## Discussion Paper

Incorporating Fisheries Related Incidental Mortality of Fraser River Spring/Summer 42/52 Chinook in the Estimation of Total Mortalities in Marine Recreational Fisheries (DFO Management Areas 18,19,20,29,121,123)

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Prepared for:

The Pacific Marine Conservation Caucus: Salmon Subcommittee

March 6, 2019

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## 1. Background

Fisheries managers, First Nations and stakeholders are becoming more aware that Fisheries Related Incidental Mortality (FRIM) can contribute significantly to total mortalities (TM) in fisheries (see Patterson et al. 2017a, 2017b). This paper examines potential FRIM and TMs in spring and summer Fraser River chinook populations designated as 'Endangered' by Canada's Committee on the Status of Endangered Wildlife in Canada (COSEWIC). This includes Fraser River $4_{2} \mathrm{~S}$ (1.2s) and $5_{2} \mathrm{~S}$ (1.3s) encountered in the Juan de Fuca Strait, Victoria area, Gulf Islands, and marine Fraser River recreational fishery (DFO fishery management areas 18,19,20,29,121,123).

Fishery regulations introduced in 2010 require the releasing of chinook greater than either 67 or 85 cm (varies by date depending on the stock of concern expected to be present). It is recognized that a high proportion of fish caught at, or above, these lengths tend to be from populations of concern, including those designated as Endangered by COSEWIC. The retained catch is made up of a mix of US and Canadian wild and hatchery stocks. Understanding the potential long-term fate of the released fish is therefore critical in any estimation of total fishery related mortalities for the populations of concern.

Fisheries and Ocean's Canada currently relies on Pacific Salmon Commission (PSC) estimates of FRIM. Both the PSC (PSC 2004) and Patterson et al. (2017a, 2017b) recognize and describe the limitations of the current approach. Because Fisheries and Oceans Canada say they are moving to a total mortality cap to manage the populations of concern, including those designated as Endangered; it is important to understand whether incorporating the elements of FRIM described in Patterson et al. (2017a,b) would have a significant impact on the estimates of total mortalities used in making fishery management and allocation decisions.

To be clear from the start, due to data limitations many assumptions are required in this analysis, some of which are described in the assumptions section (2.7). Furthermore, this is not an effort to ascribe definitive numbers of FRIM from specific fisheries to sub-stocks of Fraser River chinook, but an introductory look into the range of impacts that might be expected using the guidance provided in Patterson et al (2017a, 2017b). A simple excel worksheet was created that uses retained and release data by month and PFMA, DNA data and discrete values for drop-off, short-term and delayed mortalities to illustrate possible ranges of FRIM and TM in recreational sport fisheries. Additionally, simple Monte Carlo simulations were executed in the statistical programming language $R$ ( $R$ Core Team, 2017) using assumed distributions of parameters to create probability density plots illustrating some of the uncertainty in FRIM and TMs in various years, with respect to current methods for calculating FRIM, and the amount of TM in the marine recreational fishery relative to spawning escapements.

Patterson et al. (2017a) lays out the potential mortality ranges for each factor, however stochastic modelling can be used to characterize the variation in each individual encounter through the use of probability distributions for FRIM parameters (drop-out, capture mortality, and post-release mortality).

It is anticipated that this work will inspire discussion on this important subject, provide information to First Nations, and stakeholders on the estimation of total mortalities using the guidance provided in Patterson et al, 2017 (b) and DFO (2016), and form the basis for a much more in-depth, collaborative and robust analysis.

## 2. Methods

### 2.1 Data

Catch and release data and stock composition data (DNA) were provided by Wilf Luedtke (DFO, personal communication). For the bulk of this analysis, catches and releases from PFMA areas
$18,19,20,29,121,123$ were used. Retained and released chinook were aggregated by month for May, June, July and August across all areas included. Encounters were calculated for each month as follows:

Encounters $=$ Retained + Released

DNA data provided by DFO from their Area 19/20 creel surveys (Wilf Luedtke, DFO, personal communication) was used to determine the number of retained and released Fraser River $42 / 5_{2}$ chinook by month. DNA percentages from the UPFR, MUFR, NOTH, LWTH, LWFR-sp and LWFR-su (Fraser $4_{2}$ s and $5_{2} \mathrm{~s}$ ) groups were summed to determine the total percentage composition of these stocks in each month. This percentage was used to determine the number of retained and released FR 4-2/5-2 chinook from all areas (Assumption 1 and 2). Encounters were then calculated as above where required.

