Memorandum

To:	Wells, Rocky Reach, and Rock Island HCP Hatchery Committees, and Priest Rapids Coordinating Committee Hatchery Subcommittee	Date: October 8, 2021

From: Tracy Hillman, HCP Hatchery Committees Chairman and PRCC Hatchery Subcommittee Facilitator

cc: Larissa Rohrbach, Anchor QEA, LLC

Re: **Final Minutes of the August 18, 2021, HCP Hatchery Committees and PRCC Hatchery Subcommittee Meetings**

The Wells, Rocky Reach, and Rock Island Hydroelectric Projects Habitat Conservation Plan Hatchery Committees (HCP-HCs) and Priest Rapids Coordinating Committee's Hatchery Subcommittee (PRCC HSC) meetings were held by conference call and web-share on Wednesday, August 18, 2021, from 9:00 a.m. to 4:00p.m. Attendees are listed in Attachment A to these meeting minutes.

Action Item Summary

Joint HCP-HCs and PRCC HSC

Long-Term

- Mike Tonseth will distribute the analysis showing feasibility of the Methow Spring Chinook Salmon Outplanting plan based on historical run size data (Item I-A). (*Note: This item is ongoing; expected completion by September.*)
- Kirk Truscott will work with Colville Confederated Tribe (CCT) staff to develop a model that addresses the probability of encountering natural-origin (NOR) Okanogan River spring Chinook salmon at Wells Dam (Item I-A). (*Note: This item is ongoing; expected completion by September.*)
- Kirk Truscott will determine the number of scales that should be collected from spring Chinook salmon at Wells Dam for elemental signature analysis to discern Okanogan River spring Chinook salmon from Methow River spring Chinook salmon (Item I-A). (*Note: This item is ongoing; completion depends on the outcome of the previous action item.*)
- Keely Murdoch and Mike Tonseth will obtain estimates of pre-spawn mortality from Andrew Murdoch to update the retrospective analysis for Wenatchee spring Chinook salmon (Item I-A). (*Note: This item is ongoing; expected completion by September.*)

Near-Term (to be completed by next meeting)

- Mike Tonseth and Greg Mackey will solicit input from hatchery managers on effective methods to count surplus fish (Item I-A). (*Note: This item is ongoing.*)

- Larissa Rohrbach will file *10-year Comprehensive Review* chapters and reviewer responses on the HCP-HCs Extranet site as they are completed by lead authors and distribute them to Committees for review. (Item II-E). (*Note: This item is ongoing.*)
- The 2024–2033 Recalculation Data Summary will be further discussed with representatives in a conference call on August 31, 2021, and revised by the PUDs for approval in the September 15, 2021, meeting. The following topics will be discussed further (Item II-B):
    - Keely Murdoch will create a flow diagram showing mitigation calculations using smolt-to-adult return (SAR) values calculated at hydroprojects compared to SAR values calculated in tributaries.
    - Catherine Willard and Scott Hopkins will confirm whether Tumwater Dam counts were used as the basis for calculating Rock Island spring Chinook NOR spawning escapement.
- Grant PUD and Chelan PUD will distribute a final version of their responses to Yakama Nation (YN) comments on the draft Statements of Agreement (SOA) on Sockeye Salmon Obligation (Item II-C).
- Todd Pearsons and Catherine Willard will revise Grant and Chelan PUD's draft SOA on Sockeye Salmon Obligation for approval in the September or October meeting (Item II-C). (*Note: This item is ongoing.*)

Rock Island/Rocky Reach HCP-HCs

- None.

Wells HCP-HC

- None.

PRCC HSC

- None.

Decision Summary

- Douglas PUD's broodstock collection and mating recommendations provided in the white paper titled "*The Hankin Mating Strategy and Implementation in the Wells Hatchery Summer Chinook Programs*" were approved by the Wells HCP-HC in today's meeting.

Agreements

- None.

Review Items

- The list of *10-year Comprehensive Review* chapters that are currently available for review was distributed by Larissa Rohrbach with an updated review schedule on August 9, 2021.

