Great Blue Heron Predation on Juvenile Salmonids 2023

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Background

The Pacific Salmon Foundation and the British Columbia Conservation Foundation are interested in understanding bottlenecks to juvenile salmonid survival during their outmigration toward the ocean in southwestern British Columbia. The Pacific Great Blue Heron (*Ardea herodias fannini*) was recently found to be a notable predator of outmigrating juvenile salmonids in this region (Sherker et al. 2021). Between 2013 and 2023, nearly 400,000 fish in the region were tagged with Passive Integrated Transponder (PIT) tags. Between 2017 and 2023, researchers scanned the fecal matter at nearby heron rookeries with PIT scanners, in order to detect PIT tags that were ingested and subsequently excreted there. By linking the PIT tag detections at the heron rookeries to the original tagging data, factors affecting salmonid susceptibility to predation by herons can be explored.

The primary goal of the current analysis is to answer the following questions:

- What proportion of tagged fish are predated upon by heron?
- What is the effect of fish origin (wild vs hatchery) on the heron predation rate?
- What is the effect of fish release date on the heron predation rate?
- What is the effect of fish size on the heron predation rate?
- What are the effects of environmental variables (river discharge, water temperature, and/or air temperature) on heron predation rate?

Data Preparation

The data were prepared for analysis using R version 4.3.2 (R Core Team 2023).

Key assumptions of the data preparation included:

- 238 PIT tag codes with more than one associated length measurement were assumed to have the smallest of the recorded measurements for that fish.
- The duration of each scanning visit to a rookery was the time between the first tag and last tag detected, less any gaps in detections greater than one hour.
- Any tags detected after 9:00 pm in the evening do not represent true scanning effort.
- All visits were completed in one day, except for 3 visits to the Cowichan heron rookery which spanned 2 days (2017-08-11/2017-08-12, 2017-09-14/2017-09-15, and 2019-01-03/2019-01-04).
- The release date is the hatchery release date for hatchery fish, and the tagging date for all fish tagged in the river, beach, and purse periods, and for hatchery releases of Steelhead Trout from Robertson Creek.
- Hatchery fish were released in the river.

- The following calculations were performed to remove the confounding effects of year and day of year in the discharge data:
 - (a) Calculate a 7-day rolling average discharge in each system
 - (b) Calculate the mean annual discharge (MAD) for each system,
 - (c) Divide each 7-day average from (a) by that year's MAD from (b),
 - (d) Calculate the mean of the values in (c) for each date, across all systems,
 - (e) Divide the values in (c) by the values in (d) to get what will be referred to as "Scaled Discharge".

Statistical Analysis

Model parameters were estimated using Bayesian methods. The estimates were produced using Stan (Carpenter et al. 2017). For additional information on Bayesian estimation the reader is referred to McElreath (2020).

Unless stated otherwise, the Bayesian analyses used weakly informative normal and half-normal prior distributions (Gelman, Simpson, and Betancourt 2017). The posterior distributions were estimated from 1500 Markov Chain Monte Carlo (MCMC) samples thinned from the second halves of 3 chains (Kery and Schaub 2011, 38–40). Model convergence was confirmed by ensuring that the potential scale reduction factor $\hat{R} \leq 1.05$ (Kery and Schaub 2011, 40) and the effective sample size (Brooks et al. 2011) ESS ≥ 150 for each of the monitored parameters (Kery and Schaub 2011, 61).

Model adequacy was assessed via posterior predictive checks (Kery and Schaub 2011). More specifically, the proportion of zeros in the data and the first four central moments (mean, variance, skewness and kurtosis) in the deviance residuals were compared to the expected values by simulating new data based on the posterior distribution and assumed sampling distribution and calculating the deviance residuals.

Where computationally practical, the sensitivity of the posteriors to the choice of prior distributions was evaluated by doubling the standard deviations of all normal, half-normal and log-normal priors by an order of magnitude and then using \hat{R} to evaluate whether the samples were drawn from the same posterior distribution (Thorley and Andrusak 2017).

The parameters are summarised in terms of the point *estimate*, *lower* and *upper* 95% compatibility limits (Rafi and Greenland 2020) and the surprisal *s-value* (Greenland 2019). The estimate is the median (50th percentile) of the MCMC samples while the 95% CLs are the 2.5th and 97.5th percentiles. The s-value indicates how surprising it would be to discover that the true value of the parameter is in the opposite direction to the estimate (Greenland 2019). An s-value of > 4.32 bits, which is equivalent to a p-value < 0.05 (Kery and Schaub 2011; Greenland and Poole 2013), indicates that the surprise would be equivalent to throwing at least 4.3 heads in a row on a fair coin.

Variable selection was based on the heuristic of directional certainty (Kery and Schaub 2011). Fixed effects were included if their s-value was > 4.32 bits (Kery and Schaub 2011). Based on a similar argument, random effects were included if their standard deviation had a lower 95% CL > 5% of the median estimate.

The results are displayed graphically by plotting the modeled relationships between individual variables and the response with the remaining variables held constant. In general, continuous and discrete fixed variables are held constant at their mean and first level values, respectively, while random variables are held constant at their typical values (Kery and Schaub 2011, 77–82). Unless stated otherwise the typical value is the arithmetic mean. When informative the influence of particular variables is expressed in terms of the *effect size* (i.e., percent change in the response variable) with 95% CLs (Bradford, Korman, and Higgins 2005).

The analyses were implemented using R version 4.3.2 (R Core Team 2023) and the mbr family of packages.

Model Descriptions

Detection The data were analysed using a Cormack-Jolly-Seber (CJS) model (Kery and Schaub 2011, 170–99). In this analysis, survival probability refers to the probability that a tag remains detectable (i.e., not damaged or washed away) at a rookery, and recapture probability refers to the probability that a tag is

detected during a scanning visit, given it is detectable. Only heron rookeries with at least three scanning visits were analysed, due to an inability to separate survival and recapture probabilities for rookeries with fewer visits. A model was fit separately for each rookery meeting this criterion.

Key assumptions of the CJS model include:

- The annual PIT tag survival at rookeries is high $(\sim 90\%)$.
- The probability of PIT tag survival between visits declines exponentially as a function of the number of years between visits.
- The recapture probability varies randomly by individual tag.
- The residual variation is Bernoulli-distributed.

Additional assumptions for the Deep Bay, Pipers Lagoon, and Stanley Park heron rookeries include:

- Recapture probability varies by visit date.
- The random variation in the individual-level variation in recapture probability is normally distributed on the log-odds scale.

Additional assumptions for the Cowichan heron rookery include:

- The recapture probability varies randomly by visit date.
- The random variation in the individual-level variation in recapture probability is skew-normally distributed (Azzalini 1985) on the log-odds scale.

Prelminary analysis found that an effect of hours of scanning effort was not an informative predictor of the detection probability.