Escapement information for Fraser River $42 / 5_{2}$ chinook was provided by Gayle Brown (DFO, personal communication), but is preliminary data and rounded to reflect that other data sets may exist. However, we have used it in a purely comparative manner to our estimates of FRIM and total mortalities.

### 2.2 Fisheries Related Incidental Mortality

In Patterson et al. (2017b), guidance is given through risk factor scoring tables. We used these tables as well as local knowledge of recreational fisheries to inform our selection of FRIM mortality ranges for the simple Excel spreadsheet and the stochastic modelling work. One suggested formula for the calculation of FRIM is from the PSC as referred to in Patterson et al. (2017b):
$F R I M=($ Kept Catch $x P(N C M)+[$ Released Catch $x(P(N C M)+P(P R M))]$
Where $P(P R M)=P($ Capture Mortality $)+P($ Handling Mortality $)+P($ Injury Mortality $)+$ $P$ (Predation Mortality)

This separates mortality into a non-capture mortality rate ( $P(N C M)$ ) and post-release mortality ( $P(P R M)$ ). For the rest of this paper, NCM will be referred to as drop-out mortality (P(DOM)).

The range of the probabilities for the four sub-components of Post Release Mortality (PRM) estimates were drawn from the Table 1. The Risk Factors and Mortality Risk Ranges are taken from Appendix A in Patterson et al. (2017b). The chosen Mortality Risk Range was based on selective interviews with two experienced anglers: one an experienced guide, the other a retired biologist who fishes non-guided. We could not find any published fishery independent or dependent estimates of the Risk Factors and mortality ranges.

Table 1: Risk factors and associated mortality ranges used for capture and post-release mortality used in the simple and stochastic models.

| RISK FACTOR | CHOSEN MORTALITY RANGE | COMMENTS |
| :---: | :---: | :---: |
| CAPTURE | 5-15\% | Under 10 minutes between hooking and landing |
| HANDLING | 0-25\% | Released in water without netting to spending under 2 minutes in air (landed in, and released from, boat). The wide variation is because water release and boat release are both employed |
| INJURY | 0-5\% | Very minor injuries are reported |
| PREDATORS | 15-25\% | Daily observations of a few predators. This may be biased low as some fishing locations are reported to have relatively high numbers of predators |

We use a Multiplicative (a variant of additive) calculation as described in Patterson et al (2017b). This assumes that the cumulative impact of two or more risk factors follows a simple multiplicative risk model. Multiplicative risk is a variant of the additive interaction type that is used when the response variable (or cumulative impact) is measured with percent mortality. This implies that any two factors are independent and therefore do not interact in a synergistic or antagonistic way. Therefore, the contributions of both factors to the overall mortality risk can be simply added together.


A simple flow chart (after Patterson et al. 2017b) illustrating the various sub components used in this analysis.

An additional Risk Factor recommended by Patterson et al. (2017b) is Water Temperature. We did not employ this risk factor as most of the encounters are in the marine environment. We acknowledge this
is a potential shortcoming because some of the encounters occur adjacent to the Fraser River and the releases may soon thereafter encounter warm water which may compromise their migratory success. Further, encountering warm freshwater in their migratory phase may complicate migratory success for fish injured or stressed during release. Finally, there is a thermal change for fish brought up from deeper, cooler marine waters to surface or air temperatures.

Total mortalities in each case are calculated by a simple formula:

$$
\begin{equation*}
T M=F R I M+\text { Kept Catch } \tag{3}
\end{equation*}
$$

### 2.4 Current Methods

It is understood that the current methodology for calculating FRIM and total mortalities of Fraser River $4_{2} / 5_{2}$ chinook in Areas 19/20 follows these formulas:

FRIM $=0.15 \times$ Released Catch
$T M=$ Kept Catch $+(0.15 x$ Released Catch $)$
Note that these formulas do not include estimates of DOM and uses a relatively low point estimate of 0.15 for all post-release mortality.

The PSC uses other values for drop-out (6.9\%) and 'immediate' mortality (12.3\%), their estimates appear to be derived through the following equations:

FRIM $=($ Kept Catch $x 0.069+[$ Released Catch $x(6.9 \%+12.3 \%)]$
TM $=$ Kept Catch + FRIM (eq 7)
These values were provided by Gayle Brown (DFO, personal communication).

