rehabilitation projects that are “wired” with litz cords to monitor use of e.g., newly created or restored side channels. Juveniles can also be interrogated or tagged and released at the Lower Lemhi River RST (LLRTP) located below many of the stream rehabilitation projects before leaving the Lemhi River to the Salmon River.

Required and Recommended Items

The following example requires:

1. A recent version of R software installed (<https://cran.r-project.org/>)
2. A local copy of the PITcleanr\_lite GitHub repo (<https://github.com/Mount-Hood-Environmental/PITcleanr_lite>)
3. A PTAGIS account to create and execute queries (<https://www.ptagis.org/>)
4. Access to Biomark’s BioLogic™ web portal (<https://data3.biomark.com/>)

We additionally recommend the use of the following:

1. [RStudio](https://www.rstudio.com/) as a useful environment for R an.

R and RStudio

For step-by-step instructions on downloading and installing both R and RStudio, please visit [Appendix A](https://rstudio-education.github.io/hopr/starting.html) of the Hands-On Programming with R website.

PITcleanr\_lite

Some brief text about visiting the PITcleanr\_lite website, accessing the README, downloading, saving, etc.

Tag or Mark Data

In our example, we use two PTAGIS queries to construct a list of unique PIT-tagged juveniles tagged and/or released at the LEMTRP and HYDTRP screw traps, which we will track through the lower Lemhi River. Alternatively, a user could provide their own list of PIT-tagged individuals in a .txt or .csv file format. To complete the PTAGIS queries, the user will need to do the following:

1. Navigate to <https://www.ptagis.org>
2. Login (or Register for a new account, if necessary)
3. Navigate to the “Advanced Reporting Home Page”
4. Click “Create Query Builder2 Report”

This will take you to a list of standard queries that are provided by PTAGIS.

### Tagging Detail Query

First, we will execute a “tagging detail” query in PTAGIS to identify all newly PIT-tagged Chinook salmon and steelhead that are released at RSTs within the Lemhi River Subbasin. For the purposes of this exercise, let’s focus on fish marked starting in 2020 to present. In the left panel of the Tagging Detail Query page, the user will see a series of indices that allows one to choose which attributes to include in their export, while also allowing filtering on select attributes.

1. Report type: Tagging Detail
2. **1** Select Attributes – add the following attributes to the default:
   1. Length
   2. Weight
   3. Note: any additional attributes may be added by the user and will be included in the export, but “Length” and “Weight” must be added. Not doing so may lead to an error in the *Tag History Query* below.
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 (bottom of screen)
   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. You can organize your queries in folders, if desired.
  2. OK

1. Run Report

The above query provides us a list of all newly tagged fish released at Lemhi River RSTs. However, some juvenile Chinook salmon and steelhead are PIT-tagged using other capture methods (e.g., electrofishing) which can occur upstream of the RSTs. If the desire is to monitor all unique PIT-tagged juveniles released at the RSTs to 1) ensure representative marks and 2) bolster sample sizes, then an additional query is needed to identify juveniles that arrive at the RSTs with a PIT-tag. These fish are released with those from the *Tagging Detail Query* and can be identified using the following query:

Recapture Detail Query

1. Report type: Recapture Detail
2. **1** Select Attributes – add the following attributes to the default:
   1. Recap Length
   2. Recap Weight
   3. Note: Similar as above, any additional attributes may be added by the user to include in the export, but “Recap Length” and “Recap Weight” must be added. Not doing so may lead to an error in the *Tag History Query* below.
3. Filters
   1. **10** Mark Site Subbasin = 17060204:Lemhi
   2. **19** Recap Capture Method = Screw Trap
   3. **27** Recap Year = 2020 – Present
   4. **28** Species = Chinook, Steelhead
4. Save (bottom of screen)
   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. To can organize your queries in folders, if desired.
  2. OK

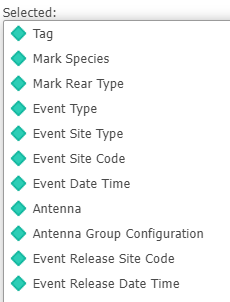
1. Run Report

The combined above *Tag Detail Query* plus *Recapture Detail Query* provides a list of all unique PIT-tagged Chinook salmon and steelhead released at RSTs in the Lemhi River, including those tagged at the trap and those that arrived at the trap with a PIT-tag. The user can then use a *Complete Tag History Query* in PTAGIS to query observations of those fish at interrogation sites (e.g., PIT-tag arrays) that are registered in PTAGIS. Note: This query only provides observations at site registered in PTAGIS, which are generally more permanent sites. To get observations at additional sites not registered in PTAGIS (e.g,, at litz cords), we will need to download those separately from BioLogic™.

Complete Tag History Query

This query filters the entire PTAGIS database for tags that are recorded in the Tag Detail Query and Recapture Detail Query and returns the associated complete tag histories to be downloaded.

1. Report type: Complete Tag History
2. **1** Select Attributes – select the following attributes:



1. Filters
   1. **6** Event Site = HYC, LRW, EVU, S2I, S2O, BHC, S3B, S3A, EVL, LLRTP, LLR
   2. This is a list of interrogation sites in the Lemhi River that are registered in PTAGIS as of the writing of this user guide.
   3. **31** Tag – Saved Report (UNION)
2. Save (bottom of screen). Unlike the first two, this report can be saved as “prompted”.
3. Run Report
   1. **several mark years and severalIn this case, we recommend running the report multiple times, either splitting out the query by mark year or event sites. As and example, the HYC site has nearly 1 million records from mark years 2020-2022 alone. Running the report for all sites causes PTAGIS to crash, but if you run the report once with event site set to “HYC” only, then again for all other sites, the issue seems to be resolved.**
4. Export
   1. Icon: 
   2. Whole report
   3. CSV file format
   4. Remaining as default
   5. Export
5. Name the downloaded file using the following naming convention:
   1. “TagHist\_basin\_sitenames\_year.csv” e.g., “TagHist\_Lemhi\_HYC\_20-22.csv”
6. Save the downloaded .csv file within the “input/PTAGIS\_data” folder in PITcleanr\_lite.

