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Nutrient Project Database Metadata

This access database contains data from Twisp River, Suspension Creek and Hancock Springs (2008-2015). There were a total of 12 Twisp River Sites used over time (TR1, TR2, TR3, TR4, TR5, TR6, TR3.1, TR3.2, TR3.3, TR4.1, TR4.2, and TR4.3. TR3 and TR3.1 were located at the same site but naming conventions changed in 2014. This is also the case for TR 4 and TR3.3. Suspension Creek was briefly sampled in 2015 and had three sample sites (SC11, SC12, SC13). Hancock Springs was composed of two reaches (Reach 1 and Reach 2) and each reach had 3 sample sites. The naming conventions for the Reach-Site combinations were Hreach#site#. Accordingly, Site one within reach two was annotated H21. When Hancock springs was only sampled at the reach level “Site” fields are identified without the second number (ie., H2 or H1). The specific sites are drawn on the attached maps.

For many of the sampling efforts, Set numbers (often referred to as “Set” in the Database) were enumerated based on the number of sampling efforts conducted in a year. For example, if Hancock Springs was electrofished in August for the 4th time in 2014, the “Set” would be labelled as 4 for all of the data collected during that sampling effort.

The current protocols for all of these datasets are currently being reviewed by monitoringmethods.com (ID# 2193, “Upper Columbia Nutrient Supplementation Project, BPA Project 2008-471-00 v1.0”).

With seven years of sampling there were substantial turnovers in staffing. Most of this database was put together by technicians employed at the time the project was terminated (3/2016). Having not been associated with the project for more than 18 months, these technicians were unfamiliar with some of the data collection efforts and associated tables in this database. Accordingly, there were some tables with columns and values that are listed as unknown. These tables were left in the database because we believe that they contain valuable information that may be important for linking future data analysis into the project. Additionally, there may be data files that were unknown to us when this database was uploaded, but could be incorporated in the future.

# Tables

Algae Taxonomy

| **Algae Taxonomy** |
| --- |
| **ID** | **Sample Date** | **Site** | **Genus** | **Division** | **Tally Rep1** | **Density (cells/mL)** | **Total Biovolume (um3/mL)** | **Sample Volume (mL)** | **Density (cells/sample)** | **Biovolume (um3/sample)** | **Notes** |
| 666 | 8/4/2008 | TR1 | Fragilaria crotonensis | Bacillariophyta | 14 | 8.00E+03 | 5.76E+06 | 190 | 1.52E+06 | 1.09E+09 |  |

Algae Taxonomy describes the species, densities and biovolume of algae found at the Twisp river site from 2008-2014, and at Hancock Springs from 2012-2014. The sample is a 30mL aliquot from the 300mL algae slurry collected by scraping the surface of cobble into a bucket of streamwater. Aliquots are also used for measuring Ash Free Dry Mass (AFDM) and Chlorophyll A & B. “ID” is a unique identifier assigned by Access for this table. “Site” refers to the river, reach, site, and repetition where applicable that the sample was collected (ie. HR11 corresponds with Hancock Springs, Reach 1, Site 1 and TR5A is Twisp River, Reach 5 all sites, sample A). “Sample Date” is the date the sample was collected. “Genus” is the genus of the algae. “Division” is the division of the algae, “Tally Rep1” could be defined by the lab. “Density (cells/mL)” is the density of the algae cells per milliliter (mL) calculated using “Density (cell/sample)” and “Sample Volume (mL).” “Total Biovolume (um3/mL)” is the volume of cells in the sample measured in cubic micrometers (µm³) per mL calculated using “Biovolume (um3/sample)” and “Sample Volume (mL)”. “Sample Volume (mL)” describes the size of the sample in mL. “Density (cells/sample)” describes the number of cells per sample. “Biovolume (um3/sample)” describes the volume of cells (biomass) found in the sample. “Notes” is a column used to define any out of the ordinary circumstances.

## BMI Hess

| **BMI Hess** |
| --- |
| **ID** | **Watershed** | **Reach** | **Site** | **SITENum** | **Habitat type** | **Set** | **UniqueID** | **Location** | **Notes** | **DateCollected** | **Rep** | **Hess** | **Row Number** | **All\_FG final** | **Taxon** | **TaxNo** | **Phylum** | **Class** | **Order** | **Family** | **Sub-family** | **Genus** | **Lengths** | **Abun(no m2)** | **Biom(g m2)** |
| 15 | Twisp | 1 | 1 |  | Open | 1 | TR1MC141016N | MC1 |  | 4/17/2012 |  | 1 |  | GC | Orthoclad sp. | 165 | ARTHROPODA | INSECTA | DIPTERA | CHIRONOMIDAE | Orthocladiinae | X1 | 1 | 1.93798449612403 | 7.36434108527132E-06 |

BMI Hess is a table of benthic macroinvertebrate (all immature/aquatic stage) samples collected with a Hess sampler in Hancock Springs (2012-2014) and the Twisp River (2012). “ID” is a unique identifier assigned by Access for this table. “Watershed” is the general location the sample was collected in (either Twisp or Hancock Springs). “Reach” and “Site” refer to the specific place the sample was collected in. SITENum is an unknown field. “Habitat type” is the type of habitat (Pool, Riffle or Open) the sample was collected in. “Set” is relative sampling effort in a given year. “UniqueID” is the file associated with the lab that identified the macroinvertebrates. “Location” is the location in the stream (Left Bank [LB], Right Bank [RB] or Mid Channel [MC]). “Notes” is any additional observations made at the time of sampling or during macroinvertebrate identification. “Rep,” “Hess,” “RowNumber,” and “All\_FG final” are unknown columns. “Taxon” is the Taxon of the individual identified. “TaxNo” is cross referenced to the “SPP\_INVERT” field in the “INVERTEBRATE\_CODES” table. “Phylum,” “Class,” “Order,” “Family,” “Sub-family” and “Genus” are the Phylum, Class, Order, Family, Sub-family and Genus, repectively, of the individuals identified. “Lengths” is an unknown column. “Abun(no m2)” was calculated in excel based on the number of individual macroinvertebrates of a given family observed and the area of stream sampled. It is the number of macroinvertebrates belonging to a given Family per square meter. “Biom(g m2)” was calculated in excel based on the weight of individuals belonging to a family observed and the area of stream sampled. It is the mass (g) of macroinvertebrates belonging to a given Family per square meter. These samples were analyzed by Invertebrate Ecology. Additional information about the data may be available by contacting them (http://www.invertebrateecology.com/about-us/).