Finalized Documents

- None.

I. Welcome

A. Review Agenda, Announcements, Approve Past Meeting Minutes, Review Last Meeting Action Items

Tracy Hillman welcomed the HCP-HCs and PRCC HSC and read the list of attendees (shown in Attachment A). The meeting was held via conference call and web-share because of travel and group meeting restrictions resulting from the coronavirus disease 2019 (COVID-19) pandemic. Hillman reviewed the agenda and asked for any changes to the agenda. The Wenatchee spring Chinook salmon retrospective analysis update including pre-spawn mortality was struck from the agenda. All HCP-HCs and PRCC HSC representatives approved the revised agenda.

Revised minutes from the July 21, 2021, meeting were reviewed and approved by all members of the HCP-HCs and PRCC HSC that were present. Kirk Truscott approved in place of Casey Baldwin for the CCT.

Action items from the HCP-HCs and PRCC HSC meeting on July 21, 2021, were reviewed and discussed *(Note: Italicized text below corresponds to action items from the previous meeting)*.

Joint HCP-HCs and PRCC HSC

Long-Term
- *Greg Mackey will work with Mike Tonseth to test a modeling approach and prepare a white paper on the method for determining a range for the number of females to be collected for a given broodstock in the upcoming year (Item I-A). (Note: This item is ongoing; expected completion by August.)*
  This item will be discussed in today's meeting. This item is complete.
- *Mike Tonseth will distribute the analysis showing feasibility of the Methow Spring Chinook Salmon Outplanting plan based on historical run size data (Item I-A). (Note: This item is ongoing; expected completion by September.)*
- *Kirk Truscott will work with Colville Confederated Tribe (CCT) staff to develop a model that addresses the probability of encountering natural-origin Okanogan River spring Chinook salmon at Wells Dam (Item I-A). (Note: This item is ongoing; expected completion by September.)*

- *Kirk Truscott will determine the number of scales that should be collected from spring Chinook salmon at Wells Dam for elemental signature analysis to discern Okanogan River spring Chinook salmon from Methow River spring Chinook salmon (Item I-A). (Note: This item is ongoing; completion depends on the outcome of the previous action item.)*
- *Keely Murdoch and Mike Tonseth will obtain estimates of pre-spawn mortality from Andrew Murdoch to update the retrospective analysis for Wenatchee spring Chinook salmon (Item I-A). (Note: This item is ongoing; expected completion by September.)*

Near-Term (to be completed by next meeting)

- *Mike Tonseth and Greg Mackey will solicit input from hatchery managers on effective methods to count surplus fish (Item I-A).*
  This item is ongoing.
- *Larissa Rohrbach will file* 10-year Comprehensive Review *chapters as they are completed by lead authors and distribute them to Committees for review in weekly batches (Item II-E).*
  This item is ongoing.
- *Brett Farman will contact Mike Haggerty and Craig Busack (National Marine Fisheries Service [NMFS]) for their responses to a set of prepared questions from the Committees and request their participation in a future meeting on the appropriateness of the existing Proportionate Natural Influence Model for spring Chinook salmon programs in the Wenatchee Basin (Item II-A).*
  This item will be discussed in today's meeting. This item is complete.
- *Todd Pearsons will add to the background information of Grant and Chelan PUD's draft Statements of Agreement (SOA) on Sockeye Salmon Obligation to provide more context on original mitigation credit agreements (Item II-C).*
  This item will be discussed in today's meeting.
- *The 2024–2033 Recalculation Data Summary will be revised by the PUDs, with outreach to other Representatives, to address the following (Item II-B):*
    - *Highlight which methods have been modified compared to the previous recalculation effort.*
    - *Add additional notes on how calculations were performed.*
    - *Share the Entiat Spring Chinook salmon spawning ground report with the PUDs for comparison to other potential adult count data sources proposed for hatchery production recalculation (Matt Cooper).*
    - *Consider whether the ratio of NOR fish at Wells Dam (run composition) should be used to adjust calculations for unclipped hatchery summer Chinook salmon and steelhead in a similar approach for both species.*
    - *Ensure that adjustments for fish that moved into the Wenatchee River are derived from stock assessments done at Dryden Dam for steelhead and Tumwater Dam for spring Chinook salmon.*

