

Wrangling and Preparing PIT Tag Data using PITcleanr

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WILDLIFE



Today's Journey

- Benefits and challenges of PIT tag data

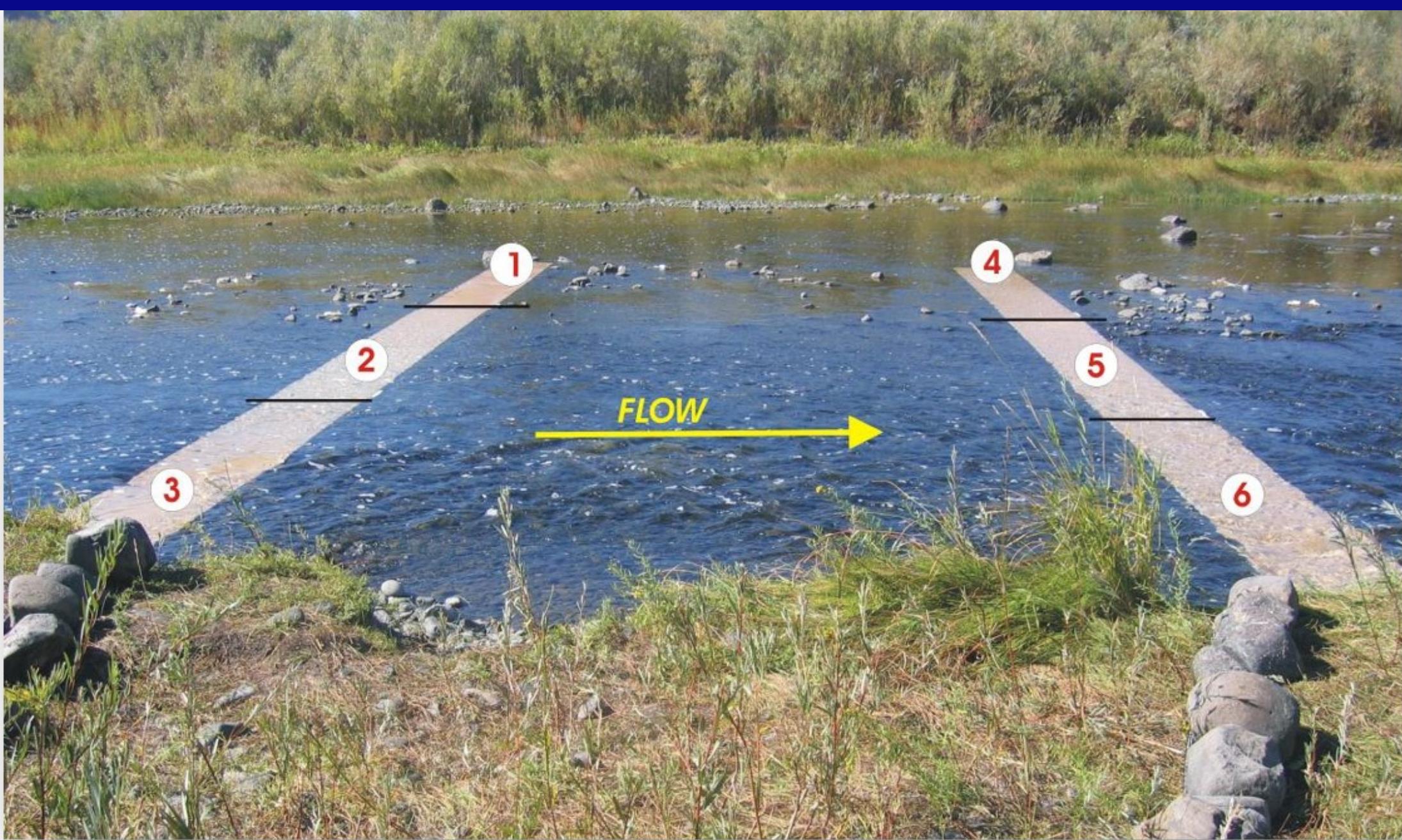
- PITcleanr:

<https://github.com/kevinsee/PITcleanr/>

- Purpose
 - Functionality
 - Package resources
- Summary



PIT Tag Data



PIT Tag Data

Benefits

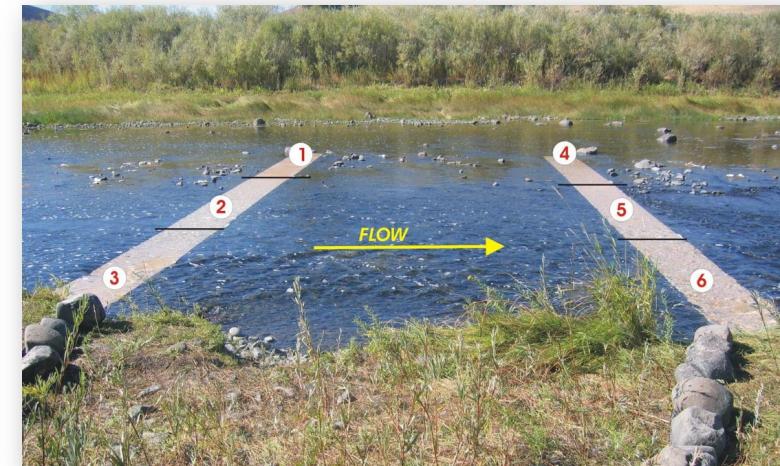
Information about individual fish

- movement
- timing
- survival



Challenges

- **TONS** of data
- Can be overwhelming
- E.g. One juvenile fish detected **681** times at single site within 12 hour period on Lemhi River



So much data...

```
# the complete tag history file from PTAGIS
ptagis_file <-
  system.file("extdata",
              "TUM_chnk_cth_2018.csv",
              package = "PITcleanr")

# read the complete tag history file into R
observations <-
  readCTH(ptagis_file,
          file_type = "PTAGIS")

n_distinct(observations$tag_code) # unique tag codes

## [1] 1406

n_distinct(observations$event_site_code_value) # unique event sites

## [1] 50

nrow(observations) # total observations

## [1] 13501
```

So much data...

												Search: <input type="text"/>
	Tag Code	Event Site Code Value	Event Date Time Value	Antenna Id	Antenna Group Configuration Value	Mark Species Name	Mark Rear Type Name	Event Type Name	Event Site Description			
	All	All	All	All	All	All	All	All	All	All	All	All
1	384.3B239AC47B	NASONC	2016-03-01T10:34:00Z	0	Chinook	Wild Fish or Natural Production	Mark	River	NASONC	2016-03-04T17:00:00Z	1	
2	384.3B239AC47B	BO3	2018-05-18T09:36:59Z	18	110	Chinook	Wild Fish or Natural Production	Observation	Adult Fishway		1	
3	384.3B239AC47B	BO3	2018-05-18T09:37:11Z	16	110	Chinook	Wild Fish or Natural Production	Observation	Adult Fishway		1	
4	384.3B239AC47B	BO3	2018-05-18T09:37:12Z	16	110	Chinook	Wild Fish or Natural Production	Observation	Adult Fishway		1	
5	384.3B239AC47B	BO3	2018-05-18T09:42:16Z	14	110	Chinook	Wild Fish or Natural Production	Observation	Adult Fishway		1	
2018-05-18T09:42:16Z												Wild Fish or