## BMI Isotope

| **BMI Isotpes Contents** |
| --- |
| **ID1** | **Concatenated** | **Site** | **Sampler** | **DateCollected** | **Abundance** | **ID** | **TaxNo** | **Phylum** | **Class** | **Order** | **Family** | **Sub-family** | **Genus** | **EcoNumber** | **Stage** | **Habitat** | **FG final** |
| 88 | HS 1.2 BMI ISO 2 | HS12 | BMI | 4/29/2013 | 1 | Tipula sp. | 150 | ARTHROPODA | INSECTA | DIPTERA | TIPULIDAE |  | Tipula |  | Immature | Aquatic | SH |

This table consists of benthic macroinvertebrates that were collected in Hancock (2013-2014) and the Twisp River (2013) and sent to a lab to be assessed for their isotopic signature. The results of the isotope analysis are not included in this table. When the results of the isotopic analysis are available, they could be linked to this table. “ID” is the unique access identifier for each record. “Concatenated” is an unknown field. “Site” is the location the data was collected from. “Sampler” was the method of collection (BMI= a Hess Sampler, Drift= a net sampler collecting macroinvertebrates floating on the surface, ISO= unknown sample method). “DateCollected” is the date the sample was collected. “Abundance” is the number of a species identified in a sample. “ID” is the species of macroinvertebrate observed. “TaxNo” is cross referenced to the “SPP\_INVERT” field in the “INVERTEBRATE\_CODES” table. “Phylum,” “Class,” “Order,” “Family,” “Sub-family” and “Genus” are the Phylum, Class, Order, Family, Sub-family and Genus, repectively, of the individuals identified. “EcoNumber” is an unknown field. “Stage” was the stage of the macroinvertebrates identified (Immature or Adult). “Habitat” is the habitat the collected individuals occupy. “FG final” is an unknown field.

Conditional Comment

| **CONDITIONAL\_COMMENT** |
| --- |
| **CODE** | **DESCRIPTION** |
|    <2 |   Descaled Between 11 and 20%   |

This is a table defining the accepted PTAGIS conditional comment codes to their descriptions. This information is also available at PTAGIS.ORG. “CODE” is a unique alpha, numeric, symbol or combination defining a common condition observed in tagged fish. “DESCRIPTION” uses words to describe the common condition observed in tagged fish.

| **Drift** |
| --- |
| **ID** | **Date** | **Site** | **Position** | **Time In** | **Time out** | **Total time deployed** | **net depth (cm)** | **net area (cm²)** | **velocity (m/s)** |
| 1 | 7/16/2012 | HS11 | LB | 10:00 | 14:30 | 4:30 | 25 | 1125 | 0.30 |

Drift

Drift describes the flow, depth, and time deployed of drift samples in the Twisp and Hancock in 2012 and 2013. The “ID” field is a unique access identifier for this table. “Date” is the date the sample was collected. “Site” corresponds with the specific river location, reach number, and site number within (ie. HS11 corresponds with Hancock Springs, Reach 1, Site 1 and TR43 is Twisp River, Reach 4, and Site 3). “Position” describes where the sample was taken. LB indicates that the sample was collected from the river left side of the stream (divided along the center of the thalweg), while RB indicates the right side. In instances where a side was too deep to sample, both nets would be put on the shallower side. For example, if the left side of a stream was too deep to sample, two samples would be collected and labelled RB-L and RB-R. “Time In” is the time the net was installed. “Time out” is the time that the net was removed and sampling ended. “Total time deployment” is the duration the net was sampling, calculated using the “Time In” and “Time out” columns. “Net depth (cm)” is the average depth the net was submerged in centimeters (cm). “Net area (cm²)” is the area of net that was actively sampling in square cm, calculated with the “net depth (cm)” and the nets width (45cm). “Velocity (m/s)” is the velocity in meters per second (m/s) measured with a Marsh McBirney flow meter at the net site prior net installation.

| **Efishing passes** |
| --- |
| **ID** | **HeaderID** | **SPECIES\_DESC** | **Passes** | **Success** |
| 210 | 75 | BROOK TROUT | 4 | Y |

Efishing passes

Efishing passes documents the number of electroshocking passes sampling a given site at Hancock Springs. “ID” is the unique identifier assigned to the record by Access. “HeaderID” is the P3 File associated with sampling that site (on a given date). “SPECIES\_DESC” is the species collected. The total number of passes (“Passes”) is dictated by the depletion rates and coefficient of variations (CV) calculated from the number of fish (of a given species) captured in each pass. As soon as the CV has dropped below the threshold, no additional passes are taken. The total number of passes ranges from two to six. If a low enough CV is never achieved then a population estimate cannot be calculated and the “Success” field will say “N”.

| **FISH\_CAPTURE** |
| --- |
| **ID** | **SITE\_ID** | **SAMPLE\_DATE** | **SPP\_FISH** | **PASS1** | **PASS2** | **PASS3** | **PASS4** | **PASS5** | **PASS6** |
| 57 | HS11 | 4/3/2012 | 3 | 11 | 2 | 1 | 1 |  |  |

Fish Capture

Fish Capture (like the Efishing Passes table) is associated with electrofishing efforts in Hancock Springs and the Twisp River (2012 only). This table totals the fish by pass and species for 2012 and 2013 (there is an issue with the Fish Capture Summary Query used to populate this table). This table was only populated through 2013. “ID” is a unique access identifier assigned to each record. “SITE\_ID” is the numbers are then used to estimate the population by species (see serber-LeCren.xls and Zippin.xls files attached in streamnet). ID is the unique identifier in Access. SITE\_ID corresponds with the specific Reach number and Site number within Hancock (ie. HR1.1 corresponds with Reach 1, Site 1). SAMPLE\_DATE is the date the sample was collected. SPP\_FISH is the species of fish collected. The letter or number codes are linked and described in the table “FISH\_CODES.” PASS1, PASS2, PASS3, PASS4 and PASS5 represent the number of fish collected in that electrofishing pass. If any of these fields are empty for a given record, that pass was not made. For example in the record listed below, only three electroshocking passes were necessary.

| **FISH\_CODES** |
| --- |
| **SPP\_FISH** | **SPECIES\_DESC** |
| 4 | SOCKEYE |

Fish Codes

Fish Codes is a table linking the PTAGIS species code to the common species name of fish. This table is linked to a few queries in this database and the information is also available at PTAGIS.ORG. “SPP\_FISH” is a single unique number or letter, “SPECIES\_DESC” uses the common species name associated with the unique number or letter.

| **FLOW** |
| --- |
| **ID** | **Date** | **Location** | **Flow (cfs)** |
| 1 | 4/4/2013 | Mouth | 11.9 |

Flow

Flow shows the cubic feet per second (cfs) at the Hancock sampling locations from 2011 to 2015. “ID” is a unique access identifier for each record. “Date” is the date the flow was collected (All flows were collected between 10:00 and 14:00). “Location” is the location within the stream that the flow was collected (see attached map). “Flow (cfs)” is the flow in cubic feet per second measured with a Marsh McBirney flow meter.