Predation Individual fish were assigned to cohorts were assigned by grouping tagged fish by river system, release day of year, outmigration year, species, and tagging period. 22,135 fish tagged in the ocean during the micro-trawling stage or tagged as adults were excluded from the analysis, because they were considered to experience negligible heron predation; none of these fish were detected at heron rookeries. 550 fish missing outmigration year data and 24 fish missing species data were excluded from analysis, as were 2 "hybrid" fish and 1 lamprey.

The Cowichan and Beacon Hill heron rookeries were the only two rookeries considered in this analysis, due to low numbers of PIT tag detections of fish with known deployment information at the other rookeries (Table 1). Cohorts were excluded from analysis if their release date was after the last scan date of the rookeries. The detection probabilities for each cohort and rookery were derived from the detection model.

Zero-or-one inflated beta regression (Ospina and Ferrari 2012) was used to model the missing values in the probability of a cohort having hatchery origin and in order to permit the extreme probabilities of 0 and 1, corresponding to cohorts with 100% wild origin and 100% hatchery origin, respectively.

Key assumptions of this model include:

- The deposition rate of tags at rookeries by herons is similar to that of double-crested cormorants (*Phalacrocorax auritus*), at 50% (95% CL 34%-70%) (Hostetter et al. 2015).
- The typical recapture probability of tags at the Beacon Hill rookery is the same as the typical recapture probability of tags at the Cowichan heron rookery.
- PIT tag codes are correctly reported.
- Cohorts with incomplete origin information have a mixture of hatchery and wild fish.
- The predation rate varies by the cohort origin, day of year the cohort was released, species, tagging period, and distance between the river system mouth and the heron rookery.
- The predation rate varies randomly by outmigration year, system-rookery combination, and cohort ID.
- The residual variation is multinomially distributed.

Reduced Predation A reduced set of data was used to explore the effects of fork length and discharge on heron predation of juvenile salmonid cohorts. This model focuses on juvenile Chinook salmon (*Oncorhynchus tshawytscha*) with known fork lengths less than 120 mm that were released in systems with known discharge.

Chinook were chosen as the species of interest for this model because they formed the majority of known tags detected at rookeries (Figure 31).

The same data preparation assumptions from the full predation model apply to this model. In addition, cohorts were grouped by length classes: the small class includes fish ≤ 70 mm, the medium class includes fish > 70 mm and ≤ 90 mm, and the large class includes fish > 90 mm and ≤ 120 mm.

The same model assumptions of the full predation model also apply to this model, except for the factors affecting the heron predation rate.

Key assumptions from this model that differ from the full predation model include:

- The predation rate varies by the cohort origin, tagging period, scaled discharge in the tagging system in the week following release, length class, and by distance between the system mouth and the heron rookery.
- The predation rate varies randomly by week within year, length class within month, and cohort ID.

Preliminary analysis indicated that day of the year and year as a random effect were not informative predictors of the heron predation rate.

Model Templates

Detection

```
.functions {
 int first_capture(array[] int y_i) {
   for (k in 1 : size(y_i)) {
     if (y_i[k]) {
       return k;
     }
   }
   return 0;
 }
 int last_capture(array[] int y_i) {
   for (k_rev in 0 : (size(y_i) - 1)) {
     int k = size(y_i) - k_rev;
     if (y_i[k]) {
       return k;
     }
   }
   return 0;
 }
 matrix prob_uncaptured(int nindividual, int ndate, matrix eRecapture, matrix eSurvival) {
   matrix[nindividual, ndate] chi;
   for (i in 1 : nindividual) {
     chi[i, ndate] = 1.0;
     for (t in 1 : (ndate - 1)) {
       int t curr = ndate - t;
       int t_next = t_curr + 1;
       t curr = ndate - t;
       t_next = t_curr + 1;
       chi[i, t_curr] = (1 - eSurvival[i, t_curr])
                         + eSurvival[i, t_curr] * (1 - eRecapture[i, t_next - 1])
                           * chi[i, t_next];
     }
   }
   return chi;
```

```
}
}
data {
  int<lower=0> nindividual;
  int<lower=2> ndate;
  real<lower=0> years_between_visits[ndate];
  array[nindividual, ndate] int<lower=0, upper=1> capture_history;
}
transformed data {
  int n_occ_minus_1 = ndate - 1;
  array[nindividual] int<lower=0, upper=ndate> first;
  array[nindividual] int<lower=0, upper=ndate> last;
  for (i in 1 : nindividual) {
    first[i] = first_capture(capture_history[i]);
  }
  for (i in 1 : nindividual) {
    last[i] = last_capture(capture_history[i]);
  }
}
parameters {
  real<lower=0, upper=1> bAnnualSurvival;
  real bRecapture;
  vector[n_occ_minus_1] bRecaptureDate;
  real<lower=0> sRecaptureDate;
  vector[nindividual] bRecaptureIndividual;
  real<lower=0> sRecaptureIndividual;
  real bSkew;
}
transformed parameters {
  matrix<lower=0, upper=1>[nindividual, n_occ_minus_1] eSurvival;
  matrix<lower=0, upper=1>[nindividual, n_occ_minus_1] eRecapture;
  matrix<lower=0, upper=1>[nindividual, ndate] chi;
  for (i in 1:nindividual) {
    for (t in 1:(first[i] - 1)) {
      eSurvival[i, t] = 0;
      eRecapture[i, t] = 0;
    }
    for (t in first[i]:n_occ_minus_1) {
      eSurvival[i, t] = bAnnualSurvival^years_between_visits[t];
      eRecapture[i, t] = inv_logit(bRecapture + bRecaptureDate[t] + bRecaptureIndividual[i]);
    }
  }
  chi = prob_uncaptured(nindividual, ndate, eRecapture, eSurvival);
}
model {
  bAnnualSurvival ~ beta(10, 1);
  bRecapture ~ normal(0, 2);
```

```
\end{lstlisting}
```

Block 1. Model description for the Cowichan heron rookery.

```
.functions {
 int first_capture(array[] int y_i) {
   for (k \text{ in } 1 : \text{size}(y_i)) 
      if (y_i[k]) {
       return k;
     }
   }
   return 0;
 }
 int last_capture(array[] int y_i) {
   for (k_rev in 0 : (size(y_i) - 1)) {
      int k = size(y_i) - k_rev;
      if (y_i[k]) {
       return k;
     }
   }
   return 0;
 }
 matrix prob_uncaptured(int nindividual, int ndate, matrix eRecapture, matrix eSurvival) {
   matrix[nindividual, ndate] chi;
   for (i in 1 : nindividual) {
      chi[i, ndate] = 1.0;
     for (t in 1 : (ndate - 1)) {
        int t_curr = ndate - t;
       int t_next = t_curr + 1;
       t_curr = ndate - t;
       t_next = t_curr + 1;
        chi[i, t_curr] = (1 - eSurvival[i, t_curr])
                         + eSurvival[i, t_curr] * (1 - eRecapture[i, t_next - 1])
                            * chi[i, t_next];
     }
   }
   return chi;
 }
```