### 2.5 Simple Model

A simple model was developed in Excel that can be used to provide discrete estimates of FRIM and TMs based on selection of parameter values (drop-out mortality, capture and post-release mortality). This was used to produce tables showing the range of discrete estimates over various parameter ranges by intervals. FRIM was calculated following equation (2) above.

Drop-out mortality (PCM) was varied between 5 and 15 to develop the FRIM tables, accommodating the uncertainty about depredation described by PSC (2014). The tables show discrete estimates at each combination of capture mortality ( $5-15 \%$ in intervals of $5 \%$ ) and total PRM ( $15-55 \%$ in intervals of 10\%) for DOMs of 5 and $15 \%$. We used 2014 DNA and catch and release data for the FRIM tables. The Total Mortality Range (not including drop-out mortality) employed in our model is $20-70 \%$.

### 2.6 Stochastic Model

The goal of this modelling work is to examine the range of FRIM that could be expected using the parameter ranges in Table 1 for some years $(2014,2017)$ where we have DNA data to inform stock composition. This process was replicated for 2018 using averaged DNA data. This is not a prescriptive approach, but rather an example of the kind of work that could be done to provide precautionary management advice. Refinement of the model, methods and inputs is encouraged.

A simplistic stochastic model was developed in R (R Core Team 2017) that uses the catch and release data, DNA data and randomly generated probability distributions for estimates of drop-out mortality (DOM), capture mortality (CM), handling mortality (HM), injury mortality (IM) and predation mortality (PM) to generate probability distributions of FRIM and TMs. This can be applied to all areas or sub-areas using DNA data from various years.

Parameter distributions were created by drawing 10,000 random samples from uniform distributions generated through 100,000 random variates within the ranges shown in Table 1. A uniform distribution (assumption 3) was used at this point, however triangular, normal or other distributions can easily be used if future work shows that they are more appropriate distributions. Sample distributions for the parameters are shown in Figure 2 and 3. Again, for the purpose of this discussion paper, uniform distributions are only a starting point. A simple Monte Carlo simulation was executed with 10,000 iterations. FRIM and TM output distributions were then plotted for each year and mortality case.

### 2.6.1 Management Sensitivity Analysis

An additional analysis was conducted to examine changes to the FRIM distributions under hypothetical management scenarios that would increase the proportion of released Fraser River $42 / 5_{2}$ chinook. Essentially, the DNA based stock composition was increased in the released chinook by 20, 40 and 60\% from the base case where the proportion of Fraser River $42 / 5_{2}$ chinook was equal in the kept catch and released catch. This was done to illustrate the effects of, for example, slot size restrictions that may increase the likelihood of larger Fraser River $42 / 5_{2}$ chinook being released. This was done for 2014, 2017 and 2018. Future work could increase the complexity of the analysis to incorporate time and area specific measures to provide a more realistic characterization.

### 2.7 Assumptions

1. DNA data from $19 / 20$ can be expanded to cover all areas.
a. This is an obviously data limited simplistic approach. It is highly likely that there are differences in the stock composition in each area, and in the timing of the chinook present as they move through their migration
2. DNA data in released catch approximates the samples from the kept catch.
a. This is likely not true in areas and times where slot sizes management measures exist. This concern is hypothetically addressed in the management scenario section (2.6.1)
3. Actual DNA data in 2018 is represented by the average of all years with DNA data (2009, 2010, 2014, 2016 and 2017).
a. Actual 2018 DNA data will be available shortly. There is considerable variation in DNA proportions of Fraser River $42 / 5_{2}$ in June which will affect the analysis if 2018 DNA is different than the mean
4. DNA sampling rates are adequate to estimate representation by stock components of interest.
a. Efforts should be made to increase the sample size, however uncertainty of DNA estimates could easily be incorporated into the model
5. Uniform distributions approximate the true distribution of mortality parameters.
a. Triangular, normal or other distributions can easily be used if future work shows that they are more appropriate distributions
6. There is no error in the catch and release data.
a. This could be addressed by providing a normal distribution around the kept catch and released catch estimates
7. Potential differential impact of high Fraser River water temperatures on released chinook versus non-encountered chinook are not incorporated.
a. Additionally, Fraser River water temperatures would be expected to increase PRM estimates in areas where releases occur much closer to the Fraser River (e.g. Area 29)
8. Compliance with regulations.
a. Uncertainty regarding compliance with fishing regulations, slot size restrictions, and catch reporting requirements in a fishery with low levels of enforcement and no fishery independent monitoring