- *Verify whether adult count data for Rock Island spring Chinook salmon reflect numbers before or after adult management (fish removal) at Tumwater Dam.*
- *Verify whether the years identified for smolt-to-adult return (SAR) data are continuous and not overlapping with the years used in the previous recalculation effort.*
- *Add SAR data sources to the data summary document.*

These updates will be discussed in today's meeting. Written responses to each comment were prepared by the PUDs and were distributed by Larissa Rohrbach on August 10, 2021.

- *Keely Murdoch will verify whether the sensitivity analysis was done for the PUD's subject fish in addition to federal hatchery subject fish for the previous hatchery production recalculation effort (Item II-B).*

Murdoch said she reviewed meeting minutes from the previous recalculation effort and distributed them to the PUDs' representatives and Tracy Hillman (they were not distributed to the entire Committees). It was agreed that Chelan PUD should not have to mitigate for mortalities caused by their projects to their own (Chelan PUD's) No Net Impact (NNI) programs. However, using Douglas PUD's 48,000 fish from Twisp River hatchery program as an example, the fish go over Wells Dam—and Douglas PUD would not mitigate for that mortality—and then go over Rocky Reach, Rock Island, Wanapum, and Priest Rapids dams. These hydroprojects are killing Douglas PUDs' mitigation production, which should be accounted for. The discussion about how to mitigate for those losses will continue during today's meeting.

- *Relevant representatives will inform the Committees of any evacuation actions or deviations from normal protocols at Methow Basin hatcheries or acclimation sites due to wildfires (Item I-A).*

Fire suppression efforts prevented the fire from spreading to facilities. This item is complete.

Wells HCP-HC

Near-Term (to be completed by next meeting)

- *All Committees members will provide feedback on the alternative mating strategies proposed for Wells Hatchery summer Chinook Salmon to Greg Mackey by August 4, 2021, for approval in next month's meeting (Item III-A).*

Mackey received no feedback; this item will be discussed in today's meeting. This item is complete.

II. Joint HCP-HCs and PRCC HSC

A. Proportionate Natural Influence Modeling for the Wenatchee Basin

Brett Farman introduced Craig Busack and summarized the intent of Busack's presentation would be to narrow the discussion around which populations should be included in the model.

Busack provided background on development of the multi-population proportionate natural influence (PNI) model. Years ago, while working on Snake River fall Chinook salmon, it became desirable to expand upon the typical two-population PNI model. Their intent was to create an area of high PNI, while allowing lower PNI elsewhere within the range for that species. They worked with Mike Ford (National Marine Fisheries Service [NMFS]) to explore the basic PNI equations and determined that the PNI model is infinitely expandable. The next use of the model was for linking the Methow spring Chinook salmon programs to the Winthrop National Fish Hatchery program. They started to call it the multi-population PNI model. This approach turned out to be a substantial advantage and solved a problem the Hatchery Scientific Review Group (HSRG) had years ago (applying the PNI model to the stepping stone model). The multi-population PNI model has become a standard tool used in almost every NMFS consultation. As many as nine different populations have been included in an analysis for the Green River, a tributary to the Puget Sound.

The approach is to start by creating a N x N matrix, where N = the component populations. The cells of the matrix are filled with the proportion of fish spawning in each location that come from the other component populations. All the proportions entered into the cells are in terms of recipients, not in terms of donors. The matrix labels are used in R code that automatically calculates PNI. The model is now automated so that it would not require input from the model developers to create a new matrix.

Busack showed an example matrix for the upper Wenatchee River component stocks, both NOR and hatchery-origin (HOR), including out-of-basin strays (Attachment B). Busack said the example is not a proposal, but it demonstrates what can be done for the Wenatchee Basin. The entries for the component populations were fine-tuned with input from Todd Pearsons.