}

```
data {
  int<lower=0> nindividual;
  int<lower=2> ndate;
  real<lower=0> years_between_visits[ndate];
  array[nindividual, ndate] int<lower=0, upper=1> capture_history;
}
transformed data {
  int n_occ_minus_1 = ndate - 1;
  array[nindividual] int<lower=0, upper=ndate> first;
  array[nindividual] int<lower=0, upper=ndate> last;
  for (i in 1 : nindividual) {
    first[i] = first_capture(capture_history[i]);
  }
  for (i in 1 : nindividual) {
    last[i] = last_capture(capture_history[i]);
  }
}
parameters {
  real<lower=0, upper=1> bAnnualSurvival;
  real bRecapture;
  vector[n_occ_minus_1] bRecaptureDate;
  vector[nindividual] bRecaptureIndividual;
  real<lower=0> sRecaptureIndividual;
}
transformed parameters {
  matrix<lower=0, upper=1>[nindividual, n_occ_minus_1] eSurvival;
  matrix<lower=0, upper=1>[nindividual, n_occ_minus_1] eRecapture;
  matrix<lower=0, upper=1>[nindividual, ndate] chi;
  for (i in 1:nindividual) {
    for (t in 1:(first[i] - 1)) {
      eSurvival[i, t] = 0;
      eRecapture[i, t] = 0;
    }
    for (t in first[i]:n_occ_minus_1) {
      eSurvival[i, t] = bAnnualSurvival^years_between_visits[t];
      eRecapture[i, t] = inv_logit(bRecapture + bRecaptureDate[t] + bRecaptureIndividual[i]);
    }
  }
  chi = prob_uncaptured(nindividual, ndate, eRecapture, eSurvival);
}
model {
  bAnnualSurvival ~ beta(10, 1);
  bRecapture ~ normal(0, 2);
  bRecaptureDate ~ normal(0, 2);
  sRecaptureIndividual ~ exponential(0.1);
  bRecaptureIndividual ~ normal(0, sRecaptureIndividual);
```

```
for (i in 1:nindividual) {
    if (first[i] > 0) {
        for (t in (first[i] + 1) : last[i]) {
            1 ~ bernoulli(eSurvival[i, t - 1]);
            capture_history[i, t] ~ bernoulli(eRecapture[i, t - 1]);
        }
        1 ~ bernoulli(chi[i, last[i]]);
    }
}
```

```
\end{lstlisting}
```

Block 2. Model description for the Deep Bay, Pipers Lagoon, and Stanley Park heron rookeries.

Predation

```
.data {
  int<lower=0> nObs;
  int<lower=0> nspecies;
  int<lower=0> nannual;
  int<lower=0> nperiod;
  int<lower=0> ncohort id;
  int<lower=0> nhatchery_disc;
  int<lower=0> nhatchery_cont;
  int<lower=0> nsystem;
  int<lower=0> hatchery_disc[nhatchery_disc];
  int<lower=0> continuous_index[nhatchery_cont];
  int<lower=0> discrete_index[nhatchery_disc];
  int<lower=0> cohort_size_cont[nhatchery_cont];
  int<lower=0> hatchery_cont_obs_bol[nhatchery_cont];
  int<lower=0> nhatchery_cont_obs;
  int<lower=0> nhatchery_cont_mis;
  int<lower=0> hatchery cont index[nhatchery cont];
  int<lower=1, upper=nhatchery_cont_obs + nhatchery_cont_mis> ii_obs[nhatchery_cont_obs];
  int<lower=1, upper=nhatchery_cont_obs + nhatchery_cont_mis> ii_mis[nhatchery_cont_mis];
  real<lower=0, upper=1> hatchery_cont_obs[nhatchery_cont_obs];
  real<lower=1, upper=366> doy[nObs];
  int<lower=0> annual[nObs];
  int<lower=0> period[nObs];
  int<lower=0> cohort_id[nObs];
  int<lower=0> system[nObs];
  real distance_beacon[nObs];
  real distance_cowichan[nObs];
  array[nObs, 3] int<lower=0> detected;
  real<lower=0, upper=1> det_prob_beacon[nObs];
  real<lower=0, upper=1> det_prob_cowichan[nObs];
}
parameters {
 real<lower=0, upper=1> bPropHatchery;
  real<lower=0, upper=1> eHatchery_cont_mis[nhatchery_cont_mis];
  real bOriginWild;
  real bOriginHatchery;
```

```
real<lower=0> bDoy;
  real<lower=0, upper=1> bPhase;
  real<lower=0, upper=1> bDeposition;
  real<lower=0> sAnnual;
  real bAnnual[nannual];
  vector[nperiod - 1] bPeriodParams;
  real<lower=0> sCohortID;
  real bCohortID[ncohort_id];
  real<lower=0> sSystemRookery;
  real bSystemBeacon[nsystem];
  real bSystemCowichan[nsystem];
  real bDistance;
}
transformed parameters {
  real hatchery_cont[nhatchery_cont];
  hatchery_cont[ii_obs] = hatchery_cont_obs;
  hatchery_cont[ii_mis] = eHatchery_cont_mis;
  vector[nperiod] bPeriod;
  real eAlpha[nhatchery_cont];
  real eBeta[nhatchery_cont];
  real eHatchery[nObs];
 real ePredation[nObs];
  real ePredationBeacon[nObs];
  real ePredationCowichan[nObs];
  real eDoy[nObs];
  real eOrigin[nObs];
  simplex[3] eScanned[nObs];
  bPeriod[1] = 0;
  for (i in 1:(nperiod - 1)) {
    bPeriod[i + 1] = bPeriodParams[i];
  }
  for (i in 1:nhatchery_disc) {
    eHatchery[discrete_index[i]] = hatchery_disc[i];
  }
  for (i in 1:nhatchery_cont) {
    eAlpha[i] = bPropHatchery * cohort_size_cont[i];
    eBeta[i] = (1 - bPropHatchery) * cohort_size_cont[i];
    eHatchery[continuous_index[i]] = hatchery_cont[i];
  }
  for (i in 1:nObs) {
    eOrigin[i] = bOriginWild * (1 - eHatchery[i]) + bOriginHatchery * eHatchery[i];
    eDoy[i] = bDoy * cos((doy[i] / 365.25 + bPhase - 0.75) * 6.283186);
    ePredation[i] = eOrigin[i] + eDoy[i] + bPeriod[period[i]] + bAnnual[annual[i]] + bCohortID[cohort_i
    ePredationBeacon[i] = inv_logit(ePredation[i] + bDistance * distance_beacon[i] + bSystemBeacon[syst
    ePredationCowichan[i] = inv_logit(ePredation[i] + bDistance * distance_cowichan[i] + bSystemCowicha
    eScanned[i, 1] = ePredationBeacon[i] * bDeposition * det_prob_beacon[i];
    eScanned[i, 2] = ePredationCowichan[i] * bDeposition * det_prob_cowichan[i];
```

```
eScanned[i, 3] = 1 - eScanned[i, 1] - eScanned[i, 2];
 }
}
model {
  bPropHatchery ~ beta(1, 1);
  bOriginWild ~ normal(-10, 4);
  bOriginHatchery ~ normal(-10, 4);
  bDoy ~ exponential(1);
  bPhase ~ beta(1, 1);
  bPeriodParams ~ normal(0, 2);
  sAnnual ~ exponential(1);
  bAnnual ~ normal(0, sAnnual);
  sCohortID ~ exponential(1);
  bCohortID ~ normal(0, sCohortID);
  sSystemRookery ~ exponential(0.2);
  bSystemBeacon ~ normal(0, sSystemRookery);
  bSystemCowichan ~ normal(0, sSystemRookery);
  bDeposition ~ beta(13, 13);
  bDistance ~ normal(-4, 2);
  for (i in 1:nhatchery_cont) {
    if (hatchery_cont_obs_bol[i]) {
      hatchery_cont_obs[hatchery_cont_index[i]] ~ beta(eAlpha[i], eBeta[i]);
    } else {
      eHatchery_cont_mis[hatchery_cont_index[i]] ~ beta(eAlpha[i], eBeta[i]);
    }
  }
  for (i in 1:nhatchery_disc) {
    hatchery_disc[i] ~ bernoulli(bPropHatchery);
  }
  for (i in 1:nObs) {
    detected[i, ] ~ multinomial(to_vector(eScanned[i, ]));
  }
}
\end{lstlisting}
Block 3. Model description.
```