## 3. Results

Using the Excel based spreadsheet tool to vary the mortality estimates illustrates the range of discrete values possible from different combinations of mortality rates (Table 2). Notably the combination of $15 \%$ DOM, $15 \%$ CM and 55\% PRM provides a FRIM estimate of more than 3 times than the lowest case of $5 \%$ DOM, $5 \%$ CM and $15 \%$ PRM. This provides support for the development of the stochastic model.

Table 2: FRIM estimates generated in the Excel based spreadsheet to illustrate the range of FRIM estimates possible of Fraser River 42/52 chinook given the range in mortality parameters in this study for 2014.

| Drop-out of 5\% |  | Capture Mortality Rate |  |  | Drop-out of $15 \%$ |  | Capture Mortality Rate |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | 5\% | 10\% | 15\% |  |  | 5\% | 10\% | 15\% |
|  | 15\% | 3373 | 3961 | 4548 | + | 15\% | 5421 | 6009 | 6596 |
|  | 25\% | 4548 | 5136 | 5723 |  | 25\% | 6596 | 7183 | 7771 |
|  | 35\% | 5723 | 6310 | 6898 |  | 35\% | 7771 | 8358 | 8946 |
|  | 45\% | 6898 | 5286 | 8072 |  | 45\% | 8946 | 9533 | 10120 |
|  | 55\% | 6461 | 8660 | 9247 |  | 55\% | 10120 | 10708 | 11295 |

Figure 4 shows the proportion of Fraser River $4_{2} / 5_{2}$ present in the DNA samples by month. Typically very few are present in May and August, June averages around $35 \%$ but is highly variable (range 16.9 to $57.7 \%$ ) and July averages around 20. Total (all stocks) encounter rates increase from May to August (Figure 5). However, Figure 6 shows that June and July are the months where the most Fraser River $42 / 5_{2}$ are present, followed by August then May.

Figures 7-9 show the FRIM and TM outputs from the stochastic model for 2014, 2017 and 2018 respectively. In all cases the entire probability distribution is higher than the estimate of FRIM or TMs using the current methods described in equation (4) and (5). Table 2 shows the estimates for various probabilities from analyses illustrated in Figures 7-9. From this table at the median value, FRIM accounts for 46,35 and $40 \%$ of the total mortalities in 2014, 2017 and 2018 respectively.

Table 2: A selection of various quantiles for FRIM and TM in 2014, 2017 and 2018. The median is highlighted in blue, and $25^{\text {th }} / 75^{\text {th }}$ are highlighted in green and the $2.5^{\text {th }} / 97.5^{\text {th }}$ (95\%) are highlighted in red. For example, there is a $95 \%$ chance that FRIM in 2014 was between 5133 and 9550, but only a $50 \%$ chance that it was between 6491 and 8146 chinook, given the specific inputs used in the stochastic model.

|  |  | Quantile |  |  |  |  |  |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | Year | $2.50 \%$ | $5 \%$ | $10 \%$ | $25 \%$ | $50 \%$ | $75 \%$ | $90 \%$ | $95 \%$ | $97.50 \%$ |
| FRIM | 2014 | 5133 | 5408 | 5804 | 6491 | 7301 | 8146 | 8866 | 9224 | 9550 |
|  | 2017 | 1787 | 1890 | 2019 | 2267 | 2548 | 2840 | 3095 | 3220 | 3339 |
|  | 2018 | 3846 | 4062 | 4350 | 4874 | 5478 | 6107 | 6646 | 6918 | 7172 |
| Total | 2014 | 13865 | 14141 | 14536 | 15223 | 16033 | 16878 | 17598 | 17956 | 18282 |
|  | 2017 | 6471 | 6574 | 6702 | 6951 | 7232 | 7523 | 7778 | 7904 | 8023 |
|  | 2018 | 12103 | 12319 | 12606 | 13131 | 13734 | 14364 | 14903 | 15174 | 15428 |

We also compared the outputs from the stochastic model to FRIM and TM estimates following DFO and PSC methods (equations 4-7) using data from 2017 and the management sensitivity analysis discussed in Section 2.6.1. Table 3 shows that estimates of FRIM derived from the stochastic model are much higher than both DFO estimates ( $>4 x$ ) and PSC estimates (approx. $2.5 x$ ). When translated to total mortalities in 2017, this corresponds to an approximately 1.5 -fold increase from the DFO estimate and $1.3 x$ from the PSC estimate.