Foam Plugs Algae Accrual

| **FOAM\_PLUG\_ALGAE\_ACCRUAL** |
| --- |
| **ID1** | **ID** | **ASL\_ID** | **Client\_ID** | **COLLECT\_DATE** | **DEPLOY\_DATE** | **TOT\_DAYS\_DEPLOY** | **Chlor\_A** | **Chlor\_A\_µg/M²** | **Chlor\_A\_mg/M²** | **Chlor\_A\_g/M²** | **DETECT\_LIMIT\_ug** | **ANALYTE** | **SITE\_ID** |
| 1 | 73 | E1002117 | Poormans Creek LB 5,19,3 | 21-Jul-08 | 7-Jul-08 | 14 | 1.3 | 1706.04 | 1.71 | 0.00 | 0.1 | Chlorophyll B | TR2.0 |

Foam Plugs Algae Accrual is a table that summarizes the standing crop in collected using a foam plug following the PESC-Winterman/DeMots Mod. –Foam method in the Twisp River and Hancock Springs from 2008 to 2012. This sampling method was no longer used after 2012. “ID1” is the unique identifier assigned by access. “ID” is the sample identifier assigned in the field. “ASL\_ID” is the unique identifier assigned by the lab. “Client\_ID” is a description of the site, but also contains stream section, and habitat unit if applicable. “COLLECT\_DATE” is the date the foam plug sample was collected. “DEPLOY\_DATE” is the date the sample was placed in stream. “TOT\_DATS\_DEPLOY” is the total number of days the sample was deployed, and is calculated using the difference in collection and deployment dates. “Chlor\_A” is the amount of Chlorophyll A in micrograms (µg) found in the sample. “Chlor\_A\_ µg/M²” is the density of Chlorophyll A in µg per square meter (m²) found using the area of the foam plug sampled. “Chlor\_A\_mg/M²” is the density of Chlorophyll A in milligrams (mg) per m² calculated by converting µg of the previous column to mg. “Chlor\_A\_g/M²” is the density of Chlorophyll A in grams (g) per m² calculated by converting mg of the previous column to g. “DETECT\_LIMIT\_µg” is the detectable lower limit of Chlorophyll A in µg. “ANALYTE” is the substance whose chemical constituents were measured by the lab. “SITE\_ID” corresponds with the specific river location, reach number, and site number within (ie. HR1.1 corresponds with Hancock Springs, Reach 1, Site 1 and TR5.0 is Twisp River, Reach 5, all sites).

| **GUILD\_CODES** |
| --- |
| **FUNCTIONAL\_GUILD** | **IDAS\_CODE** |
| Collector/Filterer | FC |

Guild Codes

Guild Codes describes the functional group of macroinvertebrates (FUNCTIONAL\_GUILD) linked to the 2 letter ID codes in the Invert Bio Update table.

Invert\_Bio\_Update, INVERT\_MASTER, INVERTEBRATE\_ABUNDANCE, INVERTEBRATE-BIOMASS, INVERTEBRATE\_DIVERSITY, INVERTEBRATE\_PRODUCTION, INVERTEBRATE\_RICHNESS

We are not familiar with any of these tables. We are leaving them in the database to be possibly updated (or associated with additional data) at a later date.

Invertebrate Codes

| **INVERTEBRATE\_CODES** |
| --- |
| **SPP\_INVERT** | **Phylum** | **Class** | **Order** | **Family** | **SUBFAMILY** | **Genus** | **Taxon** | **Index** | **FUNCTIONAL\_GUILD** | **IDAS\_CODE** |
| 0001 | ARTHROPODA | INSECTA | EPHEMEROPTERA | BAETIDAE |  | ACENTRELLA | ACENTRELLA TURBIDA | 4 | COLLECTOR/GATHERER | GC |

Invertebrate codes is used as a cross reference table for the “Lavage Contents” and other macroinvertebrate collection tables. SPP\_INVERT is a unique record identifier and the specific field that is cross referenced in the other tables. . “Phylum,” “Class,” “Order,” “Family,” “Sub-family,” “Genus” and “Taxon” are the Phylum, Class, Order, Family, Sub-family, Genus and Taxon, repectively, associated with the SPP\_INVERT id, which is cross referenced in other tables.

## **Lavage Contents**

| **Lavage Contents** |
| --- |
| **ID1** | **Init Order** | **ID** | **Year** | **Collection Date** | **Site** | **Sample Set** | **Concatenate** | **Lavage Number** | **Species** | **Age Class** | **TaxNo** | **Taxon** | **Phylum** | **Class** | **Sub-Class** | **Order** | **Family** | **Sub-family** | **Genus** | **Stage** | **Habitat** | **FG final** | **AE** | **NPE** | **No of samples** | **PropPreyInGut(Gi)** | **Abundance** | **Biomass (g)** | **summed biomass (g/taxon/fish)** | **Av Biomass (g/taxon individual/fish** |
| 1 | 1 | 2012 | 2012 | 4/4/2012 | HS11 | 1 |  | LVH15-12 | BRT | 3 | 1060 | CHIRONOMIDAE(A) | ARTHROPODA | INSECTA |  | DIPTERA | CHIRONOMIDAE |  |  | Adult | Aquatic |  | 0.75 | 0.1875 | 6 | 3.12498333333333E-05 | 1 |  | 0.000187499 | 0.000187499 |

This table is the lavaged fish stomach contents from electroshocking efforts at Hancock Springs (2012-2014) and the Twisp River (2012 only). “ID” is the unique access identifier for each record. “Init Order” and “ID” are unknown fields. “Collection Date” is the date the sample was collected on. “Site” is the site where the fish was capture prior to lavage. “Sample Set” was the relative sampling effort in a year (ie., 4 would represent the fourth time electroshocking had been conducted that year). “Concatenate” is an unknown field. “Lavage Number” is the sample number for a given sample set (each new set starts at 0). If multiple prey items were removed from a fish stomach, there will be multiple records with the same values for “Collection Date,” “Site,” “Sample Set,” and “Lavage Number.” “Species” is the species of fish the lavage sample was collected from. “Age Class” is the age class of the fish the lavage sample was collected from. “TaxNo” is cross referenced to the “SPP\_INVERT” field in the “INVERTEBRATE\_CODES” table. “Taxon,” “Phylum,” “Class,” “Sub-Class,” “Order,” “Family,” “Sub-family,” and “Genus” are the Taxon, Phylum, Class, Sub-Class, Order, Family, Sub-family and Genus of the items lavaged out of the fish. “Stage” is the life stage of the item lavaged out of the fish. “Habitat” is the habitat type used (terrestrial or aquatic) by the item lavaged out of the fish. “FG final,” “AE,” “NPE,” “No of samples” are unknown fields. We are unsure how “PropPreyInGut(Gi),” “Abundance,” “Biomass (g),” “summed biomass (g/taxon/fish),” and “Av Biomass (g/taxon individual/fish” were calculated. These samples were analyzed by Invertebrate Ecology. Additional information about the data may be available by contacting them (http://www.invertebrateecology.com/about-us/).

Par

| **Par** |
| --- |
| **ID** | **Site** | **Date Time, GMT-08:00** | **PAR, uE** |
| 37172 | HS1 | 9/14/2015 5:30 | 1.2 |

The par table shows the site, the time (every 15 minutes), and a PAR value (µE/m²s) at Hancock from 3/2015 to 9/2015. *These sensors are still in the field, and still recording. The sensor should be downloaded, and the data imported to Access before they are removed from the field.* “ID” is the unique access identifier for each record. “Site” is the location the sample was collected (see maps). “Date Time, GM-08:00” is the date and a military time for each record. “PAR µE” is the amount in millimole (µmol) photons of solar radiation in the visible spectrum (400-700 nanometers (nm)) that interact with an area measured in m², during a second (s). This is expressed in einstein units (µE/m²s).