Sub-Analysis of Predation on Chinook Salmon

```
.data {
    int<lower=0> n0bs;
    int<lower=0> nweek_annual;
    int<lower=0> nperiod;
    int<lower=0> nlength_class;
    int<lower=0> nlength_class_month;
    int<lower=0> ncohort_id;
    real distance_beacon[n0bs];
    real distance_cowichan[n0bs];
    int<lower=0> week_annual[n0bs];
    int<lower=0> period[n0bs];
```

```
int<lower=0> length_class[nObs];
  int<lower=0> length_class_month[nObs];
  int<lower=0> cohort id[nObs];
  real discharge[nObs];
  real<lower=0, upper=1> det_prob_beacon[nObs];
  real<lower=0, upper=1> det prob cowichan[nObs];
  arrav[nObs, 3] int<lower=0> detected:
  int<lower=0> nhatchery disc;
  int<lower=0> nhatchery cont;
  int<lower=0> hatchery_disc[nhatchery_disc];
  int<lower=0> continuous_index[nhatchery_cont];
  int<lower=0> discrete_index[nhatchery_disc];
  int<lower=0> cohort_size_cont[nhatchery_cont];
  int<lower=0> hatchery_cont_obs_bol[nhatchery_cont];
  int<lower=0> nhatchery_cont_obs;
  int<lower=0> nhatchery_cont_mis;
  int<lower=0> hatchery_cont_index[nhatchery_cont];
  int<lower=1, upper=nhatchery cont obs + nhatchery cont mis> ii obs[nhatchery cont obs];
  int<lower=1, upper=nhatchery_cont_obs + nhatchery_cont_mis> ii_mis[nhatchery_cont_mis];
  real hatchery_cont_obs[nhatchery_cont_obs];
}
parameters {
 real bOriginWild;
 real bOriginHatchery;
  real<lower=0, upper=1> bPropHatchery;
  real<lower=0, upper=1> eHatchery_cont_mis[nhatchery_cont_mis];
  real bDistance;
  real bDischarge;
  real<lower=0, upper=1> bDeposition;
  vector[nperiod - 1] bPeriodParams;
  vector[nlength_class - 1] bLengthParams;
  real<lower=0> sWeekAnnual;
  real bWeekAnnual[nweek_annual];
  real<lower=0> sLengthMonth;
  real bLengthMonth[nlength_class_month];
  real<lower=0> sCohortID;
  real bCohortID[ncohort_id];
}
transformed parameters {
  vector[nperiod] bPeriod;
  vector[nlength_class] bLength;
  real hatchery_cont[nhatchery_cont];
  hatchery_cont[ii_obs] = hatchery_cont_obs;
  hatchery_cont[ii_mis] = eHatchery_cont_mis;
  real eAlpha[nhatchery_cont];
  real eBeta[nhatchery_cont];
  real eHatchery[nObs];
  real ePredation[nObs];
  real ePredationCohort[nObs];
```

```
real ePredationBeacon[nObs];
  real ePredationCowichan[nObs];
  real eOrigin[nObs];
  simplex[3] eScanned[nObs];
  bPeriod[1] = 0;
  for (i in 1:(nperiod - 1)) {
   bPeriod[i + 1] = bPeriodParams[i];
  }
  bLength[1] = 0;
  for (i in 1:(nlength_class - 1)) {
   bLength[i + 1] = bLengthParams[i];
  }
  for (i in 1:nhatchery_disc) {
    eHatchery[discrete_index[i]] = hatchery_disc[i];
  }
  for (i in 1:nhatchery_cont) {
    eAlpha[i] = bPropHatchery * cohort_size_cont[i];
    eBeta[i] = (1 - bPropHatchery) * cohort_size_cont[i];
    eHatchery[continuous_index[i]] = hatchery_cont[i];
  }
  for (i in 1:nObs) {
    eOrigin[i] = bOriginWild * (1 - eHatchery[i]) + bOriginHatchery * eHatchery[i];
    ePredation[i] = eOrigin[i] + bPeriod[period[i]] + bDischarge * discharge[i] + bLength[length_class[
    ePredationBeacon[i] = inv_logit(ePredation[i] + bDistance * distance_beacon[i]);
    ePredationCowichan[i] = inv_logit(ePredation[i] + bDistance * distance_cowichan[i]);
    eScanned[i, 1] = ePredationBeacon[i] * bDeposition * det_prob_beacon[i];
    eScanned[i, 2] = ePredationCowichan[i] * bDeposition * det_prob_cowichan[i];
    eScanned[i, 3] = 1 - eScanned[i, 1] - eScanned[i, 2];
 }
}
model {
  bPropHatchery ~ beta(1, 1);
  bOriginHatchery ~ normal(-4, 2);
  bOriginWild ~ normal(-4, 2);
  bDistance ~ normal(-3, 2);
  bPeriodParams ~ normal(0, 2);
  bDischarge ~ normal(0, 2);
  bLengthParams ~ normal(0, 2);
  sWeekAnnual ~ exponential(1);
  bWeekAnnual ~ normal(0, sWeekAnnual);
  sLengthMonth ~ exponential(1);
  bLengthMonth ~ normal(0, sLengthMonth);
  sCohortID ~ exponential(0.5);
  bCohortID ~ normal(0, sCohortID);
  bDeposition ~ beta(13, 13);
  for (i in 1:nhatchery_cont) {
    if (hatchery_cont_obs_bol[i]) {
```

```
hatchery_cont_obs[hatchery_cont_index[i]] ~ beta(eAlpha[i], eBeta[i]);
} else {
    eHatchery_cont_mis[hatchery_cont_index[i]] ~ beta(eAlpha[i], eBeta[i]);
}
for (i in 1:nhatchery_disc) {
    hatchery_disc[i] ~ bernoulli(bPropHatchery);
}
for (i in 1:nObs) {
    detected[i, ] ~ multinomial(to_vector(eScanned[i, ]));
}
}
\end{lstlisting}
```

(* * (** ** 8)

Block 4. Model description.