Showing 1 to 100 of 100 entries

PITcleanr Package

PITcleanr Purpose

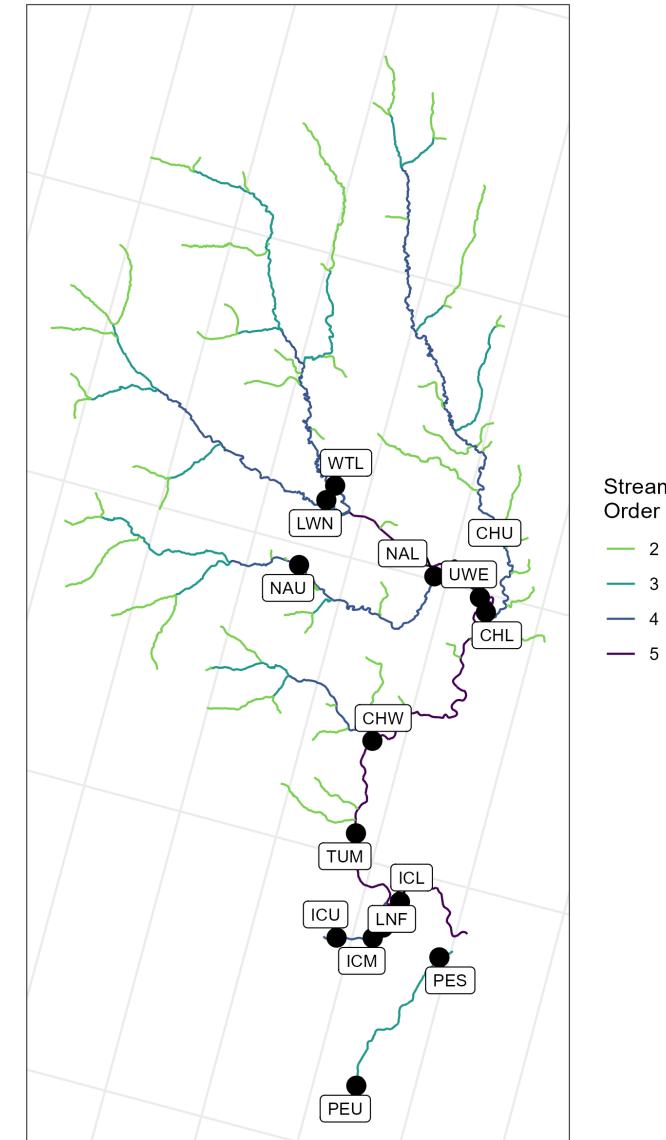
Make your life easier

- Query some data from PTAGIS
 - Metadata about sites
 - Configuration files
 - MRR files
- Read in data from PTAGIS or non-PTAGIS sources
 - Consistent format
 - Identify orphan or disowned tags
- Compress observations
 - Reduce redundant detections
- Determine movement direction
 - Based on parent-child table
 - Includes tools to build parent-child table
- Estimate array/site efficiency

Example Data

Adult Spring Chinook

- Tagged at Tumwater Dam on Wenatchee River as adults
- Goal is to estimate movement or survival past each site



Read in Data

Complete tag histories from PTAGIS

- Start with a list of tags
- Need certain columns

```
print(cth_file_nm)  
## [1] "TUM_chnk_cth_2018.csv"
```

Read in Data

Complete tag histories from PTAGIS

- Start with a list of tags
- Need certain columns

```
print(cth_file_nm)  
## [1] "TUM_chnk_cth_2018.csv"
```

Use `readCTH()` function:

```
# read the complete tag history file into R  
cth_df ←  
  system.file("extdata",  
              cth_file_nm,  
              package = "PITcleanr") ▷  
  readCTH(file_type = "PTAGIS")
```

- PTAGIS not the only format
 - Biologic
 - Raw .log, .xlsx, or .txt files
- Change `file_type`

Compress data

Key feature of PITcleanr

Map each site / antenna to a *node*

Start with:

- 13,501 observations of
- 1,406 unique tags from
- 50 different sites.

```
comp_obs <- compress(cth_df)
```

End with 4,435 rows of data.

- 32.8% of original data

Compress data

Search:

	Tag Code	Node	Slot	Event Type Name	N Dets	Min Det	Max Det
	All	All	All	All	All	All	All
1	384.3B239AC47B	NASONC	1	Mark	1	2016-03-04T17:00:00Z	2016-03-04T17:00:00Z 0
2	384.3B239AC47B	B03	2	Observation	18	2018-05-18T09:36:59Z	2018-05-18T12:00:05Z 143.1 1158757
3	384.3B239AC47B	B04	3	Observation	7	2018-05-18T13:03:11Z	2018-05-18T13:09:29Z 6.3 63.1
4	384.3B239AC47B	TD1	4	Observation	4	2018-05-20T17:20:39Z	2018-05-20T17:20:44Z 0.1 3131.2
5	384.3B239AC47B	J01	5	Observation	2	2018-05-21T17:49:21Z	2018-05-21T17:51:20Z 2 1468.6
6	384.3B239AC47B	MC2	6	Observation	12	2018-05-24T09:04:38Z	2018-05-24T09:54:53Z 50.2 3793.3

Showing 1 to 100 of 100 entries

Compress data

1. Shrink size of data
2. Assign observations to node of your choice
3. First, last and number of detections on each node
4. Total duration between first and last detections
5. Travel time from previous node

Configuration File

Configuration file

Map each detection to a user-defined node

Node could be:

- Individual antenna
- Array (group of antennas)
- Site
- Group of sites

Configuration file

Map each detection to a user-defined node

Node could be:

- Individual antenna
- Array (group of antennas)
- Site
- Group of sites

Can use PTAGIS site metadata to construct

```
my_config ← buildConfig(node_assign = "site")
```

Configuration file

Essential columns

Search:

	Site Code	Antenna Id	Config
	All	All	All
1	0HR	01	100 0HR
2	0HR	02	100 0HR
3	0HR	03	100 0HR
4	158	D1	100 158
5	158	D2	100 158
6	158	D3	100 158
7	158	D4	100 158
8	158	D5	100 158
9	158	D6	100 158