Periphyton

| **Periphyton** |
| --- |
| **ID** | **Site** | **Location** | **Sample date** | **Ash Free Dry Mass (g)** | **AFDM g/m^2** | **Weight-Dry Material (g)** | **Chlorophyll A (ug)** | **ChlA g/m^2** | **Chlorophyll B (ug)** | **ChlB g/m^2** | **Chlorophyll A&B (ug)** | **ChlA&B g/m^2** | **A\_paper (cm)** | **W\_paper (g)** | **W\_rock silhouette (g)** | **A\_rock (cm)** | **Water Volume sampled (mL)** | **Sub-sample size (mL)** | **Sub-sample rock area** | **Notes** |
| 1162 | HS23 | 5 | 12/29/2015 |  | 0 |  |  | 0 |  | 0 |  | 0 |  |  |  | 34.5 | 300 | 30 | 3.446 |  |

Periphyton is a table displaying measurements of Ash Free Dry Mass, Chlorophyll A & B measurements (g/m2) from the Twisp River and Hancock Springs from 2012 to 2014. “ID” is the unique access identifier for each record. “Site” is the location the sample was collected (see maps). “Location” is the sample number of each rock taken from the reach. “Ash Free Dry Mass (g)” is the mass (g) of periphyton scraped from rocks (weighed and measured in a lab). “AFDM g/m^2” is the weight per m² of Ash Free Dry Mass. This is based on the area of the rock scrubbed and the lab measured weight of the periphyton. “Weight-Dry Material (g)” is the weight of the dried periphyton measured by the lab in g. “Chlorophyll A (µg)” is the weight of the Chlorophyll A scrubbed from rock samples and measured in a lab in µg. “ChlA g/m^2” is the weight per m² of the Chlorophyll A based on lab measurements and the area of the rock scraped measured in g/m². “Chlorophyll B (µg)” is the weight of the Chlorophyll B scrubbed from rock samples and measured in a lab in µg. “ChlB g/m^2” is the weight per meter squared of the Chlorophyll B based on lab measurements and the area of the rock scraped in g/m². “Chlorophyll A&B (µg)” is the combined weight of the Chlorophyll A and Chlorophyll B scrubbed from rock samples and measured in a lab in µg. “Chl A&B g/m^2” is the combined weight per meter squared of the Chlorophyll A and Chlorophyll B based on lab measurements and the area of the rock scraped in g/m². “A\_paper (cm),” “W\_paper (g),” “W\_rock silhouette (g),” “A\_rock (cm),” were all used to calculated the area of each rock that was scraped to collect periphyton. “A\_paper (cm),” is the total area (cm2) of the piece of paper each scraped rock was traced on. “W\_paper (g)” is the weight (g) of the paper the rock was traced on. “W\_rock silhouette (g),” is the weight (g) of the rock-tracing cut-out from the whole piece of paper. “A\_rock (cm),” is the calculated rock area (cm2) based on the relative weight of the rock tracing compared to the entire piece of paper. “Notes” is used to describe any anomalies that occurred with the sample, or “TAX” was used to note the sample from which the aliquot for algae taxonomy was taken. In 2015 we started using ImageJ, a program that calculates the area of a traced silhouette in cm². We have areas for the samples taken in 2015 but the samples have not yet been processed. The Twisp river was not sampled in 2014.

| **PIT\_ANTENNAS** |
| --- |
| **TIMESTAMP** | **PITTAG** | **READER** |
| 1/6/2016 3:26:00 PM | 3D9.1C2C372EB3 | A2 |

PIT Antennas

Pit antennas is a table that simply shows the detections of PIT tagged fish in the PIT arrays in Hancock spring. TIMESTAMP is the time and date of the detection. PITTAG is the identification of the fish passing the antenna. READER is the antenna coil ID reading the detection (A1 and A2 are at the bottom of reach 1; B1 and B2 are at the bottom of reach 2; and C1 and C2 are at the mouth of Hancock springs where it enters the Methow River). This data ranges from April 2013 to January 2016. Also, this information can be found on the PTAGIS.ORG website, along with antenna downtimes and other issues.

| **REDDS** |
| --- |
| **YEAR** | **SITE** | **SPP\_FISH** | **REDD\_COUNT** | **GPS\_LOCATION\_LAT** | **GPS\_LONG** | **DATE\_DETECTED** | **NOTES** |
| 2014 | HS11 | 3 | 1 | 48.534722 | 120.334167 | 4/28/2014 |  |

Redds

Redds shows counts (conducted from visual bank surveys) of salmonid redds at Hancock from 2012 to 2015. “YEAR” is the year the redds were detected. “SITE” is the Site the redds were detected in (see map). Before 2013 redd counts were only enumerated within reaches (Reach 1 = H1 and Reach 2 = H2). “SPP\_FISH” is the species of fish the redd was associated with. These codes are described and linked in the FISH\_CODES table. “REDD\_COUNT” is the number of redds that were counted in a given site (or reach). “GPS\_LOCATION\_LAT and GPS\_LONG” is the latitude and longitude of the redd. This information was not always collected and sometimes redds were only enumerated at the reach or site scale. “DATE\_DETECTED” is the exact date the survey was conducted (DD/MM/YYYY). “NOTES” is any additional observations the surveyor made.

Sonde Calibrations

| **Sonde Calibrations** |
| --- |
| **ID** | **Cali File** | **Date (MM/DD/YYYY)** | **Time (HH:MM:SS)** | **Temp °C** | **Cond µS/cm** | **TDS mg/L** | **SpCond µS/cm** | **Sal psu** | **Chlorophyll RFU** | **Chlorophyll µg/L** | **BGA-PC RFU** | **BGA-PC µg/L** | **ODO % sat** | **ODO mg/L** |
| 1 | CH10212014 | 2/12/2014 | 12:06:29 | 5.729 | 90 | 59 | 143 | 0.07 | 0.56 | 2.05 | 0.04 | 0.04 | 93 | 11.65 |

This is a table of the calibration files for each sonde. Date, time, sonde, battery life, % sat DO, and DOmg/L are displayed. The calibration file was used to document and troubleshoot any sonde issues that would come up. “ID” is the unique access identifier for each record. “Site” is the location the sample was collected (see maps). “Cali File” is the unique name the file was saved under. The rest of the columns are identical to, and define in the Sonde Data table below.

Sonde Data

| **Sonde Data** |
| --- |
| **ID** | **Site** | **Date (MM/DD/YYYY)** | **Time (HH:MM:SS)** | **Temp °C** | **Cond µS/cm** | **TDS mg/L** | **SpCond µS/cm** | **Sal psu** | **Chlorophyll RFU** | **Chlorophyll µg/L** | **BGA-PC RFU** | **BGA-PC µg/L** | **ODO % sat** | **ODO mg/L** |
| 1 | HS2 | 12/10/2013 | 12:40:50 | 5.09 | 89 | 58 | 144 | 0.07 | 20.75 | 83.27 | 3.49 | 3.49 | 96.9 | 12.34 |

Sonde data shows the site, date and time, a handful of parameters that were never calibrated as well as dissolved oxygen (DO) data for the two Hancock sites from 4/2013 to 1/2016. *These sensors are still in the field, and still recording. The sensor should be downloaded, and the data imported to Access before they are removed from the field.* “ID” is the unique access identifier for each record. “Site” is the location the sample was collected (see maps). “Date” is the date that the measurement was collected. “Time” is the military time, in hours, minutes and seconds that the measurement was collected. “Temperature °C” is the temperature in degrees Celsius (°C). “Cond µS/cm” is the conductivity measured in microSiemens (µS) per cm. “TDS mg/L” is a measure of total dissolved solids in mg/liter(L). “SpCond µS/cm” is the specific conductivity in µS/cm. “Sal psu” is salinity measured in practical salinity units (PSU) based on the properties of sea water conductivity. “Chlorophyll RFU” is a chlorophyll measurement in relative florescent unit (RFU). “Chlorophyll µg/L” is a measure of Chlorophyll in µg/L. “BGA-PC RFU” is a blue-green algae measurement in RFU. “BGA-PC µg/L” is a blue-green algae measurement in µg/L. And finally, “ODO % sat” is a measurement of the percent saturated with dissolved oxygen the water is. “ODO mg/L” is a measurement of the amount of oxygen dissolved in the water in mg/L.