For each production unit, one needs to know what proportion of spawners come from the other stocks. Arrangement of the columns is arbitrary, but every cell needs a value. For the hatchery programs, the proportions are the proportion of natural-origin broodstock and proportion of hatchery-origin broodstock values. Groups can be left out of the model (zero's entered) but the user needs to ensure they are left out completely as a production unit and as a contributor to spawning. Pearsons noted that out-of-basin strays could be all HOR or NOR. Busack said you could set it up to consider all strays as one segregated group, or as separate groups if proportion of natural-origin broodstock is known for those groups. There is a need to determine a reasonable way to deal with multiple PNI values for each group. Each PNI value can be weighted based on total production, a decision made by the user, and a weighted average PNI can be calculated. This tool would allow for the user to see component PNI and overall PNI.

Todd Pearsons said some discussion was desired on the appropriate PNI value that should be reported for two purposes, monitoring and evaluation (M&E) and permit requirements. Farman said this matrix could be used to parse out where effects on PNI might be greatest or to obtain feedback

on individual programs, but from a reporting standpoint, NMFS is predominantly looking at impacts to the total Wenatchee Basin population. An update could be made to the Biological Opinion, or an amendment to the permit, to include this type of reporting. Busack said he intentionally did not explore the regulatory obligations but noted there has been a PNI for Chiwawa and a PNI for Nason reported in the past. Tracy Hillman said these PNI values are not currently rolled up to a Wenatchee Basin PNI and were calculated using the previous formula provided by Busack. Busack said this approach would allow those to be rolled up into an estimate for average PNI with detail to support it. If a consultation were to be initiated today, given that most of this information is currently available, he would encourage them to develop the PNI calculation with this matrix. Hillman agreed that it could be done but has concerns about how to come up with weights, which could have a large effect on the overall PNI calculation.

Busack said what is known about the production of a given area can have a big impact on the weighting. Special situations can be considered. For instance, proportion of hatchery-origin spawners on one of the Clatskanie populations was very large but turned out to be occurring all in one small creek that swamped the calculation of proportion of hatchery-origin spawners for the entire basin. Oregon Department of Fish and Wildlife argued strongly that this was a production sink with a lot of HOR, but low productivity from those HOR. On the Kalama River, Washington Department of Fish and Wildlife (WDFW) installed a large, expensive weir and many fish spawned below it, so the above weir and below weir spawning was weighted separately. Any place where the relative importance of the spawning component can be considered with flexibility and transparency should be considered.

Pearsons asked how different the internal workings of this model are from the former model. Busack said they are not different at all. Pearsons said the PNI has been calculated for the different component populations and they could be weighted.

Bill Gale said he would like to see a consistent approach being used in both the Wenatchee and Methow basins. Busack said that is feasible with this matrix; there is of course a big difference in management complexity between the Methow and Wenatchee basins with different administrative obligations. In the Wenatchee Basin there is a need to conserve the Chiwawa, Nason, and White River spawning groups.

Gale asked Busack about his scientific perspective on including strays in the model. Gale said the PNI model is typically used to express the relationship between two or more populations that are intentionally allowed to mix, whereas there is nothing intentional about stray hatchery fish and no intent to reach genetic equilibrium for those fish in that population. Busack said, in terms of program design, they probably should not be included, but in terms of understanding impacts, they probably should. For instance, including Leavenworth National Fish Hatchery (LNFH) strays will help us to understand their impacts on Wenatchee Basin conservation programs. This may create problems for operators if it's discovered that a hatchery program is having impacts—that were previously