Showing 1 to 200 of 200 entries

Configuration file

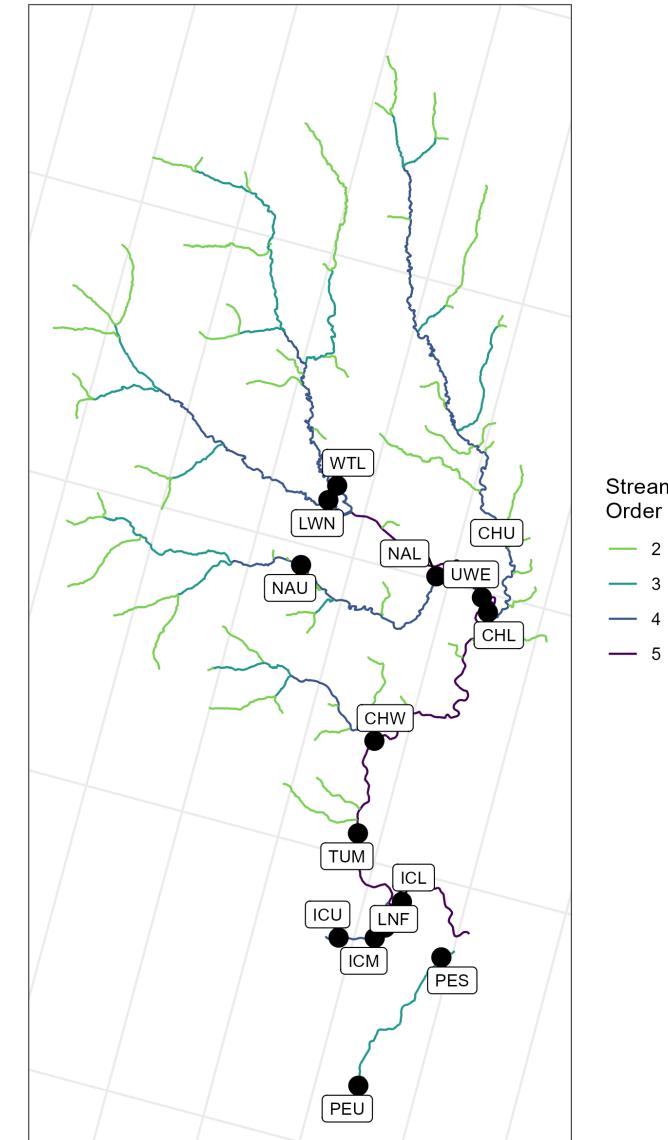
But PTAGIS columns include:

```
names(my_config) >  
janitor::make_clean_names("title")  
  
## [1] "Site Code"          "Config Id"         "Antenna Id"        "Node"  
## [5] "Start Date"         "End Date"          "Site Type"         "Site Name"  
## [9] "Antenna Group"      "Site Description" "Site Type Name"   "Rkm"  
## [13] "Rkm Total"          "Latitude"         "Longitude"
```

Directionality

Map of Sites

- Which sites are upstream / downstream of one another?
- What are possible paths a fish might take?



Parent-Child Table

- Moving upstream, tags move from parent sites to child sites
- Details which sites are upstream of a particular site
- Can be reversed for downstream movement
- Can be made by hand...
- PITcleanr has tools to help

```
parent_child >
  select(parent, child)

## # A tibble: 14 x 2
##       parent    child
##       <chr>     <chr>
## 1     ICL      LNF
## 2     ICL      ICM
## 3     TUM      ICL
## 4     TUM      UWE
## 5     TUM      CHL
## 6     TUM      PES
## 7     TUM      CHW
## 8     ICM      ICU
## 9     UWE      LWN
## 10    UWE      WTL
## 11    UWE      NAL
## 12    CHL      CHU
## 13    PES      PEU
## 14    NAL      NAU
```

Parent-Child Table

- PITcleanr has a `buildParentChild()` function.
- Requires an `sf` point object of sites
 - Build yourself or use `extractSites()`
- Requires an `sf` line object of the NHDPlus flowlines, downloaded from USGS.
 - Use `queryFlowlines()` to download it