Table 3: FRIM estimates from DFO, PSC and our stochastic model under the different cases from our management regulation sensitivity analysis. The base case assumes that the proportion of Fraser River $42 / 5_{2}$ chinook is equal in the kept catch and released catch. The 20/40/60\% scenario assumes that the proportion of Fraser River $42 / 5_{2}$ chinook in the released catch is 20/40/60\% higher than in the kept catch.

|  |  |  |  | $50 \%$ Probability <br> from Stochastic | Increase <br> from DFO <br> $(\%)$ | Increase <br> from PSC <br> $(\%)$ |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | Case | DFO | PSC | Model | 2547 | $447 \%$ |
|  | base | 570 | 1052 | $242 \%$ |  |  |
| FRIM | $20 \%$ | 684 | 1198 | 2964 | $433 \%$ | $247 \%$ |
|  | $40 \%$ | 798 | 1344 | 3379 | $423 \%$ | $251 \%$ |
|  | $60 \%$ | 911 | 1490 | 3792 | $416 \%$ | $254 \%$ |
|  | base | 5253 | 5736 | 7232 | $138 \%$ | $126 \%$ |
| Total | $20 \%$ | 5367 | 5882 | 7648 | $143 \%$ | $130 \%$ |
| Mortalities | $40 \%$ | 5481 | 6028 | 8063 | $147 \%$ | $134 \%$ |
|  | $60 \%$ | 5595 | 6174 | 8476 | $151 \%$ | $137 \%$ |

As an additional comparison to highlight the importance of work to improve the certainty of FRIM estimates, we compared the model output median values to FRIM estimates using DFO and PSC methods to preliminary escapement estimates of Fraser River $42 / 5_{2}$ chinook. The high levels of FRIM and TM in years such as 2009 and 2018 illustrate the need to have a better understanding of FRIM mortality factors and how they should be applied following the guidance in Patterson et al. (2017b).

Table 4: A comparison of escapement and FRIM estimates using DFO and PSC methods and the median value from the stochastic model. Total mortalities from the stochastic model are also included. Only years with DNA analysis are included, except for 2018 where DNA results are not available yet. In 2018 the proportion of Fraser River 42/52 chinook was estimated as the average by month over all years with DNA data (2009, 2010, 2014, 2016 and 2017).

|  | Escapement of <br> Fraser River | DFO |  | FRIM at 50\% <br> Probability | TM at 50\% <br> Probability |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| Year | $\mathbf{4}_{\mathbf{2}} / \mathbf{5}_{\mathbf{2}}$ <br> chinook | FRIM <br> Estimate | PSC FRIM <br> Estimate | Stochastic <br> Model | Stochastic <br> Model |
| 2009 | 48100 | 1656 | 3081 | 7438 | 21374 |
| 2010 | 45400 | 416 | 851 | 1982 | 6591 |
| 2011 | 32500 |  |  |  |  |
| 2012 | 32300 |  |  |  |  |
| 2013 | 34100 |  |  |  |  |
| 2014 | 81900 | 1762 | 2858 | 7301 | 16033 |
| 2015 | 64700 |  |  |  |  |
| 2016 | 32200 | 687 | 1265 | 3068 | 8658 |
| 2017 | 19800 | 570 | 1052 | 2547 | 7523 |
| $2018^{1}$ | 16000 | 1274 | 2201 | 5478 | 13734 |

## 4. Discussion

Our analysis suggest total mortalities associated with south coast recreational chinook fisheries impacting Fraser $4_{2} / 5_{2}$ chinook populations may be much higher than currently estimated by DFO and the PSC. We also illustrate the uncertainty incorporated in all estimates.

DFO says they are moving towards a total mortalities cap to manage Fraser chinook populations designated as 'Endangered' by COSEWIC. Since a key management measure employed to reduce harvest impacts on these populations is the releasing of chinook assumed - based on length - to be from these populations; it is important to incorporate an estimate of FRIM that incorporates best practices and the associated uncertainty.