Tag Detail

| **TAGDETAIL** |
| --- |
| **HeaderID** | **DetailID** | **PITCode** | **Sequence** | **ForkLength (mm)** | **Weight (g)** | **Species** | **Run** | **RearingType** | **AgeClass** | **IsotopeNum** | **LavageNum** | **DNANum** | **AdditionalComment** | **ConditionalComment** | **TextualComment** | **Pass** |
| 8 | 85 | 3D9.1C2D9F1627 | 3 | 215 | 116 | 3 | R | W | 4 |  |  |  |  |  |  |  |

Tag Detail documents each individual fish that is handled at by the crew. It is uploaded to the PTAGIS.ORG database. This is the bulk of the fish data; the table is queried to determine daily growth, biomass, and production. The “HeaderID” is used to link to tag header information like date, temperature, tagger and so forth in the TAGHEADER table to each fish. “DetailID” is the unique identifier assigned by Access. “PITCode” displays the unique Passive Integrated Transponder (PIT) tag implanted in the fish, or is blank if the fish was not tagged. “Sequence” is a whole number starting at 1 that defines what position in the P3 file the fish was sampled for each file. “ForkLength (mm)” is a measurement from the tip of the snout to the trough of the tail in millimeters (mm), sculpin do not have a forked caudal, and should be considered measurements of total length from snout to the tip of the tail. “Weight (g)” is the weight in grams measured by an OHAUS digital scout pro scale (For the 2014 and 2015 sampling seasons weights were imported directly from the scale to the tagging file). “Species” is a number or letter that describes the fish species, descriptions of these codes can be found in the FISH\_CODE table or at PTAGIS.ORG. “Run” is a single number that describes the run of the fish, descriptions of these codes can be found at PTAGIS.ORG. “Rearing Type” is a code describing the rearing type of the fish, descriptions of these codes can be found at PTAGIS.ORG. “AgeClass” describes the age class of the fish. These values were determined based on length-frequency histograms produced in R. This has only been completed through the 2013 data. “IsotopeNum” is the sample ID associated with the fin clip taken for isotope analysis. “LavageNum” is the sample ID associated with the lavage sample taken. Isotope and lavage samples are only collected on 5 fish from each species per site per sample set if available. Both IsotopeNum and LavageNum are populated using the AdditionalComment column when the data is uploaded to the database. “DNANum” signifies the number associated with samples taken for genetic analysis and scale cards, it is populated from the TextualComment column when the data is uploaded to the database. “AdditionalComment” is the column that lavage and isotope numbers are entered into in the field, and redistributed to individual columns when uploaded to the database. “ConditionalComment” is a unique alpha, numeric, symbol or combination defining a common condition observed in tagged fish as described in CONDITIONAL\_COMMENT table and found on PTAGIS.ORG. “TextualCommnet” is used to describe any anomalies that occurred with the sample, and starting in July 2013 to present this column was used to note what e-fishing pass the sample was collected in (p1-6=pass 1-6, PNA=not associated w/ a pass). “Pass” is used to record what pass each fish is from, and is populated when tag detail data is imported to the database using data initially recorded in the TextualComment column.

Tag Header

| **TAGHEADER** |
| --- |
| **HeaderID** | **Name** | **TemplateID** | **Created** | **Modified** | **FileName** | **SessionMessage** | **TagDate** | **Tagger** | **MigratoryYr** | **TagSite** | **RacewayTransect** | **CaptureMethod** | **TaggingTemp** | **TaggingMethod** | **Organization** | **CoordinatorID** | **ReleaseSite** | **ReleaseRiverKM** | **ReleaseRiverKMExt** |
| 214 | TNA15343.H21 | 22 | 12/9/2015 1:35:28 PM | 12/9/2015 1:52:10 PM | TNA15343.H21 | STH:0%CV; BRK:3.4%CV; CHK:0%CV; SCL:14.0%CV | 12/9/2015 1:34:00 PM | FISH T | 15 | HANSPC | HS21 | SHOCK | 6.5 | HAND | YINN | TNA | HANSPC | 843.097 | 001 |

Tag Header describes tagging information for the associated TAGDETAIL table. The “HeaderID” links the TAGHEADER information to the TAGDETAIL for each fish. “Name” is the name of the file as it is saved locally in the program P3, and online at PTAGIS.ORG. “TemplateID” describes which of the saved P3 templates was used to create the tag file. “Created” is the date the file was created. “Modified” describes the date for the last modification of the table. “FileName” is the unique name of the P3 file. “SessionMessage” is a column that is used to describe the sampling purpose, any anomalies that occurred during, and since 2014 a list of the %CV for population estimates for each species generated in the field. “TagDate” shows the date the fish were tagged. “Tagger” describes the person tagging by their last name and first initial. “MigratoryYr” is the year the fish were tagged. “TagSite” is the river or location the fish were tagged at. A list and description of tag sites can be found at PTAGIS.ORG. “RacewayTransect” describes the site the fish were sampled from (see map). “CaptureMethod” describes the method used to capture the sample. A list and description of capture methods can be found at PTAGIS.ORG. “TaggingTemp” is the temperature of the anesthesia bath in °C. “TaggingMethod” describes the method of tagging. A list and description of tagging methods can be found at PTAGIS.ORG. “Organization” notes the organization responsible for the tags. “CoordinatorID” is a unique identifier associated with the project. “ReleaseSite” is the location fish were released at after sampling. “ReleaseRiverKM” is the location in river kilometer (km) of the mouth of the release site. “ReleaseRiverKMExt” is the distance up the release site river, in km, that the fish were released after sampling.

| **TEMP\_HS** |
| --- |
| **ID** | **Location** | **Date Time, GMT-08:00** | **Temp, °C** |
| 2 | Hancock Source | 1/26/2012 15:30 | 5.154 |

Temp HS

This table shows the location, date, time, and temperature recorded every 30 minutes of the five Hancock hobo loggers from 1/2012 to 9/2015. *These loggers are still actively logging and should be downloaded, and imported to the database when they are removed from the field.* “ID” is a unique identifier assigned by Access for this table. “Location” refers to the location of the logger. “Date Time, GMT-0800” is the date and military time of the measurement. “Temp, °C” is the water temperature in °C measured by the recorder. The loggers are housed in PVC to protect from the sun, and placed in pools near shore that will hold water year round, but occasionally extreme low flows cause the loggers to go dry where they will continue to record, but measure air temperature instead of water.

| **TEMP\_TWISP** |
| --- |
| **ID** | **Location** | **Date Time, GMT-07:00** | **Temp, °C** |
| 1 | TR 3.1 | 8/2/2012 15:00 | 14.84 |

Temp Twisp

This table shows the location, date, time, and temperature recorded every 30 minutes of the six Twisp river hobo loggers from 1/2012 to 9/2015. *These loggers are still actively logging and should be downloaded, and imported to the database when they are removed from the field.* “ID” is a unique identifier assigned by Access for this table. “Location” refers to the location of the logger. “Date Time, GMT-0800” is the date and military time of the measurement. “Temp, °C” is the water temperature in °C measured by the recorder. The loggers are housed in PVC to protect from the sun, and placed in pools near shore that will hold water year round, but occasionally high flows, ice dams and extreme drought cause the loggers to go dry where they will continue to record, but measure air temperature instead of water.