Build sf object of sites

One way

```
# extract sites from detection file
sites_sf <-  
  extractSites(cth_file = cth_df,  
               as_sf = T,  
               # drop juvenile detection/marking sites  
               min_date = "20180501")  
  
# focus on sites within Wenatchee subbasin, and drop a few sites we don't care about
sites_sf <-
  sites_sf %>%
  # all sites in the Wenatchee have a river kilometer that starts with 754
  filter(str_detect(rkm, "^754."),  
        type != "MRR",  
        site_code != "LWE") %>%  
  mutate(across(site_code,  
              ~ recode(.,  
                        "TUF" = "TUM")))
```

Build sf object of sites

Another way

```
# type site codes by hand
sites_sf <-
  tibble(site_code =
    c("ICL", "TUM", "ICM", "UWE", "CHL", "PES", "NAL",
      "LNF", "CHW", "ICU", "LWN", "WTL", "CHU", "PEU",
      "NAU")) %>
  left_join(my_config %>
    select(site_code,
           site_name,
           site_type_name,
           site_type,
           rkm,
           site_description,
           latitude,
           longitude) %>
    distinct(),
            by = join_by(site_code)) %>
  st_as_sf(coords = c("longitude",
                     "latitude"),
            crs = 4326) %>
  arrange(rkm)
```

Query Flowlines

```
# query the flowlines
nhd_list <-  
  queryFlowlines(sites_sf = sites_sf,  
                 root_site_code = "TUM",  
                 min_strm_order = 2,  
                 dwnstrm_sites = T,  
                 dwn_min_stream_order_diff = 2)  
  
# join the upstream and downstream flowlines
flowlines <-  
  nhd_list$flowlines %>%  
  rbind(nhd_list$dwn_flowlines)
```

```
flowlines >  
  st_drop_geometry() >  
  select(COMID,  
         Hydroseq,  
         UpHydroseq,  
         DnHydroseq)
```

```
## # A tibble: 386 x 4  
##       COMID Hydroseq UpHydroseq DnHydroseq  
##   <int>    <dbl>      <dbl>      <dbl>  
## 1 23080784 50063945  50070238  50058967  
## 2 23080786 50070238  50078399  50063945  
## 3 23080788 50078399  50089588  50070238  
## 4 23080790 50089588  50106483  50078399  
## 5 23080792 50106483  50137781  50089588  
## 6 23080794 50137781  50220575  50106483  
## 7 23081176 50089577  50106469  50078388  
## 8 23080910 50106479  50137746  50033323  
## 9 23081092 50031394  50032319  50030525  
## 10 23081090 50030525  50031394  50029716  
## # i 376 more rows
```

Build Parent-Child Table

```
parent_child <-  
  suppressWarnings(  
    buildParentChild(sites_sf,  
                      flowlines))
```

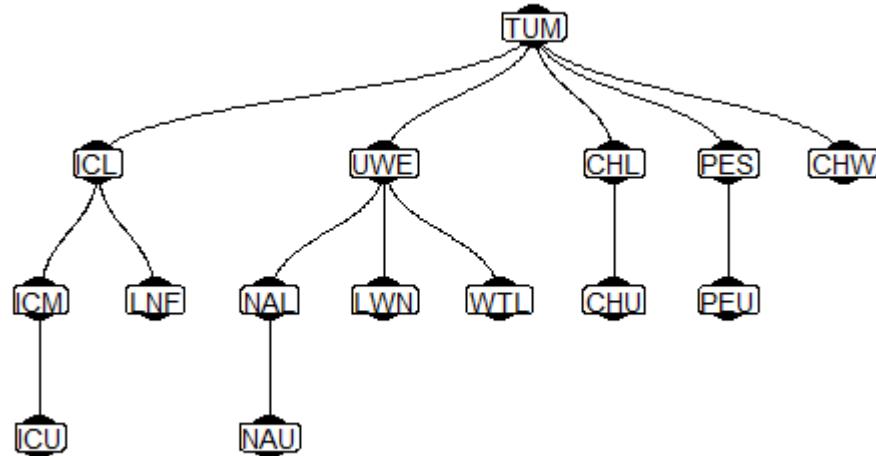
```
parent_child <-  
  editParentChild(parent_child,  
                  fix_list =  
                    list(c(NA, "PES", "TUM"),  
                          c(NA, "LNF", "ICL"),  
                          c(NA, "ICL", "TUM"),  
                          c("PES", "ICL", "TUM")),  
                  switch_parent_child =  
                    list(c("ICL", 'TUM')))
```

```
# view corrected parent_child table  
parent_child %>  
  select(parent, child)
```

```
## # A tibble: 14 x 2  
##       parent child  
##       <chr>  <chr>  
## 1 ICL    LNF  
## 2 ICL    ICM  
## 3 TUM   ICL  
## 4 TUM   UWE  
## 5 TUM   CHL  
## 6 TUM   PES  
## 7 TUM   CHW  
## 8 ICM   ICU  
## 9 UWE   LWN  
## 10 UWE  WTL  
## 11 UWE  NAL  
## 12 CHL  CHU  
## 13 PES  PEU  
## 14 NAL  NAU
```