There are many more steps needed to complete a complex and robust model incorporating variation in input parameters such as area and time specific management restrictions, area specific water temperatures, and area specific predation rates, to note a few. And there are many more areas where this model could be improved. For example, Patterson et al. (2017b) suggest that predation may be a significant factor in some areas where high seal density is present. This area specific predation rate could be applied differentially in a subset of areas given evidence to suggest actual pinniped presence. However, the variation incorporated currently in the input parameters for DOM, CM, HM, IM and PM should capture some of that.

Fisheries managers require accurate estimates of mortality to better account for total mortality from fishing, while fishers desire guidance on strategies for reducing mortality and maintaining the welfare of released fish. The emergent theme in recent research is that post-release rates of mortality are
consistently context-specific and can be affected by a suite of interacting biotic and abiotic factors. The fishing gear used, location of a fishery, water temperature, and handling techniques employed by fishers each can dramatically affect survival of the salmon they release (Raby et al. 2015). Future research requires a collaboration between stakeholders, managers, and researchers - similar to Cook et al. (2017, $2018)$, Bass et al. (2017) and Donaldson $(2011,2013)$ - where mortality factors associated with particular fisheries are identified and the necessary research conducted as recommended in Patterson et al. (2017b). Stock estimates for exploited populations that do not account for non-retention mortality overestimate the number of reproductively viable fish. Unaccounted mortality and interannual variation in the magnitude of this mortality may prevent accurate estimates of viable spawners, confound our understanding of the relationship between stock size and recruitment, impede optimal management and obscure the ecosystem impacts of migratory stocks (Baker and Schindler, 2011).

## 5. Recommendations

## 1. Model improvements

In the stochastic model the Kept Catch term is added across the FRIM probability distribution. Additional work could be done to quantify the error (and may have been done already in creel estimates) in both the Kept Catch and Released Catch variables, in which case uncertainty around those estimates could easily be incorporated into the model. Additionally, the uncertainty in the DNA stock composition data could be easily incorporated, and may be a valuable addition given the generally small sample sizes. Area and time specific management measures could be incorporated. Area and time specific mortality risk ranges could be incorporated.
2. DNA sampling

DNA sampling effort should be increased to other areas than just 19/20 (and to our understanding it has been recently), and an effort to increase sample size in all areas should be made. DNA collection kits could be provided to guides to take small tissue samples from fins or other areas in a non-lethal manner for those fish released due to slot-size restrictions, in an effort to examine the assumption that the proportion of Fraser River $42 / 5_{2}$ chinook is equal in kept and released catch.
3. Capture mortality

Additional information on capture mortality and the behaviour of fishers in recreational fisheries with regards to kept and released capture mortalities should be gathered. For example, depending on size restrictions and licence regulations, fish that are captured (brought on board) dead may be kept or discarded. Additional information on this would be helpful in scaling the capture mortality term and/or separating it from the PRM term in FRIM calculations.
4. Pinniped density and short-term predation mortality

Research should be conducted to gain a better understanding of short-term mortality of released fish in areas with relatively high pinniped density.

## 5. Long-term post release mortality

Research using telemetry (similar to Cook et al. (2017)) should be undertaken to better understand longterm mortality.
6. Surveys and fishery independent observations

Surveys, accommodated by fishery independent observations, should be used to obtain better estimates of the mortality ranges associated with identified Risk Factors.

## 6. References

Baker, M.R. and D.E. Schindler. 2009. Unaccounted mortality in salmon fisheries: non-retention in gillnets and effects on estimates of spawners. Journal of Applied Ecology 46:752-761. doi:
10.1111/j.1365-2664.2009.01673.x

Bass, A.L., Hinch, S.G., Patterson, D.A., Cooke, S.J., Farrell, A.P. 2018. Location-specific consequences of beach seine and gillnet capture on upriver-migrating sockeye salmon migration behavior and fate. Canadian Journal of Fisheries and Aquatic Sciences 75(11): 2011-2023.

Cook, K. V., Hinch, S. G., Drenner, S. M., Halfyard, E. A., Raby, G. D., and Cooke, S. J. 2017. Populationspecific mortality in coho salmon (Oncorhynchus kisutch) released from a purse seine fishery. ICES Journal of Marine Science, doi:10.1093/icesjms/fsx129.