unknown—on a conservation program. One approach would be to adjust the PNI goals for the conservation programs to limit the effect of the stray populations. Gale said he would think the approach would be to manage for the LNFH's stray target, which is already very low. Busack noted that this falls in the interaction between biology and regulatory decisions. Farman noted that unless there was an extreme situation, those data can be weighted to reduce their effect on the overall PNI calculation, but he would not exclude them just because they are not part of the program structure and some other program's issue. Gale said if all out-of-basin programs are lumped into one column, it is unclear whether LNFH fish have the same effect as Yakima, Snake, or Methow River fish straying into the basin. One catch-all column may not be very meaningful. Busack said this is not a recommendation; this shows, analytically, the maximum extent of what people may be interested in looking at. LNFH could be added as its own population. Decisions on what to do if a problem is identified are a separate issue. For instance, if there are strays from a segregated program that is using a composite or out-of-basin stock, what is the impact compared to an integrated program or strays from an integrated program from far away? In Puget Sound, a lot of strays from all types of programs have been observed, and sorting out how to deal with them differently is a source of discussion. The disadvantages are risk of domestication and outbreeding depression (losing adaptation because the fish came from somewhere else) or both, so it can get complicated.

Farman said the Committees will need to discuss whether this matrix will provide the answers managers are looking for. From a regulatory perspective, the Committees will have to agree that the chosen model represents what is actually happening in the Wenatchee Basin. If there is an agreeable model, it will provide a better snapshot of what's happening in the Wenatchee Basin compared to the simpler 2-population PNI model. Busack said the interest may be to simply focus on how the Wenatchee Basin hatchery programs are interacting with the natural populations. Gale said one decision could be to only include strays in the model if they exceed a target stray rate. Farman agreed and said the rate may be so low or infrequent that it may not inform what's relevant for the Basin. Pearsons said those estimates for recipient populations are available in the chapter on strays in the 10-Year Comprehensive M&E Report. They found that in some cases, the primary hatchery contributing strays is a single hatchery, and in some cases it is from a mix of hatcheries that collectively create a larger stray proportion. Gale asked whether that result was based on expansion of coded wire tags (CWTs) observed in spawner surveys? Pearsons said he believes that is the case for spring Chinook salmon. Gale said that would represent a maximum value, because many of those ad-clipped fish would be removed at Tumwater Dam. Farman said to be clear, when discussing stray rates in this context, the impact is to the recipient population.

Hillman projected the HCP-HCs and PRCC HSC's original list of questions about PNI (first discussed on June 16, 2021; Attachment C) noting that Busack provided answers about the analytical component, but the Committees will have to further discuss the production components and weighting of individual PNI values in the model. A question remained about the scale at which PNI

should be evaluated. Gale said he did not recommend looking below Tumwater Dam; the scale to be discussed is whether all three tributaries should be evaluated separately or in one average. Gale said his recommendation would be to calculate PNI for the major spawning aggregates and perhaps not the minor spawning areas. Hillman said to keep in mind that PNI would be calculated for the other species as well, which would require a different scale. Catherine Willard said the permit states that PNI should be calculated for the Wenatchee River population and suggested that this overall calculation should be included with the Chiwawa and Nason River component population PNI values reported in the annual report.

Mike Tonseth said the question is whether PNI should be calculated per the permit requirements, or for consistency with other programs, and whether the multi-population model could be run for the Wenatchee Basin. Tonseth summarized that Busack has confirmed that it can be done and there seems to be agreement to start calculating PNI using the multi-population method. To be clear, this was not something that NMFS brought to us; we asked for their input. Permits expire in 2026 and Tonseth questioned the value of requesting re-consultation. Busack indicated this analysis would be done anyway during a new consultation. Perhaps the effort is best spent confirming which populations should be included as part of NMFS' expectation for the next consultation phase. Keely Murdoch said she agrees with Tonseth. Murdoch is not interested in amending the Biological Opinion; this is an internal process that the Committees initiated. It is important to report PNI as described in the Permit, but it would be informative to explore the multi-population model to put the programs in a better position with 4 to 5 years of data prior to the next consultation. Farman said he does not have a strong opinion either way but clarified that, from NMFS perspective, amendments to the permit can be as simple as an email exchange as a record of an agreement to start using a new approach.

This item will be included on future meeting agendas to continue this conversation.