Plot Parent-Child Table

```
plotNodes(parent_child,
          point_size = 10,
          label_size = 5)
```



All possible fish pathways

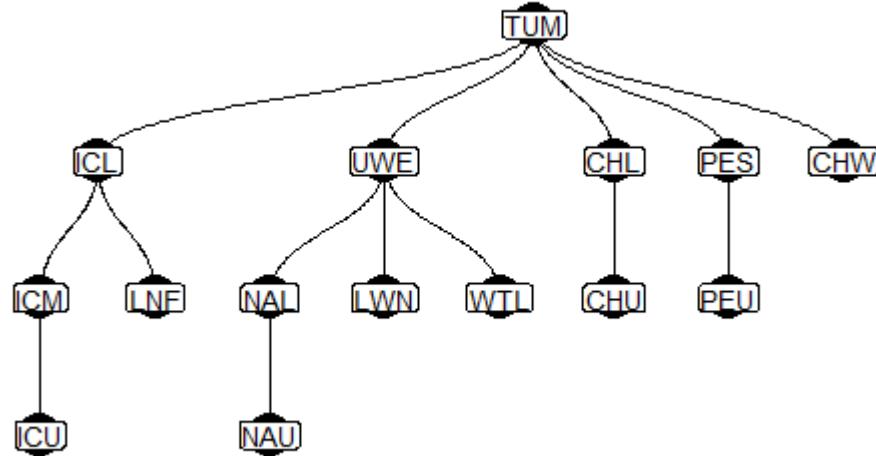
```
buildNodeOrder(parent_child)
```

```
## # A tibble: 15 x 3
##       node    node_order path
##   <chr>      <dbl> <chr>
## 1 TUM         1 TUM
## 2 CHL         2 TUM CHL
## 3 CHU         3 TUM CHL CHU
## 4 CHW         2 TUM CHW
## 5 ICL         2 TUM ICL
## 6 ICM         3 TUM ICL ICM
## 7 ICU         4 TUM ICL ICM ICU
## 8 LNF         3 TUM ICL LNF
## 9 PES         2 TUM PES
## 10 PEU        3 TUM PES PEU
## 11 UWE        2 TUM UWE
## 12 LWN        3 TUM UWE LWN
## 13 NAL        3 TUM UWE NAL
## 14 NAU        4 TUM UWE NAL NAU
## 15 WTL        3 TUM UWE WTL
```

Add Direction

```
comp_dir <-  
  addDirection(compress_obs = comp_obs,  
               parent_child = parent_child)  
  
comp_dir %>  
  select(tag_code,  
         node,  
         min_det,  
         node_order,  
         path,  
         direction)  
  
## # A tibble: 3,257 x 6  
##   tag_code     node min_det           node_order path      direction  
##   <chr>       <chr> <dttm>          <dbl> <chr>    <chr>  
## 1 384.3B239AC47B TUM 2018-06-16 15:26:31      1 TUM      start  
## 2 384.3B239AC47B UWE 2018-06-23 22:03:13      2 TUM UWE   forward  
## 3 384.3B239AC47B NAL 2018-07-01 00:06:16      3 TUM UWE NAL  forward  
## 4 3DD.003B9DD720 TUM 2018-06-17 09:39:26      1 TUM      start  
## 5 3DD.003B9DD725 TUM 2018-06-19 09:33:08      1 TUM      start  
## 6 3DD.003B9DD725 CHU 2018-06-28 21:34:58      3 TUM CHL CHU forward  
## 7 3DD.003B9DDAB0 TUM 2018-07-17 11:51:44      1 TUM      start  
## 8 3DD.003B9F123C TUM 2018-06-21 09:45:14      1 TUM      start  
## 9 3DD.003B9F123C UWE 2018-07-01 12:55:31      2 TUM UWE   forward  
## 10 3DD.003BC7A654 TUM 2018-06-09 22:36:03     1 TUM      start  
## # i 3,247 more rows
```