Cook, K.V., Hinch, S.G., Watson, M.S., Patterson, D.A., Reid, A.J., Cooke, S.J. 2018. Experimental capture and handling of chum salmon reveal thresholds in injury, impairment, and physiology: Best practices to improve bycatch survival in a purse seine fishery. Fisheries Research 206: 96-108.

Donaldson, M.R., Hinch, S.G., Patterson, D.A., Hills, J., Thomas, J.O., Cooke, S.J., Raby, G.D., Thompson, L.A., Robichaud, D., English, K.K., Farrell, A.P. (2011) The consequences of angling, beach seining, and confinement on the physiology, post-release behaviour and survival of adult sockeye salmon during upriver migration. Fisheries Research 108: 133-141.

Donaldson, M.R., Raby, G.D., Nguyen, V.N., Hinch, S.G., Patterson, D.A., Farrell, A.P., Rudd, M., Thompson, L.A., O’Connor, C.M., Colotelo, A.H., McConnachie, S.H., Cook, K.V., Robichaud, D., English, K.K., Cooke, S.J. (2013) Evaluation of a simple technique for recovering Pacific salmon from capture stress: integrating comparative physiology, biotelemetry, and social science to solve a conservation problem. Canadian Journal of Fisheries and Aquatic Sciences 70: 90-100.

DFO. 2016. Review and Evaluation of Fishing-Related Incidental Mortality for Pacific Salmon. DFO Can. Sci. Advis. Sec. Sci. Advis. Rep. 2016/049.

Patterson, D.A., Robinson, K.A., Lennox, R.J., Nettles, T.L., Donaldson, L.A., Eliason, E.J., Raby, G.D., Chapman, J.M., Cook, K.V., Donaldson, M.R., Bass, A.L., Drenner, S.M., Reid, A.J., Cooke, S.J., and Hinch, S.G. 2017a. Review and Evaluation of Fishing-Related Incidental Mortality for Pacific Salmon. DFO Can. Sci. Advis. Sec. Res. Doc. 2017/010. ix + 155 p.

Patterson, D.A., Robinson, K.A., Raby, G.D., Bass, A.L., Houtman, R., Hinch, S.G., and Cooke, S.J. 2017b. Guidance to Derive and Update Fishing-Related Incidental Mortality Rates for Pacific Salmon. DFO Can. Sci. Advis. Sec. Res. Doc. 2017/011. vii + 56 p.

Pacific Salmon Commission Joint Technical Committee Report. 2004. Estimation and application of incidental fishing mortality in chinook salmon management under the 1999 agreement to the pacific salmon treaty. Report TCCHINOOK (04)-1. vii + 56 p.

R Core Team (2017). R: A language and environment for statistical computing. R Foundation for statistical Computing, Vienna, Austria. URL https://www.R-project.org/.

Raby, G.D., Donaldson, M.R., Hinch, S.G., Clark, T.D., Eliason, E.J., Jeffries, K.M., Cook, K.V., Teffer, A., Bass, A.L., Miller, K.M., Patterson, D.A., Farrell, A.P., Cooke, S.J. 2015. Fishing for effective conservation: context and biotic variation are keys to understanding the survival of Pacific salmon after catch-andrelease. Integrative and Comparative Biology 55(4):554-576.

## 7. Glossary of Terms

FRIM: Fisheries Related Incidental Mortality
TM: Total Mortalities
DOM, NCM and PCM: Drop-out, non-capture mortality, pre-capture mortality are equivalent terms
PRM: Post-release mortality
CM: Capture mortality
HM: Handling mortality
IM: Injury mortality
PM: Predation mortality
Fraser River $\mathbf{4}_{\mathbf{2}} / \mathbf{5}_{\mathbf{2}}$ chinook: Chinook from the spring and summer $4_{2}(1.2)$ and $5_{2}(1.3)$ populations in the Fraser River, including Upper Fraser spring/summer $5_{2}$, Middle/Upper Fraser spring/summer $5_{2}$, Lower Fraser spring and summer, North Thompson spring/summer $5_{2}$ and Lower Thompson spring $4_{2}$ populations. These populations rear for 1 year in freshwater and the return after either 3 years ( $4_{2}$ ) or 4 years $\left(5_{2}\right)$ at sea.