Results

Tables

Scanning Visits Table 1. Summary of visits to heron rookeries.

	Number of	Mean Scanning	Number of Unique	Proportion of Tags Linked to
Heron Rookery	Visits	Effort (hours)	Tags Detected	Deployment Information
Beacon Hill	2	1.4916667	222	0.9909910
Park				
Chemainus	1	0.6105556	3	0.6666667
Cowichan	40	5.4064653	974	0.9229979
Heron Rookery				
Deep Bay	3	2.5674074	126	0.0079365
Deer Lake	1	3.5333333	4	0.0000000
Little	1	0.3816667	8	0.0000000
Qualicum				
Piercy Road	2	0.9416667	5	0.0000000
Pipers Lagoon	3	1.3666667	6	1.0000000
2				
Stanley Park	3	4.5555556	604	0.0000000

Detection Table 2. Parameter descriptions.

Parameter	Description
bAnnualSurvival	The annual survival rate of PIT tags at the rookery
bRecaptureDate	Effect of the t^{th} visit on bRecapture
bRecaptureIndividual	Effect of the i th individual tag on bRecapture
bRecapture	<pre>Intercept for logit(eRecapture[i, t])</pre>
bSkew	Term controlling the skewness of the random effect of
	bRecaptureIndividual (Cowichan rookery only)
<pre>capture_history[i, t]</pre>	Whether or not the i^{th} individual tag was detected on the t^{th} visit
chi[i, t]	Probability that the i th individual is never captured again, if it is
	alive at time t

Parameter	Description
eRecapture[i, t]	Expected recapture probability of the \mathtt{i}^{th} individual tag during the \mathtt{t}^{th} visit
eSurvival[i, t]	Expected survival probability of tags between the ${\tt t}$ – ${\tt 1}^{\rm th}$ and ${\tt t}^{\rm th}$ visit
first[i]	The first visit the i th individual tag was detected at a rookery
last[i]	The last visit the i^{th} individual tag was detected at a rookery
n_occ_minus_1	Number of scanning visits to the rookery, less one
ndate	Number of scanning visits to the rookery
nindividual	Number of individuals
sRecaptureDate	Standard deviation of the random effect of bRecaptureDate (Cowichan rookery only)
sRecaptureIndividual	Standard deviation of the random effect of bRecaptureIndividual
<pre>years_between_visits[t]</pre>	The number of years between the t^{th} visit and the previous visit

Cowichan Heron Rookery Table 3. Model coefficients.

term	estimate	lower	upper	svalue
bAnnualSurvival	0.955	0.944	0.966	10.6
bRecapture	3.200	2.580	3.790	10.6
bSkew	-13.100	-20.700	-7.070	10.6
sRecaptureDate	1.820	1.460	2.400	10.6
sRecaptureIndividual	1.500	1.360	1.650	10.6

Table 4. Model convergence.

n	Κ	nchains	niters	nthin	ess	rhat	converged
36038	5	3	500	5	267	1.006	TRUE

Table 5. Model sensitivity.

all	analysis	sensitivity	bound
all	1.006	1.009	1.059

Deep Bay Table 6. Model coefficients.

term	estimate	lower	upper	svalue
bAnnualSurvival	0.931	0.698	0.997	10.600
bRecapture	3.580	0.932	6.340	7.090
bRecaptureDate1	2.880	0.187	5.670	4.820
bRecaptureDate2	0.602	-1.920	2.920	0.637
sRecaptureIndividual	2.700	0.992	4.950	10.600

Table 7. Model convergence.

n	Κ	nchains	niters	nthin	ess	rhat	converged
378	5	3	500	15	444	1.006	TRUE

Table 8. Model sensitivity.

all	analysis	sensitivity	bound
all	1.006	1.006	1.261

Pipers Lagoon 2 Table 9. Model coefficients.

term	estimate	lower	upper	svalue
bAnnualSurvival	0.942	0.741	0.998	10.600
bRecapture	0.573	-3.330	4.220	0.383
bRecaptureDate1	0.223	-3.500	4.130	0.141
bRecaptureDate2	0.387	-3.490	3.830	0.231
sRecaptureIndividual	9.070	1.200	42.200	10.600

Table 10. Model convergence.

n	Κ	nchains	niters	nthin	ess	rhat	converged
18	5	3	500	15	880	1.002	TRUE

Table 11. Model sensitivity.

all	analysis	sensitivity	bound
all	1.002	1.002	1.008

Stanley Park Table 12. Model coefficients.

term	estimate	lower	upper	svalue
bAnnualSurvival	0.9000	0.553	0.996	10.6000
bRecapture	-0.0195	-2.390	2.570	0.0174
bRecaptureDate1	0.8390	-1.430	3.120	1.0500
bRecaptureDate2	-0.9640	-3.270	1.510	1.2000
sRecaptureIndividual	3.4200	2.630	6.680	10.6000

Table 13. Model convergence.

n	Κ	nchains	niters	nthin	ess	rhat	converged
1812	5	3	500	40	232	1.02	TRUE

Table 14. Model sensitivity.

all	analysis	sensitivity	bound
all	1.02	1.068	1.074

Predation Table 15. Parameter descriptions.

Parameter	Description
annual[i]	Outmigration year of the i th cohort
bAnnual	Effect of annual on ePredation
bCohortID	Effect of cohort_id[i] on ePredation
bDeposition	Probability that tags eaten by heron are excreted at a rookery
bDistance	Effect of distance_beacon and distance_cowichan on
	<pre>logit(ePredationBeacon) and logit(ePredationCowichan), respectively</pre>
bDoy	Effect of doy on ePredation using a seasonal cosine wave with period of 1 year
bOriginHatchery	Effect of hatchery origin on eOrigin
bOriginWild	Effect of wild origin on eOrigin
bPeriodParams[1]	Effect of being tagged in the beach period compared to the river period
bPeriodParams[2]	Effect of being tagged in the purse period compared to the river period
bPeriod	Effect of period on ePredation
bPhase	Phase shift of seasonal cosine wave describing day of year effect on ePredation
bPropHatchery	The expected proportion of fish in a cohort that are of hatchery origin
bSpecies	Effect of species on ePredation
bSystemBeacon	Effect of system on logit(ePredationBeacon)
bSystemCowichan	Effect of system on logit(ePredationCowichan)
cohort_id[i]	The ID of the i th cohort
cohort_size_cont[i]	Number of individuals in the i th cohort with a proportion of hatchery fish between 0 and 1 or with missing hatchery information
<pre>continuous_index[i]</pre>	Indexes of hatchery that are between 0 and 1 or are unknown
det_prob_beacon[i]	Estimated detection probability at the Beacon Hill heron rookery for the i^{th} cohort
<pre>det_prob_cowichan[i]</pre>	Estimated detection probability at the Cowichan heron rookery for the i^{th} cohort
detected[i, 1]	The number of tags in the i th cohort detected at the Beacon Hill heron rookery
detected[i, 2]	The number of tags in the i th cohort detected at the Cowichan heron rookery
detected[i, 3]	The number of tags in the i th cohort that were not detected at the Beacon Hill or Cowichan rookeries
discrete index[i]	Indexes of hatchery that are either 0 or 1
distance_beacon[i]	Standardized distance between the Beacon Hill heron rookerv and
	mouth of the system the i th cohort was tagged in
distance_cowichan[i]	Standardized distance between the Cowichan heron rookery and mouth of the system the <i>i</i> th cohort was tagged in
doy[i]	Day of year the i th cohort was released
eAlpha[i]	First parameter of the beta distribution describing hatchery values between 0 and 1