## TMI Pan Traps

| **TMI Pan Traps** |
| --- |
| **ID** | **Date** | **Site** | **Stage** | **Habitat** | **Guild** | **Species** | **TaxNo** | **Phylum** | **Class** | **Order** | **Family** | **Sub-family** | **Genus** | **Length** | **AbunConv** | **BiomConv** |
| 26 | 7/28/14 | HS22 | Immature | Aquatic | GC | Orthoclad sp. | 165 | ARTHROPODA | INSECTA | DIPTERA | CHIRONOMIDAE | Orthocladiinae |  | 2 | 1 | 2.28164022822184E-05 |

This table is all of the terrestrial macroinvertebrate data collected in pan traps in Hancock Springs in 2014. “ID” is the unique identifier assigned to each record by Access. “Date” is the date the pan traps were collected (all pan traps were deployed for 72 hrs before being collected). “Site” is the Site the pan traps were deployed in. “Stage” is the lifestage of the observed macroinvertbrate. “Habitat” is the normal habitat occupied by the insect collected. “Guild” is the functional guild of the observed macroinvertebrate. This code can be cross referenced with the IDAS\_CODE and FUNCTIONAL\_GUILD in the “INVERTEBRATE CODES” table. “TaxNo” is cross referenced to the “SPP\_INVERT” field in the “INVERTEBRATE\_CODES” table. “Species,” “Phylum,” “Class,” “Order,” “Family,” “Sub-family” and “Genus” are the Species, Phylum, Class, Order, Family, Sub-family and Genus, repectively, of the individuals identified. “Length” is an unknown field. We are not sure how “AbunConv,” and “BiomConv” were calculated. Additional information about the data may be available by contacting them (http://www.invertebrateecology.com/about-us/).

Water Chem

| **WATER\_CHEM** |
| --- |
| **ID** | **LabID** | **Sample Date** | **SITE** | **Subsite** | **Location** | **TP** | **TDP** | **SRP** | **NH4** | **NO2\_NO3** | **TN** | **ALKALINITY** | **DIN** | **TOC** | **TEMP\_C** | **TIME** | **DISCHARGE** |
| 978 | TR6.020111026R | 10/26/11 0:00 | TR6 | B | RB | 2.00 | 2.00 | 1.00 | 10.00 | 10.00 | 56.56 |  |  | 28235.29 | 6.0 | 10:00 | 83 |

This table documents the location and chemical components of samples taken from Hancock Springs (2012-2015), Twisp (2008-2015, intermittent), and Suspension Creek (2015, limited data). “ID” is a unique identifier assigned by Access for this table. “LabID” is a unique identifier assigned for the sample by the lab. “Sample Date” is the date the water samples were collected. “SITE” is the location the sample was collected at and corresponds with the river, reach number, and site number within (ie. HS11 corresponds with Hancock Springs, Reach 1, Site 1 and TR43 is Twisp River, Reach 4, and Site 3). “Subsite” is used if more than one sample was taken from a single location. “TP” is the total phosphorous in µg/L found in the sample. “TDP” is the total dissolved phosphorous in µg/L found in the sample. “SRP” is soluble reactive phosphorous in µg/L found in the sample. “NH4” is the amount of ammonium in µg/L discovered in the sample. “NO2\_NO3” is the amount of nitrite and nitrate in µg/L in the sample. “TN” is the total µg/L nitrogen found in the sample. “AKALINITY” is a measure of calcium carbonate ([Ca](https://en.wikipedia.org/wiki/Calcium)[C](https://en.wikipedia.org/wiki/Carbon)[O](https://en.wikipedia.org/wiki/Oxygen)3) in µg/L discovered in the sample. “DIN” is the deposition of inorganic nitrogen in µg/L measured in the sample. “TOC” refers to the total organic carbon in µg/L found in the sample. “TEMP\_C” is the water temperature in °C measured with a thermometer at the location and time of the sample. “TIME” is the time the sample was collected. “DISCHARGE” is recorded in cfs as measured by USGS real time water database for the Twisp or as flows measured with a Marsh McBirney flow meter taken in conjunction with water chemistry samples.

| **YrSet** |
| --- |
| **ID** | **HeaderID** | **YrSet** | **SetDate** |
| 1 | 214 | 15.6 | 12/7/2015 |

YrSet This table helps simplify reading several queries by identifying the date of a sample session (without having to look at the “TAGHEADER” table. “HeaderID” matches the value in the HEADERID table associated with a YrSet and SetDate. In the example listed in the row pictured, this was the sampling set number 6 collected in 2015 (YrSet = 15.6) and the mean date of this sampling set (SetDate) was 12/7/2015.

# Queries

## Fish\_Capture\_Summary

* This update query updates the table “Fish Capture” (which can be used to estimate the populations of species in reaches). It is not currently working but could be fixed in the future.

## Fish Counts

| **Fish Counts** |
| --- |
| **HeaderID** | **Site** | **SPECIES\_DESC** | **Passes** | **Success** | **Total Catch** | **AvgOfWeight** | **StDevOfWeight** | **<>** | **1** | **2** | **3** | **4** | **5** | **6** |
| 108 | H13 | CHINOOK | 3 | Y | 16 | 9.05625006556511 | 1.7746243930377 |  | 12 | 3 | 1 |  |  |  |

* This query summarizes fish captures and electrofishing passes **SINCE MARCH 2013**. The limited data collected in 2012 is not included in this query.
* “HeaderID” is the P3 file specifically associated with electrofishing this site-and set. “Site” corresponds to the Hancock site number being electrofished. “Passes” is the number of electrofishing passes that were conducted for a given species on a given day (in order to meet the coefficient of variation threshold).
* “Success” indicates whether or not the coefficient of variation was low enough to calculate the population. The relative CV values were calculated in an excel spreadsheet (see attached) ”Serber-LeCren.xlsx” was used if only 2 passes were made. “Zippin.xlsx” was used if 3 or more passes were made.
* “Total Catch” is the total number of that species caught electrofishing in a single site on a single date.
* “AverageOfWeight” and “StDevOfWeight” were the average and standard deviation of the weight of that species of fish observed in that site-set combination.
* Columns “1,” “2,” “3,” “4,” “5,” and “6” tally the number of fish captured in that electrofishing pass. For example in the row pictured above there were 11, 2 and 4 brook trout capture in the first, second and third electroshocking passes, respectively.

## Morts

| **Morts** |
| --- |
| **Year** | **BROOK TROUT** | **CHINOOK** | **SCULPIN** | **STEELHEAD** |
| 2012 |  |  |  | 1 |

* This table is used for report writing and calculates the number of mortalities of each species that occurred in each year. “Year” is the year mortalities are calculated for. “BROOK TROUT,” “CHINOOK,” “SCULPIN,” and “STEELHEAD” is the number of brook trout, chinook, sculpin and steelhead mortalities that occurred in a year (if blank there were no mortalities).

