**File name: Kaylor et al\_JoAE\_density\_sampled.csv**

|  |  |
| --- | --- |
| **Variable** | **Description** |
| CombID | CombID is a unique ID for all stream segments within Catherine Creek and Upper Grande Ronde. Segments are approximately 15x bankfull width. |
| Site | The unique site ID. |
| Subbasin | The subbasin the stream segment is within (either CC or UGR). |
| UTM\_zone | UTM zone which is 11N for all segments |
| UTM\_E | UTM easting for a point at the middle of each stream segment (CombID). |
| UTM\_N | UTM northing for a point at the middle of each stream segment (CombID). |
| Reach\_length | Total stream length (m) of each segment (CombID). |
| Reach\_Area | Total area (m2) of each segment (CombID). |
| Width\_BF | Mean bankfull width (m) of segment. |
| Pool\_percent | Percent pool area of each segment. |
| Pools\_per\_100m | Number of pools per 100 m within each segment |
| Wood\_count\_100m | Number of pieces of wood within the bankfull channel per 100 m. |
| Aug\_mean\_temp | Mean August temperature of the site. This was derived from the NORWEST model (Isaak et al. 2015) and represents |
| ReddCount | Number of redds located within 2 km upstream of the segement. |
| Gradient | Gradient of the site (change in elevation divided by length) |
| CH\_per\_100m | Estimated number of Chinook Salmon parr per 100 m. Snorkel counts were translated to the abundance scale using local habitat variables (see Staton et al. 2021). |
| CH\_per\_100m\_lowerCI | Lower 80% confidence interval for the estimated number of Chinook Salmon parr per 100 m. Snorkel counts were translated to the abundance scale using local habitat variables (see Staton et al. 2021). |
| CH\_per\_100m\_upperCI | Upper 80% confidence interval for the estimated number of Chinook Salmon parr per 100 m. Snorkel counts were translated to the abundance scale using local habitat variables (see Staton et al. 2021). |

**File name: Kaylor et al\_JoAE\_Fish diets.csv**

|  |  |
| --- | --- |
| **Variable** | **Description** |
| Subbasin | Subbasin of site |
| SiteID | Unique ID for each site |
| UTM\_zone | UTM zone which is 11N for all sites |
| UTM\_E | UTM easting for a point at the middle of site. |
| UMT\_N | UTM northing for a point at the middle of site. |
| Date | Date of sample collection |
| Diet\_ID | Unique ID for each diet sample. This can be linked to fish data in Kaylor et al\_JoAE\_Fish raw data.csv. |
| Species | Species of fish sampled. Chinook Salmon for all diet samples. |
| Fish\_length | Fork length of sample fish in mm. |
| Fish\_weight | Weight of fish in grams. |
| Prey\_Taxon | Lowest identified taxonomic resolution of prey item. |
| Count | Number of prey items included in this row. If many individuals of a taxa were of similar size, an average length was obtained and remaining individuals were counted. |
| Life\_stage | Life state of prey item (e.g. larve, adult) |
| Origin | Whether the prey item is aquatic or terrestrial in origin. |
| Comment | Any comments by the individual identifying and measuring prey items. |
| Body\_length\_mm | Body length of the prey item in mm. |
| Dry\_mass\_mg | Estimated dry mass of the prey item based on length-mass regressions. |
| Dry\_mass\_regression | The regression equation used to estimate dry mass from length. |
| Regression\_taxa | The taxa used to estimate dry mass from length. |
| Regression\_ref | The reference from which the regression equation was obtained from. |
| Intercept\_a | The intercept in the regression equation. |
| Coefficient\_b | The beta coefficent for the regression equation. |
| Calories\_per\_mg | The estimated calories per mg of dry mass. |
| Calories\_taxa | The taxa used to estimate calories per mg dry mass. |
| Calories\_per\_preyItem | The estimated calories per prey item. |
| Kingdom | Kingdom of prey item. |
| Phylum | Phylum of prey item. |
| Class | Class of prey item (if identified). |
| SubClass | SubClass of prey item (if identified). |
| Order | Order of prey item (if identified). |
| Family | Family of prey item (if identified). |

**File name: Kaylor et al\_JoAE\_Fish raw data.csv**

|  |  |
| --- | --- |
| **Variable** | **Description** |
| Subbasin | Subbasin of site |
| SiteID | Unique ID for each site |
| UTM\_zone | UTM zone which is 11N for all sites |
| UTM\_E | UTM easting for a point at the middle of site. |
| UMT\_N | UTM northing for a point at the middle of site. |
| Date | Date of sampling |
| Species | Species of fish sampled. Chinook Salmon. |
| Fork\_length | Fork length of sampled fish in mm. |
| Weight | Weight of fish in grams. |
| Mark\_recapture | If the fish received a PIT-tag, this indicates whether the fish was marked or subsequently recaptured. |
| PIT\_tag\_ID | Unique ID of the PIT-tag associated with this fish |
| Diet\_ID | If a diet sample was taken from the fish, this indicates the unique ID of that diet sample. |

**File name: Kaylor et al\_JoAE\_SSN\_prediction sites.csv**

|  |  |
| --- | --- |
| **Variable** | **Description** |
| CombID | CombID is a unique ID for all stream segments within Catherine Creek and Upper Grande Ronde. Segments are approximately 15x bankfull width. These CombIDs were not sampled for fish size, density, or growth. Spatially explicit habitat measurements were obtained from the Aquatic Inventories Project (Moore et al., 2017). |
| Subbasin | The subbasin the stream segment is within. |
| UTM\_zone | UTM zone which is 11N for all segments |
| UTM\_E | UTM easting for a point at the middle of each stream segment (CombID). |
| UTM\_N | UTM northing for a point at the middle of each stream segment (CombID). |
| Reach\_length | Total stream length (m) of each segment (CombID). |
| Reach\_area | Total area (m2) of each segment (CombID). |
| Width\_BF | Mean bankfull width (m) of segment. |
| Pool\_percent | Percent pool area of each segment. |
| Pools\_per\_100m | Number of pools per 100 m within each segment |
| Wood\_count\_100m | Number of pieces of wood within the bankfull channel per 100 m. |
| ReddCount\_2km | Number of redds located within 2 km upstream of the segement. |
| Predicted | Indicator of whether response variables (density, size, growth, pCmax) were predicted at segment. Note that there are many segments where we did not predict response variables. These are not within the juvenile Chinook Salmon rearing extent. However, in order to run SSN models, segments need to be continuous and connect at a single outlet. Values of -999 indicate that no data were available. |

**File name: Kaylor et al\_JoAE\_Temperature.csv**

|  |  |
| --- | --- |
| **Variable** | **Description** |
| Subbasin | Subbasin of site |
| SiteID | Unique ID for each site |
| UTM\_E | UTM easting for sensor |
| UTM\_N | UTM northing for sensor |
| Date | Date of measurement. |
| Time | Time of measurement. Pacific Standard Time. |
| Temp\_C | Temperature in degrees celcius. |
| Emerge\_estimated | Indicator for whether we estimated Chinook Salmon emergence timing at this site. |