Parameter	Description
eBeta[i]	Second parameter of the beta distribution describing hatchery
	values between 0 and 1
eHatchery[i]	Expected proportion of a cohort that is of hatchery origin
eHatchery_cont_mis[i]	Expected proportion of hatchery fish for the i th cohort missing
	hatchery information
eOrigin[i]	Intercept for ePredation
ePredationBeacon[i]	Expected predation rate on the i th cohort at the Beacon Hill
	rookery
ePredationCowichan[i]	Expected predation rate on the i th cohort at the Cowichan rookery
ePredation[i]	Expected heron predation rate on the i th cohort, on the log-odds
	scale, without the effect of distance
eScanned[i, 1]	Expected probability of the i th cohort being scanned at the Beacon
	Hill rookery
eScanned[i, 2]	Expected probability of the i th cohort being scanned at the
	Cowichan rookery
eScanned[i, 3]	Expected probability of not being detected at the Beacon Hill or
	Cowichan rookeries
hatchery[i]	Proportion of the i th cohort that is of hatchery origin
hatchery_cont_index	Indexes for imputing the missing values in hatchery
hatchery_cont_obs_bol[i]	Logical variable describing whether or not the i^{th} cohort has a
	hatchery value between 0 and 1
hatchery_cont_obs	Observed hatchery values between 0 and 1
hatchery_cont	Combined observed and expected values of hatchery between 0 and
hatchery_disc[i]	Proportion of cohort of hatchery origin for cohorts that are entirely hatchery (1) or entirely wild (0)
ii_mis	Indexes to combine the missing hatchery values between 0 and 1
ii_obs	Indexes to combine the observed hatchery values between 0 and 1
nObs	Number of observations
nannual	Number of outmigration years
ncohort_id	Number of cohorts
nhatchery_cont_mis	Number of cohorts with an unknown proportion of hatchery fish
	between 0 and 1
nhatchery_cont_obs	Number of cohorts with a known proportion of hatchery fish
	between 0 and 1
nhatchery_cont	Number of cohorts with a proportion of hatchery fish between 0 and
	1 or with missing hatchery information
nhatchery_disc	Number of cohorts with a known proportion of hatchery fish that
	are either 0 or 1
nperiod	Number of tagging periods
nspecies	Number of species
nsystem	Number of systems
period[i]	The tagging period of the i th cohort
sAnnual	SD of the random effect of bAnnual
sCohortID	SD of the random effect of bCohortID
sSpecies	SD of the random effect of bSpecies
sSystemRookery	SD of the random effects of bSystemBeacon and bSystemCowichan
<pre>species[i]</pre>	The species of the i th cohort
system[i]	River system the i th cohort was tagged in

Table 16. Model coefficients.

term	estimate	lower	upper	svalue
bDeposition	0.508	0.328	0.686	10.6
bDistance	-6.020	-8.420	-3.760	10.6
bDoy	1.010	0.437	1.630	10.6
bOriginHatchery	-12.400	-14.700	-10.500	10.6
bOriginWild	-12.000	-14.300	-10.100	10.6
bPeriodParams1	-1.100	-1.550	-0.675	10.6
bPeriodParams2	-2.290	-2.910	-1.700	10.6
bPhase	0.357	0.279	0.446	10.6
bPropHatchery	0.528	0.521	0.535	10.6
sAnnual	0.562	0.313	1.070	10.6
sCohortID	0.710	0.585	0.862	10.6
sSystemRookery	2.300	1.280	4.180	10.6

Table 17. Model convergence.

n	Κ	nchains	niters	nthin	ess	rhat	converged
3266	12	3	500	10	309	1.011	TRUE

Table 18. Model sensitivity.

all	analysis	sensitivity	bound
all	1.011	1.009	1.086

Table 19. Model posterior predictive checks.

moment	observed	median	lower	upper	svalue
zeros	0.9381506	0.9406001	0.9347826	0.9467238	1.263996
mean	-0.0386290	-0.0510068	-0.0645017	-0.0376838	3.810241
variance	0.0994496	0.1241778	0.1053152	0.1468309	6.644818
skewness	2.6620485	1.4341148	0.5165607	2.2784063	7.381783
kurtosis	30.0105476	21.6927790	17.6590024	26.7738030	6.851268

Sub-Analysis of Predation on Chinook Salmon Table 20. Parameter descriptions.

Parameter	Description
bCohortID	Effect of cohort_id[i] on ePredation
bDeposition	Probability that tags eaten by heron are excreted at a rookery
bDischarge	Effect of discharge on ePredation
bDistance	Effect of distance_beacon and distance_cowichan on
	<pre>logit(ePredationBeacon) and logit(ePredationCowichan), respectively</pre>
bLengthMonth	Effect of length_class_month on ePredation
bLengthParams[1]	Effect of being in the medium length class compared to the small length class
bLengthParams[2]	Effect of being in the large length class compared to the small length class