BioLogic™

PTAGIS only provides the user with PIT-tag interrogations at sites registered with PTAGIS; however, many interrogations may also occur at sites not registered with PTAGIS e.g., at temporary, project-specific sites like the litz cords installed at stream rehabilitation projects in the Lemhi River to monitor the use of side channels and off-channel habitats, particularly by juveniles. In this case, much of those sites are installed and managed by Biomark, Inc. and so the data are available in the BioLogic™ database. Here, we provide an example of how to download observation data from BioLogic™ managed sites in the Lemhi River.

After logging in to BioLogic™, the Site Module should show each Site Name that the user’s account has access to. We’ll need to download data from each site, individually. Note: some sites may have multiple or several readers, in which case, one download for the site will contain the observation data for each of its readers. In this example, we will download data for one site (0HR) with one reader and one site (0LL) with several readers. 0HR is an instream array located just upstream of the Henry’s Reach project in the Lemhi River designed to provide juvenile rearing habitat in multiple restored side channels. 0LL contains several readers, each a litz cord, laid across several side channels within the Henry’s Reach project.

1. Navigate to the BioLogic™ web portal (<https://data3.biomark.com/>).
2. Login
   1. If you don’t have a login, please contact…
3. Click on Site Name: Henry’s Ranch Instream Array (0HR)
4. Navigate to the Download tab 
5. From: 01/01/2020
6. To: E.g., Present Day
7. Files to generate: TAG FILE
8. After the file generates, click on the filename to download.
9. Repeat steps 3-8 for the 0LL site.

BioLogic™ data downloads should be saved to the “input/biologic\_data” folder and must include the string “biologic” in the filename (e.g., “0HR\_tagobs\_biologic\_20220929”).

## Site Metadata

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

Tag Filtering

If the user desires to filter observations from some PIT-tags out of the results (e.g., test tags), those tag IDs can be entered into the “input/tag\_filter/filter\_tags.csv” file. List all the tags to be filtered out in the “tag\_num” column.

Site Configuration

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. An alternative way to think of this is by stream order – lower stream orders (tributaries) are the “children” of mainstem reaches. This is because PITcleanr was constructed to handle both downstream migration of smolts as well as upstream migration of adults. Therefore, adults move upstream from parent to child reaches, and juveniles move downstream from child to parent reaches. The upstream or downstream direction of fish movement is defined by the “direction” argument in the **addDirectionWrap()** function of the workflow (see *Running the Scripts*).
* **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)

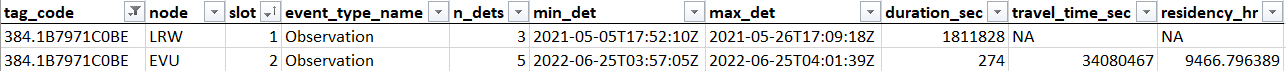
Running the Scripts

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. **AddDirectionWrap()**
         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, and a fourth optional .csv with the final paths for all detected fish. 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. **Optional:** 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.

Data Interpretation

“TagObs\_Compressed\_YY-MM-DD.csv”

This file contains all tag observation data. Each record is the number and duration of observations for a single tag at one node. For example, the first record below reads as: The first observation (slot = 1) for tag “384.1B7971C0BE” was at node LRW. There were 3 detections from 2022-05-05 at 17:52:10Z to 2022-05-26 at 17:09:18Z (which is 1,811,828 seconds). Then, the second node that the fish was detected at was EVU (slot = 2). The amount of time that elapsed between the final detection at LRW and first detection at EVU was 9,466 hours (or 34,080,647 seconds). As default, each detection of a unique tag at a new node is given a “slot”. In the example below, the fish was first detected at LRW, so this set of 3 detections at LRW is assigned slot #1. Next, the fish went to EVU for 5 detections, which is assigned slot #2. If the fish was detected at LRW **after** the 5 detections at EVU, then the next set of LRW detections would get a new row and have slot #3.



“TagObs\_Wide\_YY-MM-DD.csv”

This file takes the nodes and number of detections from the “compressed” file and pivots it wide. Here, each row describes the number of detections that the tag had at all nodes. In the example below, tag “3DD.003D57FB85” was detected 1 time at HYC, 2 times at LRW, 7 at SRSC1, 1 at HRSC6, and so on.



“TagObs\_Directionality\_YY-MM-DD.csv”

This file uses the “node\_direction” metadata file to estimate fish movement. Like the “compressed” data, each record contains the number and duration for a set of detections at a node. “path” and “direction” columns are also added. In the case that node locations were grouped when adding directionality, a “node\_id” column is also present to detail the specific node where the fish was detected. In the “direction” column there are 1 of 5 possible values, depending on the previous node where the fish was detected:

* **Start:** The first observation of the fish within the zone designated by the “node\_direction” file.
* **Forward:** Between the previous observation and the current observation, the fish has moved in the direction designated by the “node\_direction” file.
* **Backward:** Between the previous observation and the current observation, the fish has moved in the opposite direction as designated by the “node\_direction” file.
* **Unknown:** The direction between the previous and current observations could not be determined.
* **No movement:** The previous fish detection was at the same location, but under a different “slot” number.

“TagObs\_FinalPaths\_YY-MM-DD.csv”

This file subsets data from the “directionality” file so that there is a maximum of one record per unique tag. This record is the last node location where the fish was observed, so that the “path” column shows a possible path that the fish may have followed.