Strange Directions



```
## # A tibble: 8 x 6
##   tag_code      node min_det          node_order path      direction
##   <chr>        <chr> <dttm>           <dbl> <chr>    <chr>
## 1 3DD.003BC80D81 TUM  2018-06-21 16:14:26     1 TUM      start
## 2 3DD.003BC80D81 UWE  2018-06-29 15:29:19     2 TUM UWE   forward
## 3 3DD.003BC80D81 NAL  2018-06-30 01:35:27     3 TUM UWE NAL  forward
## 4 3DD.003BC80D81 LWN  2018-07-05 23:05:02     3 TUM UWE LWN  unknown
## 5 3DD.003BC80D81 NAL  2018-07-08 03:06:42     3 TUM UWE NAL  unknown
## 6 3DD.003BC80D81 UWE  2018-07-17 21:52:42     2 TUM UWE   backward
## 7 3DD.003BC80D81 NAL  2018-07-20 21:50:13     3 TUM UWE NAL  forward
## 8 3DD.003BC80D81 NAU  2018-07-30 22:40:06     4 TUM UWE NAL NAU  forward
```

Filter Observations

```
comp_filter <- filterDetections(compress_obs = comp_obs,
                                 parent_child = parent_child,
                                 max_obs_date = "20180930")

comp_filter %>
  filter(tag_code %in% examp_tag) %>
  select(tag_code, node, min_det, direction,
         path,
         ends_with("keep_obs"))

## # A tibble: 8 x 7
##   tag_code node  min_det      direction path  auto_keep_obs user_keep_obs
##   <chr>    <chr> <dttm>     <chr>    <chr> <lgl>        <lgl>
## 1 3DD.003~ TUM  2018-06-21 16:14:26 start    TUM  TRUE        NA
## 2 3DD.003~ UWE  2018-06-29 15:29:19 forward  TUM ~ FALSE       NA
## 3 3DD.003~ NAL  2018-06-30 01:35:27 forward  TUM ~ FALSE       NA
## 4 3DD.003~ LWN  2018-07-05 23:05:02 unknown  TUM ~ FALSE       NA
## 5 3DD.003~ NAL  2018-07-08 03:06:42 unknown  TUM ~ FALSE       NA
## 6 3DD.003~ UWE  2018-07-17 21:52:42 backward TUM ~ TRUE        NA
## 7 3DD.003~ NAL  2018-07-20 21:50:13 forward  TUM ~ TRUE        NA
## 8 3DD.003~ NAU  2018-07-30 22:40:06 forward  TUM ~ TRUE        NA
```

Other Functionality

Array Efficiency

Based on tags detected at an array, and any tags detected upstream of that array

Array Efficiency

Based on tags detected at an array, and any tags detected upstream of that array

Start by building a description of how each node is connected to others

```
node_order ←  
  buildNodeOrder(parent_child)  
  
node_order
```

```
## # A tibble: 15 x 3  
##   node    node_order path  
##   <chr>    <dbl> <chr>  
## 1 TUM        1 TUM  
## 2 CHL        2 TUM CHL  
## 3 CHU        3 TUM CHL CHU  
## 4 CHW        2 TUM CHW  
## 5 ICL        2 TUM ICL  
## 6 ICM        3 TUM ICL ICM  
## 7 ICU        4 TUM ICL ICM ICU  
## 8 LNF        3 TUM ICL LNF  
## 9 PES        2 TUM PES  
## 10 PEU       3 TUM PES PEU  
## 11 UWE       2 TUM UWE  
## 12 LWN       3 TUM UWE LWN  
## 13 NAL       3 TUM UWE NAL  
## 14 NAU       4 TUM UWE NAL NAU  
## 15 WTL       3 TUM UWE WTL
```

Array Efficiency

Based on tags detected at an array, and any tags detected upstream of that array

```
estNodeEff(comp_obs,  
           node_order)
```

If no node is supplied, calculated for all nodes

Search:

	node	tags_at_node	tags_above_node	tags_resighted	est_tags_at_node			
	All	All	All	All	All	All	All	All
1	ICL	6	20	1	72	34.1	0.083	0.039
2	CHL	441	454	165	1211	59	0.364	0.018
3	NAL	168	133	83	269	12.7	0.625	0.029
4	UWE	361	256	175	528	16	0.684	0.021
5	TUM	1406	1039	1039	1406	0	1	0
6	CHU	454	0	0	454	0	1	0