Parameter	Description
bLength	Effect of length_class on ePredation
bOriginHatchery	Effect of hatchery origin on eOrigin
bOriginWild	Effect of wild origin on eOrigin
bPeriodParams[1]	Effect of being tagged in the beach period compared to the river period
bPeriodParams[2]	Effect of being tagged in the purse period compared to the river period
bPeriod	Effect of period on ePredation
bPropHatchery	The expected proportion of fish in a cohort that are of hatchery origin
bWeekAnnual	Effect of week annual on ePredation
cohort id[i]	The ID of the i th cohort
continuous index[i]	Indexes of hatcherv that are between 0 and 1 or are unknown
det_prob_beacon[i]	Estimated detection probability at the Beacon Hill heron rookery for the <i>i</i> th cohort
det_prob_cowichan[i]	Estimated detection probability at the Cowichan heron rookery for the i th cohort
detected[i, 1]	The number of tags in the i th cohort detected at the Beacon Hill heron rookery
detected[i, 2]	The number of tags in the i th cohort detected at the Cowichan heron rookery
detected[i, 3]	The number of tags in the i th cohort that were not detected at the Beacon Hill or Cowichan rookeries
discharge[i]	Scaled discharge in the system the <i>i</i> th cohort was released, in the week following release
discrete_index[i]	Indexes of hatchery that are either 0 or 1
distance_beacon[i]	Standardized distance between the Beacon Hill heron rookery and mouth of the system the <i>i</i> th cohort was tagged in
distance_cowichan[i]	Standardized distance between the Cowichan heron rookery and mouth of the system the <i>i</i> th cohort was tagged in
eAlpha[i]	First parameter of the beta distribution describing hatchery values between 0 and 1
eBeta[i]	Second parameter of the beta distribution describing hatchery
eHatchery[i]	Expected proportion of a cohort that is of hatchery origin
eHatchery cont mis[i]	Expected proportion of a cohort that is of natchery origin
	hatchery information
eOrigin[i]	Intercept for ePredation
ePredationBeacon[i]	Expected predation rate on the i th cohort at the Beacon Hill rookery
ePredationCowichan[i]	Expected predation rate on the i th cohort at the Cowichan rookery
ePredation[i]	Expected heron predation rate on the i th cohort, on the log-odds scale, without the effect of distance
eScanned[i, 1]	Expected probability of the i^{th} cohort being scanned at the Beacon Hill rookerv
eScanned[i, 2]	Expected probability of the i th cohort being scanned at the Cowichan rookery
eScanned[i, 3]	Expected probability of not being detected at the Beacon Hill or Cowichan rookeries
hatchery[i]	Proportion of the i th cohort that is of hatchery origin
hatchery_cont_index	Indexes for imputing the missing values in hatchery

Parameter	Description
hatchery_cont_obs_bol[i]	Logical variable describing whether or not the i th cohort has a hatchery value between 0 and 1
hatcherv cont obs	Observed hatchery values between 0 and 1
hatchery_cont	Combined observed and expected values of hatchery between 0 and 1
hatchery_disc[i]	Proportion of cohort of hatchery origin for cohorts that are entirely hatchery (1) or entirely wild (0)
ii_mis	Indexes to combine the missing hatchery values between 0 and 1
ii_obs	Indexes to combine the observed hatchery values between 0 and 1
length_class[i]	The length class of the i th cohort
length_class_month[i]	The length class and month of release of the i th cohort
nObs	Number of observations
ncohort_id	Number of cohorts
nhatchery_cont_mis	Number of cohorts with an unknown proportion of hatchery fish between 0 and 1
nhatchery_cont_obs	Number of cohorts with a known proportion of hatchery fish between 0 and 1
nhatchery_cont	Number of cohorts with a known proportion of hatchery fish between 0 and 1
nhatchery_disc	Number of cohorts with a known proportion of hatchery fish that are either 0 or 1
nlength_class_month	Number of length class-month combinations
nlength_class	Number of length classes
nperiod	Number of tagging periods
nweek_annual	Number of week-annual combinations
period[i]	The tagging period of the i th cohort
sCohortID	SD of the random effect of bCohortID
sLengthMonth	Standard deviation of the random effect of bLengthMonth
sWeekAnnual	Standard deviation of the random effect of bWeekAnnual
<pre>species[i]</pre>	The species of the i th cohort
week_annual[i]	The week and year the i^{th} cohort was released

Table 21. Model coefficients.

term	estimate	lower	upper	svalue
bDeposition	0.503	0.3220	0.6880	10.60
bDischarge	-1.390	-2.4100	-0.4460	7.09
bDistance	-3.510	-4.3000	-2.9100	10.60
bLengthParams1	-0.536	-1.4500	0.2980	2.78
bLengthParams2	-1.030	-2.2300	0.0375	4.14
bOriginHatchery	-2.480	-4.6800	-0.5160	6.16
bOriginWild	-6.640	-7.9500	-5.3400	10.60
bPeriodParams1	-1.350	-1.8000	-0.8760	10.60
bPeriodParams2	-2.310	-2.9700	-1.6500	10.60
bPropHatchery	0.189	0.1780	0.2000	10.60
sCohortID	0.668	0.4970	0.8700	10.60
sLengthMonth	0.342	0.0743	0.9680	10.60
sWeekAnnual	0.446	0.1400	0.7090	10.60

Table 22. Model convergence.

n	Κ	nchains	niters	nthin	ess	rhat	converged
1182	13	3	500	10	284	1.029	TRUE

Table 23. Model sensitivity.

all	analysis	sensitivity	bound
all	1.029	1.079	1.05

Table 24. Model posterior predictive checks.

moment	observed	median	lower	upper	svalue
zeros	0.8553299	0.8620981	0.8460237	0.8773266	1.209634
mean	-0.0744831	-0.1007408	-0.1335486	-0.0682637	3.004814
variance	0.2233268	0.2800047	0.2395459	0.3270826	6.464245
skewness	1.5992580	0.9880963	0.3349272	1.5420807	4.936998
kurtosis	10.0354794	7.1873680	5.4718685	9.8445390	4.669065

Movement of Tags between Systems and Rookeries

Tagged Fish Detected at Rookeries Table 25. Number of fish with known deployment information which were detected at heron rookeries, by tagging system and the rookery they were detected at.

Tagging System	Heron Rookery	Count
Big Qualicum	Pipers Lagoon 2	1
Robertson Creek	Cowichan Heron Rookery	1
Millstone	Pipers Lagoon 2	1
Nanaimo	Pipers Lagoon 2	4
Nanaimo	Cowichan Heron Rookery	1
Koksilah	Cowichan Heron Rookery	9
Cowichan	Deep Bay	1
Cowichan	Chemainus Rookery	2
Cowichan	Cowichan Heron Rookery	886
Cowichan	Beacon Hill Park	3
Goldstream	Cowichan Heron Rookery	2
Goldstream	Beacon Hill Park	163
Millstream	Beacon Hill Park	54

Tagged Fish Not Detected at Rookeries Table 26. Number of fish with known deployment information which were not detected at heron rookeries, by tagging system.

Tagging System	Count
Big Qualicum	23698
Black Creek	32430
Cowichan	128512
Englishman	9739
Goldstream	17457
Heydon	3589

Tagging System	Count
Koksilah	1448
Little Qualicum	14879
Millstone	1982
Millstream	3912
Nanaimo	49548
Oyster	768
Puntledge	35253
Quinsam	33551
Robertson Creek	14887

Figures

Scanning Visits



Figure 1. Number of tags scanned by hours of scanning effort, rookery, and proportion of tags linked to deployment information, for visits with known scanning effort.

Detection



Figure 2. The predicted recapture probability (on the log-odds scale) by date and rookery (with 95% CIs).



Figure 3. The predicted annual tag survival probability (on the log-odds scale) by rookery (with 95% CIs).