## CoC: Lavage and ISO

| **CoC: Lavage and ISO** |
| --- |
| **TagDate** | **Site** | **SPECIES\_DESC** | **IsotopeNumber** | **LavageNumber** |
| 12/1/2015 2:09:00 PM | H13 | CHINOOK | ISO61 | LV61 |

* This table was generated for each sampling set and printed as a chain of custody (CoC) packaged with the lavage and isotope samples. Only fish that were lavaged will appear in this query. “TagDate” is the date and time the fish was tagged. “Site” is the site the fish was captured in. “IsotopeNumber” and “LavageNumber” are the corresponding isotope/lavage idenfication number FROM THE SAME SET.

## Fish Metrics:

| **Fish Metrics** |
| --- |
| **Name** | **Site** | **SetDate** | **YrSet** | **HeaderID** | **DetailID** | **PITCode** | **SPECIES\_DESC** | **ForkLength (mm)** | **Weight (g)** | **CF** | **Pass** | **TextualComment** | **AdditionalComment** | **ConditionalComment** | **Outlier** |
| TNA15188.H12 | H12 | 7/12/2015 | 15.3 | 171 | 11431 | 3D9.1C2D9BDFB3 | CHINOOK | 68 | 3.29999995231628 | 1.05 | 1 | P1 |  |  |  |

* A query derived from the “Tag Detail” Table. This query is intended to select data from fish captured electrofishing in Hancock Springs. “Name” is the name of the P3 file the record originated from. “Site” is the site the fish was captured in. “SetDate” is the median date of the set (usually each set took approximately 9 days to complete). “YrSet” is the Year and Set number of the fish capture. In the example listed above the fish was captured in 2015 in the third set. “HeaderID” and “DetailID” are linked to the exact record in P3 of the fish capture. “PITCode” is the PIT tag identification (if the fish was tagged). If the fish was not tagged, only dots (…….) will be in this field. “SPECIES\_DESC” is the species of fish observed. “ForkLength (mm)” is the Fork Length in mm (or total length for sculpin) of the fish observed. “Weight” is the total wet weight in g of the species observed. “CF” is the condition factor calculated as (Weight/((ForkLength/10)^3))\*100). “Pass” is the electrofishing pass number this fish was captured in. This may be as high as 6 but is usually closer to 2. “TextualComment” is any observations that were made at the time of capture. This field is not coded so anything can be written. “AdditionalComment” enumerates the corresponding isotope and lavage sample number (from the set) IF the fish was lavaged (Up to 5 individuals were lavaged from each species in each site during each set). “ConditionalComment” is a coded comment field in P3. Each abbreviation is listed out in the CONDITIONAL\_COMMENT table. “Outlier” is linked to the QAQC LenWeight query. If this query indicated the fish was an outlier, this “Outlier” field will say “OUT.”

## Growth Queries:

* Four queries **(Growth 1, Growth 2, Growth 3, and Growth 4)** were used to calculate average daily growth (grams/day) for each Site Species combination (ie. H11, 2015, Brook Trout).

| **Growth1** |
| --- |
| **Name** | **DetailID** | **Site1** | **PITCode** | **SPECIES\_DESC** | **ForkLength (mm)** | **Weight (g)** | **RE** | **YrSet.YrSet** | **SetDate** |
| TNA13084.H11 | 2289 | H11 | 3D9.1C2DDA24D3 | STEELHEAD | 79 | 5.4 |  | 13.1 | 3/29/2013 |

* Growth 1 queries all recaptured fish based on repeated PITtag values in the “Fish Metrics” query. “Name” is the P3 file name associated with the fish capture. “DetailID” is the unique identifier associated with individual fish observations. “Site1” is the site the fish was capture in. “PITCode” is the unique identifier of the PIT tag each fish was associated with. All of the fish in these queries have PIT tags (the only way to identify if a fish is recaptured). “SPECIES\_DESC” is the species captured. “ForkLength (mm)” is the fork length in mm (or total length for sculpin) of the individual at the time of captured. “Weight (g)” is the wet weight in grams of the individual at the time of capture. “RE” indicates if this is the first capture event (blank field) or a recapture (field will say “RE”). “YrSet” is the Year and Set number (in the example above it was set number one in 2013) of the capture event. “SetDate” was the median set date of a sample set (Sample sets usually lasted approximately nine days).

| **Growth2** |
| --- |
| **PITCode** | **Site1** | **SPECIES\_DESC** | **FirstOfSetDate** | **FirstWeight(g)** |  |
| 384.3B23A4E556 | H21 | STEELHEAD | 12/7/2015 | 4.59999990463257 |  |

* Growth 2 groups fish by PITCode and Site (ie. All brook trout caught, and recaptured in Hancock reach 1, site 1) and then establishes the first capture date and first capture weight associated with each PITCode-Site grouping. “PITCode” is the unique identifier of the PIT tag in a tagged fish. “Site” is the Site the fish was capture in. “SPECIES\_DESC” is the type of species captured. “FirstOfSetDate” is the first date an individual fish was caught in a site. “FirstWeight (g)” is the wet weight of a fish at the first date of capture.

| **Growth3** |
| --- |
| **Site1** | **DetailID** | **PITCode** | **SPECIES\_DESC** | **ForkLength (mm)** | **Weight (g)** | **YearSet** | **SetDate** | **DaysSinceFirstDetection** | **GrowthSinceFirstDetection** | **GramsPerDayGrowth** |
| H13 | 13687 | 3D9.1C2D9FE158 | CHINOOK | 94 |  | 15.4 | 8/15/2015 | 34 |  |  |

* Growth 3 calculates the weight difference (g) and time difference (days) between the first capture and the recapture event in a specific site. This query only contains fish that were recaptured (initial capture events are not included). “Site1” is the Site the fish was captured in. “DetailID” is the P3 unique identifier attached to the recapture event. “PITCode” is the unique identifier of the PIT tag each fish was associated with. “SPECIES\_DESC” is the species captured. “ForkLength (mm)” is the fork length in mm (or total length for sculpin) of the individual at the time of capture. “Weight (g)” is the wet weight in grams of the individual at the time of capture. “YearSet” is the Year and Set number (in the example above it was set number four in 2015) of the capture event. “SetDate” was the median set date of a sample set (Sample sets usually lasted approximately nine days). “DaysSinceFirstDetection” is the number of days since the fish was first captured in the site. “GrowthSinceFirstDetection” is the amount of growth in g since the fish was first detected in the site. “GramsPerDayGrowth” is the average weight gain per day since the first capture event.

| **Growth4** |
| --- |
| **Site** | **SPECIES\_DESC** | **AvgDailyGrowth (g)** | **SDDailyGrowth** | **VarianceDailyGrowth** | **AvgDaysBetweenDetections** | **NumObservations** |
| H11 | BROOK TROUT | 0.157256278230764 | 0.115304257598785 | 0.013295071820407 | 231.959016393443 | 243 |

* Growth 4 calculates the average weight change per day (g/day) for each Site-Species combination. “Site” is the site the fish was captured AND recaptured in. “SPECIES\_DESC” is the species. “AvgDailyGrowth (g)” is the average daily growth for a given species in a given site. “AvgDaysBetweenDetections” is the average number of days between capture and recapture events for that species in that site. “SDDailyGrowth” and “VarianceDailyGrowth” are the standard deviation and variance of the average daily growth calculation. “NumObservations” counts the number of growth calculations used to calculate average daily growth.