B. Hatchery Production Recalculation: Data Source Review (continued)

Tracy Hillman projected the revised draft of the *2024–2033 Recalculation Data Summary* and a comment response distributed by email to address topics raised in the last meeting (distributed by Larissa Rohrbach on August 10, 2021; Attachment D). Data source and calculation diagrams were updated to more clearly show how calculations were done. A few updates were made to the datasets, although the method for calculating mitigation was not changed. Hillman reviewed the schedule for recalculation. In September, the plan is to approve the data sources and review sensitivity analysis results. Hillman asked if there are any other concerns with the data sources so the PUDs can continue to work on resolving the issues before the September meeting.

Smolt-to-adult Return Data

Keely Murdoch said it became clear that for SAR data, there was not a lot of data available for consecutive years used in the last recalculation effort. Before the meeting, Catherine Willard shared

with Murdoch which SAR years were going to be used in this effort and why, and Murdoch agreed with the approach.

Murdoch questioned the appropriateness of using SAR data that are calculated from counts at a given hydroproject versus SAR calculated from counts returning to the basin in which the subject hatchery produced the fish. Murdoch said she could not find documentation from the last effort but noted that most of the data were taken from annual reports, and some data looked like it was from passive integrated transponder (PIT)-tag detections at hydroprojects, and sometimes different types of data were combined together for a given hatchery. The Biological Assessment and Management Plan (BAMP) calculation is about mortality at the projects and the number calculated is adult equivalents that have to be replaced by juvenile production, which makes sense because mortality is coming from the projects not the tributaries. But those adult fish are missing from the spawning grounds, and the intent is that their replacements should make it back to the spawning grounds.

Brett Farman said he needs to review more carefully how the SAR numbers are calculated for this effort but needs to think more about what sources of mortality are included in the SAR calculation and which sources should not be included.

Kirk Truscott asked Murdoch to expound on this issue. Murdoch said the number of fish that need to be replaced using hatchery production is set at a given dam. But there is a need to replace those fish all the way back to the tributary using the tributary SAR to ensure enough fish return to the spawning ground. Farman said it is unclear what needs to happen to the calculation to legally show replacement but agrees that mitigation to the tributaries is what should occur.

Todd Pearsons said his understanding is that the PUDs are trying to achieve numbers of fish to replace the mortality at the dams. The intent of using NOR back to a hydroproject is to match up the SAR to generate the number of fish needed for mitigation back to the hydroproject. In the past, SAR was calculated from CWTs on spawning grounds because those were the best data available. Now there is a lot more data from PIT tags back to hydroprojects, which allows programs to pinpoint SAR calculation back to the area of interest and a reason why there are differences between the last recalculation effort and the current one. Greg Mackey said he recollects that this issue was discussed in the past but concurs with Pearsons that SARs at the dam should be used to replace mortality at the dams.

Murdoch said the BAMP formula was intended to use the hatchery SAR. For example, if replacing 100 adults that would have come back, if not killed as juveniles by a hydroproject, those 100 adults are missing from the tributaries if a SAR to the project is used. Using a tributary or hatchery-based SAR ensures that number of replacement adults makes it back to tributaries. If using the dam-based SAR, the SAR value is going to be slightly higher and, as a result, the mitigation obligation would be reduced because it does not account for mortality from dam to tributary and perhaps only 90 of

those replacement fish are arriving at spawning grounds and terminal fisheries. So that component of the population is not being fully replaced.

Farman asked, who is responsible for mitigating for that mortality that may occur from the project to the tributary? Calculating the SAR back to the hydroproject by default assumes that no mortality occurs from the impoundment itself, and once those fish pass the project, those fish are "returned." Farman added that this assumption may not be totally correct. Calculating mitigation numbers to produce a total value of returning adults to the tributary is more correct.

Pearsons said if the mitigation responsibility is to spawning or harvesting, and if there is 90% pre-spawn mortality due to bad habitat (e.g., high water temperatures), that means programs would continue to add more hatchery fish into the system, but that habitat problem shouldn't be the responsibility of the PUDs Hatchery Programs. It does get at the question of where the PUDs responsibility begins and ends. The conversion between dams is very high for the most part, but pre-spawn mortality in the tributaries can be high, which is not a responsibility of the PUDs Hatchery Programs. The PUDs' responsibility is to ensure fish return back to their hydroprojects.