Predation



Figure 4. Predation rate (on the log-odds scale) by cohort origin (with 95% CIs).



Figure 5. Predation rate (on the log-odds scale) by tagging year for river-released cohorts (with 95% CIs).



Figure 6. Predation rate (on the log-odds scale) by tagging period (with 95% CIs).



Figure 7. Predation rate by tagging day of year for river-released cohorts (with 95% CIs).



Figure 8. Predation rate by distance between tagging system mouth and rookery for river-released cohorts (with 95% CIs).



Figure 9. Predation rate (on the log-odds scale) by distance between rookery and system mouth, system, and rookery for river-released cohorts (with 95% CIs).

Sub-Analysis of Predation on Chinook Salmon



Figure 10. Predation rate (on the log-odds scale) by cohort origin, for medium-sized fish from river-released cohorts (with 95% CIs).



Figure 11. Predation rate (on the log-odds scale) by tagging period for medium-sized fish from river-released cohorts (with 95% CIs).



Figure 12. Predation rate (on the log-odds scale) by month and fork length class, for river-released cohorts (with 95% CIs).



Figure 13. Predation rate (on the log-odds scale) by week and year for medium-sized fish from river-released cohorts (with 95% CIs).



Figure 14. Predation rate by scaled discharge (MAD / mean weekly MAD) for medium-sized fish from river-released cohorts (with 95% CIs).



Figure 15. Predation rate by distance between tagging system mouth and rookery for medium-sized fish from river-released cohorts (with 95% CIs).



Figure 16. Predation rate by distance (km) between tagging system and rookery, tagging system, and rookery, for medium-sized fish from river-released cohorts (with 95% CIs).



Figure 17. Length frequency distributions of Chinook salmon less than 120 mm from Nanaimo and Cowichan



Rivers used in the predation sub-analysis, by origin. The red dotted lines represent the cutoffs between size classes (70 mm, 90 mm, and 120 mm).

Figure 18. Scaled discharge (MAD / mean weekly MAD) by day of year, system, and outmigration year. A scaled discharge value of 1.0 represents an average MAD value for that week and year.

Movement of Tags between Systems and Rookeries

All Tagged Fish



Figure 19. A visual depiction of the proportion of all known deployed tags that end up at rookeries. The sections on the left of the plot represent the tagging locations of fish in this analysis. The sections on the right are the rookeries that tags were detected at. The relative height of each section represents the proportion of tags belonging to that category. Both tagging systems and rookeries are ordered by latitude, with southern sites at the bottom and northern sites at the top.

Tagged Fish Detected at Rookeries

Big Qualicum Robertson Creek Milistone Nanaimo	Deep Bay Pipers Lagoon 2 Chemainus	_
Cowichan	Cowichan Heron Rookery	
Goldstream	Beacon Hill Park	
Millstream		

Figure 20. A visual depiction of the movement of fish tags from tagging system to rookery for tags with known deployment information ultimately detected at a rookery. The sections on the left of the plot represent the tagging locations of fish in this analysis. The sections on the right are the rookeries that these tags were detected at. The relative height of each section and the linkage paths represent the proportion of tags belonging to that category. Both tagging systems and rookeries are ordered by latitude, with southern sites at the bottom and northern sites at the top.



Figure 21. A visual depiction of the movement of fish tags from tagging system to rookery for tags with known deployment information ultimately detected at rookeries. The sections on the left of the plot represent the tagging locations of fish in this analysis. The sections on the right are the rookeries that these tags were detected at. The colours of the linkages represent the species of fish. The relative height of each section and the linkage paths represent the proportion of tags belonging to that category. Both tagging systems and rookeries are ordered by latitude, with southern sites at the bottom and northern sites at the top.

Detection Histories



Figure 22. Detection history of tags scanned at Beacon Hill Park, by fish, date of first session of visit, and whether or not tags were linked to deployment information. Note that time differences between scan dates on the x-axis may not be uniform.



Figure 23. Detection history of tags scanned at Chemainus, by fish, date of first session of visit, and whether



or not tags were linked to deployment information. Note that time differences between scan dates on the x-axis may not be uniform.

Figure 24. Detection history of tags scanned at Cowichan Heron Rookery, by fish, date of first session of visit, and whether or not tags were linked to deployment information. Note that time differences between scan dates on the x-axis may not be uniform.



Figure 25. Detection history of tags scanned at Deep Bay, by fish, date of first session of visit, and whether or not tags were linked to deployment information. Note that time differences between scan dates on the x-axis may not be uniform.



Figure 26. Detection history of tags scanned at Deer Lake, by fish, date of first session of visit, and whether

or not tags were linked to deployment information. Note that time differences between scan dates on the x-axis may not be uniform.



Figure 27. Detection history of tags scanned at Little Qualicum, by fish, date of first session of visit, and whether or not tags were linked to deployment information. Note that time differences between scan dates on the x-axis may not be uniform.



Figure 28. Detection history of tags scanned at Piercy Road, by fish, date of first session of visit, and whether or not tags were linked to deployment information. Note that time differences between scan dates on the x-axis may not be uniform.



Figure 29. Detection history of tags scanned at Pipers Lagoon 2, by fish, date of first session of visit, and

whether or not tags were linked to deployment information. Note that time differences between scan dates on the x-axis may not be uniform.



Figure 30. Detection history of tags scanned at Stanley Park, by fish, date of first session of visit, and whether or not tags were linked to deployment information. Note that time differences between scan dates on the x-axis may not be uniform.

Tagged Fish Detected at Rookeries



Figure 31. Number of tags detected at heron rookeries with known deployment information, by outmigration year, species, and heron rookery.



Figure 32. Number of tags detected at heron rookeries with known deployment information, by tagging year, tagging system, and heron rookery.



Figure 33. Number of tags detected at heron rookeries, by tagging period.



Figure 34. Number of detected tags by fork length (mm) and heron rookery, for fish with known fork lengths.

Recommendations

Recommendations include:

- Continue more scans at the heron rookeries:
 - Aim to scan those rookeries with >50 tags twice per year (Cowichan, Beacon Hill, Deep Bay, Stanley Park), once around a month after the majority of hatchery releases in nearby systems, and again 6 months later.
 - Aim to scan those rookeries with < 50 tags once every two years (Chemainus, Deer Lake, Little Qualicum, Piercy Road, Pipers Lagoon), around 2 months after the majority of hatchery releases in nearby systems.
- Use the tag scanner that collects coordinates of the tags scanned at rookeries as much as possible, and particulary at the Cowichan rookery, to further reduce uncertainty in the detection probabilities at the rookeries.
- Attempt to link more of the tags detected at rookeries to tagging deployment data.
- Get more information on heron deposition rate of ingested tags at rookeries following the methods of Hostetter et al. (2015).
- Collect and provide information on as detailed fish length information as possible for hatchery fish cohorts (individual fork lengths linked to PIT tag ID or as narrow as possible bins of fork lengths).

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