Capture Histories

May need matrix of 1s and 0s

```
buildCapHist(comp_filter,  
             parent_child = parent_child,  
             configuration = my_config)
```

```
## # A tibble: 1,406 x 2  
##   tag_code      cap_hist  
##   <chr>        <chr>  
## 1 384.3B239AC47B 100000000010100  
## 2 3DD.003B9DD720 100000000000000  
## 3 3DD.003B9DD725 101000000000000  
## 4 3DD.003B9DDAB0 100000000000000  
## 5 3DD.003B9F123C 100000000010000  
## 6 3DD.003BC7A654 100000000010110  
## 7 3DD.003BC7F0E3 100000000010110  
## 8 3DD.003BC80A3C 100000000010100  
## 9 3DD.003BC80D81 100000000010110  
## 10 3DD.003BC80F20 100000000000100  
## # i 1,396 more rows
```

Capture Histories

May need matrix of 1s and 0s

```
buildCapHist(comp_filter,  
             parent_child = parent_child,  
             configuration = my_config)
```

```
## # A tibble: 1,406 x 2  
##   tag_code      cap_hist  
##   <chr>        <chr>  
## 1 384.3B239AC47B 100000000010100  
## 2 3DD.003B9DD720 100000000000000  
## 3 3DD.003B9DD725 101000000000000  
## 4 3DD.003B9DDAB0 100000000000000  
## 5 3DD.003B9F123C 100000000010000  
## 6 3DD.003BC7A654 100000000010110  
## 7 3DD.003BC7F0E3 100000000010110  
## 8 3DD.003BC80A3C 100000000010100  
## 9 3DD.003BC80D81 100000000010110  
## 10 3DD.003BC80F20 100000000000100  
## # i 1,396 more rows
```

What do columns stand for?

```
defineCapHistCols(parent_child = parent_child,  
                   configuration = my_config) >>  
  as_tibble()  
  
## # A tibble: 15 x 1  
##   value  
##   <chr>  
## 1 TUM  
## 2 CHL  
## 3 CHU  
## 4 CHW  
## 5 ICL  
## 6 ICM  
## 7 ICU  
## 8 LNF  
## 9 PES  
## 10 PEU  
## 11 UWE  
## 12 LWN  
## 13 NAL  
## 14 NAU  
## 15 WTL
```

Package Resources

Package Website

- <https://kevinsee.github.io/PITcleanr/>

PITcleanr 3.0.0 FUNCTIONS VIGNETTES ▾ NEWS

PITcleanr



Description

`PITcleanr` is an R package for preparing PIT tag data for further analysis. The package can help import complete tag histories from [PTAGIS](#), build a configuration file to help assign each detection to a "node", and compress those detections into a smaller file. It contains functions to determine which detection locations are upstream or downstream of each other, build a parent-child relationship table describing whether detection locations are upstream or downstream in relation to each other, and assign directionality of movement between each detection location. For analyses that focus on one-way directional movement (e.g., straightforward CJS models), `PITcleanr` can help determine which detections fail to meet that one-way movement assumption and should be examined more closely, and which detections can be kept.

It was originally conceived as a companion to the [DABOM](#) package for estimating abundance of returning anadromous adult fish moving upstream. `PITcleanr` was designed to prepare the raw PIT tag observations from [PTAGIS](#) for use in the [DABOM](#) package.

The user can find more information related to installation and use of this package on the package website, <https://kevinsee.github.io/PITcleanr>.

Installation Instructions

The `PITcleanr` package can be installed as an R package from GitHub by using Hadley Wickham's `devtools` package:

```
# install and load packages if necessary
```

Links

[Browse source code](#)
[Report a bug](#)

License

[Full license](#)
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Community

[Contributing guide](#)

Citation

[Citing PITcleanr](#)

Developers

Kevin See
Author, maintainer

Dev status

[launch binder](#)

Package Website

- <https://kevinsee.github.io/PITcleanr/>



Articles

Getting Started

[Querying, Compressing, and Making Sense of PIT Tag Detection Data](#)

Specific components

[Reading PIT Tag Data Into R](#)

[Configuration Files](#)

[Compressing PIT Tag Data](#)

[Parent-Child Tables](#)

DABOM

Vignettes aimed at preparing data for DABOM

[DABOM Data Prep 'Cheatsheet'](#)

Contact Developers

- **Kevin See:** Kevin.See@dfw.wa.gov
- **Mike Ackerman:** MikeA@nezperce.org
- **Ryan Kinzer:** RyanK@nezperce.org

A wide-angle photograph of a landscape at sunset. The sun is low on the horizon, casting bright rays of light across the scene. The sky is filled with dark, textured clouds. In the foreground, there are rolling hills covered in green grass and some small, orange flowers. The overall atmosphere is peaceful and dramatic.

Questions?