## QAQC LenWeight Query:

| **QAQC LenWeight** |
| --- |
| **FileName** | **HeaderID** | **Sequence** | **DetailID** | **PITCode** | **SPECIES\_DESC** | **ForkLength (mm)** | **Weight (g)** | **ConditionalComment** | **Comment** | **Calculated Weight** | **Outlier** |
| TNA11228.T08 | 15 | 5 | 126 | 3D9.1C2D9CD3BC | STEELHEAD | 128 | 143.5 |  | DNA 517, YN1 POS 17 | 21.8845247053043 | OUT |

* Used to find outliers based on the length field. This query is only applied to fish greater than 10 grams. Length-Weight regressions were developed in R based on all of the length and weight observations collected to date (12/2015). The equations derived from each species (“calculated weight” field) were:
	+ BROOK TROUT: 10^(-5.092+3.0552\*((Log(ForkLength))/Log(10)))
	+ CHINOOK: 10^(-5.332+3.194\*((Log(ForkLength))/Log(10)))
	+ STEELHEAD: 10^(-4.9836+3.001\*((Log(ForkLength))/Log(10)))
	+ SCULPIN: 10^(-5.353+3.226\*((Log(ForkLength))/Log(10))) (10))
* For all species EXCEPT SCULPIN outliers were flagged if the calculated weight was less than 60% of the observed weight or greater than 140% of the observed weight. For SCULPIN outliers were flagged if the calculated weight was less than 50% of the observed weight or greater than 150% of the observed weight.
* “FileName,” “HeaderID” and “Sequence” are unique P3 identifiers. These are helpful when you want to change a value in P3 based on the presence of an outlier in this query. “PITCode” is the unique identifier of the PIT tag each fish was associated with. “SPECIES\_DESC” is the species captured. “ForkLength (mm)” is the fork length in mm (or total length for sculpin) of the individual at the time of capture. “Weight (g)” is the wet weight in grams of the individual at the time of capture. “ConditionalComment” is a coded comment field in P3. Each abbreviation is listed out in the CONDITIONAL\_COMMENT table. “Comment” is a field with any additional observations made at the time of capture. “Calculated Weight” is the estimated weight of a fish based on the equations listed above. “Outlier” will say “OUT” if a fish weight does not meet the criteria listed above. Otherwise this field will be blank.

## QAQC Recap Queries

* These queries **(QAQC Recaps\_1, QAQC Recaps\_2)** were designed for the field laptop to check that all recapped fish were labelled with “RE” before uploading the data to Pitagis. These queries are run on the field laptop before any data is imported into the database. Accordingly, in this database the results of QAQC Recaps\_2 are issues that have not been resolved- as of March 2016 there were four records in this query) .

| **QAQC Recaps\_1** |
| --- |
| **PITCode** | **MinOfDetailID** |
| 384.3B23A4B091 | 18383 |

* QAQC Recaps\_1 queries PITCodes (unique identifier of the PIT tag each fish was associated with) from the “Recap’d fish” query and finds the Detail ID associated with the first capture event (“MinOfDetailID”).

| **QAQC Recaps\_2** |
| --- |
| **HeaderID** | **DetailID** | **PITCode** | **ConditionalComment** | **TextualComment** |
| 204 | 18126 | 3D9.1C2D9F216B | M | PNA, PIT tag found in previous 7R lavage sample |

* QAQC Recaps\_2 selects all recapped fish that were NOT in QAQC\_Recaps 1 and that DON’T have “RE” in the conditional comments. “HeaderID” and “DetailID” are unique P3 identifiers. These are helpful when you want to add “RE” in P3 based on the results of this query. “PITCode” is the unique identifier of the PIT tag each fish was associated with. “SPECIES\_DESC” is the species captured. “ConditionalComment” is a coded comment field in P3. Each abbreviation is listed out in the CONDITIONAL\_COMMENT table. “TextualComment” is a field with any additional observations made at the time of capture.

## QAQC Species ID

| **QAQC Species ID** |
| --- |
| **Site1** | **HeaderID** | **DetailID** | **PITCode** | **SPECIES\_DESC** | **ForkLength (mm)** | **Weight (g)** | **TextualComment** |
| H11 | 211 | 19942 | 384.3B23A44EE2 | CHINOOK | 86 | 6.40000009536743 | P1 |
| H11 | 204 | 18259 | 384.3B23A44EE2 | STEELHEAD | 85 | 6.40000009536743 | P1 |

* This query was designed for the field laptop to check that all recaptured species were labelled with the same species when they were tagged (and any following capture event). As of March 2016, there were 11 records in this table. In the example above the fish was labelled as a steelhead the first time it was captured and a chinook the second time it was captured. Accordingly, the results of this query represent unresolved issues (we were not able to tell with certainty what the actual species was so no changes were made). “Site1” is the site the fish was captured in. “HeaderID” is a unique P3 identifier helpful when you want to change a species in P3 based on results from this query. “DetailID” is a unique identifier associated with a capture event. “PITCode” is the unique identifier of the PIT tag each fish was associated with. “SPECIES\_DESC” is the species captured. “ForkLength (mm)” is the fork length in mm (or total length for sculpin) of the individual at the time of capture. “Weight (g)” is the wet weight in grams of the individual at the time of capture. The fork length and weight fields can be helpful in determining what the actual species was (which record contained the error). “TextualComment” is a field with any additional observations made at the time of capture.

## Recap’d Fish

| **Recap'd Fish** |
| --- |
| **Name** | **HeaderID** | **DetailID** | **Site1** | **SetDate** | **PITCode** | **SPECIES\_DESC** | **ForkLength (mm)** | **Weight (g)** | **CF** | **TextualComment** | **Outlier** | **ConditionalComment** |
| TNA15338.H11 | 211 | 19942 | H11 | 12/7/2015 | 384.3B23A44EE2 | CHINOOK | 86 | 6.40000009536743 | 1.01 | P1 |  | RE |

* This query was designed to select all fish (PITtags) that had been recaptured. This query will list the records from the first capture and all recapture events. “Name,” “HeaderID” and “DetailID” are unique P3 identifiers associated with each capture event. “Site1” is the site the fish was captured in. “SetDate” was the median set date of a sample set (Sample sets usually lasted approximately nine days). “PITCode” is the unique identifier of the PIT tag each fish was associated with. “SPECIES\_DESC” is the species captured. “ForkLength (mm)” is the fork length in mm (or total length for sculpin) of the individual at the time of capture. “Weight (g)” is the wet weight in grams of the individual at the time of capture. “CF” is the condition factor calculated as (Weight/((ForkLength/10)^3))\*100). “TextualComment” is a field with any additional observations made at the time of capture. “Outlier” is linked to the QAQC LenWeight query. If this query indicated the fish was an outlier, this “Outlier” field will say “OUT.” “ConditionalComment” is a coded comment field in P3. Each abbreviation is listed out in the CONDITIONAL\_COMMENT table. This field will also indicate if the record is a recapture (field will say “RE”).