Farman said there are circumstances of mortality that have nothing to do with the PUDs activities. These comments are for discussion, not official direction from NMFS. An assumption of a conversion rate to the mouth of the tributary or to the hatchery could be used. He understands it's not the responsibility of the PUDs to replace fish because of poor habitat and agrees adding fish to poor habitat may not be advisable. The conversion rate from dams to tributaries may be high enough that nothing is changed. The question is where to delineate the line for where the fish have "returned." From NMFS' legal standpoint, there is an interest in ensuring fish return to areas where they can spawn and increase production.

Willard noted that the Tributary Habitat Programs fund actions that improve tributary habitat conditions. NNI is achieved as a result of both the Hatchery and Habitat Programs. It should not be the responsibility of the Hatchery Programs to produce fish lost because of poor habitat conditions within tributaries upstream from the hydroprojects.

Peter Graf said the BAMP calculation for NOR deals with this. The BAMP calculation uses NOR to a hydroproject. The calculations ask how many adults would have returned to the hydroproject absent project mortality. It is the obligation of the PUD to ensure those additional fish return. The intent is to release a suitable number of fish to erase the hydroproject effects. The hydroproject is both the starting and end point; that's why those two numbers are linked. Murdoch said when the BAMP was written, the hatchery SAR was used; the BAMP does not say anywhere that SAR should be measured at the hydroproject. There was supposed to be an incentive to improve hatchery practices to increase SARs and reduce the amount of mitigation needed.

Because it appears SARs were calculated at both hydroprojects and within tributaries during the last recalculation, Hillman asked whether there is a mandate to calculate SARs at a specific location if the data exist. Murdoch said the HCPs direct programs to recalculate "considering the methods in the BAMP."

Mike Tonseth said the SAR calculated back to the hydroproject area should be used if that's where those fish are being released (e.g., Chelan Falls Dam, Priest Rapids Dam). But many programs are intended to supplement naturally spawning populations and fish are released outside of the hydroproject area. This puts into question the purpose of all the M&E and management done in the tributaries to ensure the performance of those fish. Tonseth said the hatchery production is intended not just to mitigate for mortality at the projects but also for the productivity of those populations.

Pearsons agrees the PUDs should continue with efforts to support species recovery in the tributaries and the PUDs do care greatly about what happens to the adult fish after they pass the projects; but in terms of the recalculation, he agrees with what Graf described. Graf said, for example, using redd counts as a starting point, and using a SAR back to redds (e.g., if 100 redds, there would have been 107 without the project) the project effect would be relatively similar.

Tonseth suggested we look to annual reports to see how that SAR metric was measured. Murdoch said, for example, the reported SAR for the Chiwawa spring Chinook salmon program in the annual report included all estimated recoveries. Those fish are no longer available for harvest in the Icicle River or spawning in the tributaries. There is a need to replace those fish all the way to the end destination. We are not asking for PUDs to replace more fish due to mortality between projects and final destination.

Graf said the hydroproject is the destination. Using the counts at the project, we then ask how many fish are needed for replacement. Mackey said if 107 fish would have come back to a project location absent the project, but because of the project only 100 fish come back, mitigation needs to create 100+7=107 back to the project. The fish that were missing that would have returned absent the project (7 fish), and the fish that replace the missing fish (7 fish), would both experience the same upstream mortality, and so the same number of fish would end up in the tributary whether the project is in place or not. Therefore there are no missing fish in the tributary from the calculation.

Murdoch said there are missing fish. If you use the SAR back to the dam it will be slightly higher than the SAR to the tributary, but those fish will be missing. Tonseth said 107 fish come back to the dam because the SAR is based on the returns to the dam, you are not mitigating for that additional 7 fish that were lost upstream of the dam. Ending the calculation at the dam assumes no mortality can be attributed to the impoundment itself, which may not be correct. It is unclear whether this could be accounted for in another way, but this would be accounted for by calculating SAR back to the tributary. That conversion rate is probably quite high in most cases to the mouth of the tributary. It

makes sense to calculate SAR back to the point they should return rather than truncating it at the projects.