Figure 1: Map of the PFMAs and Southern Resident Killer Whale Critical Habitat. From Resource Management, Pacific Region.


Figure 2: Probability density plot used in the stochastic model for drop-out mortality. The dashed vertical line represents the median value.


Figure 3: Parameter plots used in the stochastic model for the post-release mortalilty. Note that capture mortality is included in this term although technically it occurs before release. The dashed line indicates the median values. Although the density plots overlap 0 , no values less than 0 were generated using the runif() function in R.

Percent Fraser 42/52 DNA in Area 19/20 Creel by Month


Figure 4: Percent DNA in samples taken from the area 19/20 creel surveys by month (including 2009, 2010, 2014, 2016 and 2017). The solid line represents the median, the star the mean and the points are outliers. The grey boxes represent the 25 th and 75 th quantiles.


Figure 5: Retained and released chinook from areas 18,19,20,29,121 and 123 by month from years where DNA samples were taken (including 2009, 2010, 2014, 2016 and 2017). The solid line represents the median, the star the mean and the points are outliers. The grey boxes represent the 25th and 75th quantiles.

Retained and Released 42/52 Chinook by Month (for years with DNA data)


Figure 6: Assumed retained and released Fraser River spring/summer 42/52 chinook from areas $18,19,20,29,121$ and 123 by month from years where DNA samples were taken (including 2009, 2010, 2014, 2016 and 2017). The solid line represents the median, the star the mean and the points are outliers. The grey boxes represent the 25th and 75th quantiles.


Figure 7: Probability density plots of stochastic model outputs for FRIM and total mortality estimates using DNA and catch and release data from 2014. Vertical solid lines represent the median (blue), mean (red) and current estimate (see methods - black). Given the size of the sample and the nature of the distributions the mean and median are typically very close. The vertical dashed lines indicate the $25^{\text {th }} / 75^{\text {th }}$ (grey) and the $10^{\text {th }} / 90^{\text {th }}$ (blue) quantiles.


Figure 8: Probability density plots of stochastic model outputs for FRIM and total mortality estimates using DNA and catch and release data from 2017. Vertical solid lines represent the median (blue), mean (red) and current estimate (see methods - black). Given the size of the sample and the nature of the distributions the mean and median are typically very close. The vertical dashed lines indicate the $25^{\text {th }} / 75^{\text {th }}$ (grey) and the $10^{\text {th }} / 90^{\text {th }}$ (blue) quantiles.


Figure 9: Probability density plots of stochastic model outputs for FRIM and total mortality estimates using DNA and catch and release data from 2018. Vertical solid lines represent the median (blue), mean (red) and current estimate (see methods - black). Given the size of the sample and the nature of the distributions the mean and median are typically very close. The vertical dashed lines indicate the $25^{\text {th }} / 75^{\text {th }}$ (grey) and the $10^{\text {th }} / 90^{\text {th }}$ (blue) quantiles.


Figure 10: Probability density plots of stochastic model outputs for FRIM using DNA and catch and release data from 2014, under different hypothetical management regimes (see methods). The vertical solid lines (black) represents the current estimate (see methods). The vertical dashed lines indicate the respective medians.


Figure 11: Probability density plots of stochastic model outputs for TM using DNA and catch and release data from 2014, under different hypothetical management regimes (see methods). The vertical solid lines (black) represents the current estimate (see methods). The vertical dashed lines indicate the respective medians.


Figure 12: Probability density plots of stochastic model outputs for FRIM using DNA and catch and release data from 2017, under different hypothetical management regimes (see methods). The vertical solid lines (black) represents the current estimate (see methods). The vertical dashed lines indicate the respective medians.


Figure 13: Probability density plots of stochastic model outputs for TM using DNA and catch and release data from 2017, under different hypothetical management regimes (see methods). The vertical solid lines (black) represents the current estimate (see methods). The vertical dashed lines indicate the respective medians.


Figure 14: Probability density plots of stochastic model outputs for FRIM using DNA and catch and release data from 2018, under different hypothetical management regimes (see methods). The vertical solid lines (black) represents the current estimate (see methods). The vertical dashed lines indicate the respective medians.


Figure 15: Probability density plots of stochastic model outputs for TM using DNA and catch and release data from 2018, under different hypothetical management regimes (see methods). The vertical solid lines (black) represents the current estimate (see methods). The vertical dashed lines indicate the respective medians.