Hillman asked if the calculation should include sources of mortality outside of impacts of the projects, or just mitigating for the impacts of the projects. Murdoch said there is a need to ensure that that number of fish that were killed by the projects are brought all the way back to the tributary. Hillman said there are agents of mortality that occur that are independent of the hydroproject mortality, and there are also fish that do not arrive on the release location but do survive to spawn in the other locations (e.g., Chiwawa River program spawning in the tributaries). Murdoch said those fish would be included in the tributary-based SAR if the CWTs from all fish on the spawning grounds are collected.

Hillman said it would be useful to have a flow diagram showing the agents of mortality associated with calculating SARs at the hydroprojects and within tributaries. Murdoch agreed to create a flow diagram comparing the two approaches with SAR numbers taken from the annual reports.

Pearsons said one reason for the variation in data sources used in the last recalculation may be that a priority was put on using data from PIT tags when they were available.

In the proposal to use SARs to the projects, Truscott asked whether those SARs would be based solely on PIT tags. Mackey said it would be based on PIT tags plus harvest downstream of hydroprojects, which is mainly based on CWTs. Truscott said there is likely many more CWT recoveries compared to PIT detections at dams and the precision may be different between the methods. Pearsons said part of the precision issue is what the detection efficiencies are for CWTs or PIT tags passing the dams. Truscott asked if the overall sample size matters too. Pearsons said yes, but detection efficiency can have a larger effect. Truscott asked if an analysis was done to make a comparison. Pearsons said the PUDs tried to produce the most accurate estimate possible, in this case, that accuracy was related to where the detection occurred.

Tonseth said there was a robust discussion in the past on PIT-tag detection efficiencies, which resulted in the direction for the number of PIT tags to be released to allow for smolt-to-smolt survival estimates, not just SARs. Willard said Skalski Statistical Services was contracted to calculate a samples size analysis that directed the number of fish to be tagged within each program. Truscott said for some species (e.g., summer Chinook salmon) there can be a considerable holding period for adults and mortality would be captured in a hatchery SAR estimate from CWTs. Just because fish pass a project doesn't mean there is no project-associated mortality.

Tom Kahler pointed out that the behavior of returning summer Chinook adults holding at the mouths of warm tributaries while waiting for them to cool, is ubiquitous in both managed and unmanaged river systems, and not associated with the Projects. If those fish are harvested by fisheries authorized by others, are those losses "project effects," and if so, by what mechanism?

Indeed, those mortalities would be captured in a CWT-based hatchery SAR, but as a harvest effect. Furthermore, we currently have no mechanism for attributing non-harvest losses to the projects. Even considering all sources of adult mortality (not just project-related), adult mortality between projects is very low, with survival generally exceeding 99 percent. Thus, any project-related mortality occurring in the reservoir between the concrete and project boundary at the tributary mouths is extremely low. Kahler noted that for brood years 2010 and 2011, the conversion rate from Wells Dam to Winthrop National Fish Hatchery (WNFH) for PIT-tagged WNFH spring Chinook detected at Wells Dam was 98 percent and 93 percent, respectively. The mortality rate in the reservoir must have been extremely low to achieve those conversion rates. Kahler also reported that for brood years 2009-2013, detections of PIT-tagged Methow-origin spring Chinook upstream of Wells Dam averaged 86 percent of the fish detected at Wells Dam, even though the detection probability beyond the hydrosystem is dramatically lower than at the mainstem projects. Kahler reminded the Committees to look beyond the hatchery-centric perspective of these committees to the entirety of the HCP. Hatchery compensation obligations compensate for unavoidable Juvenile Project Mortality. Kahler quoted the Wells HCP as stating that, the establishment of the Plan Species Account to fund tributary habitat actions "will be used to fully compensate for adult mortality…." Kahler emphasized that the calculation of hatchery production obligations must focus only on mitigating for juvenile losses as specified by the HCPs, since adult losses were negligibly low (in the scheme of the subject calculations) and already mitigated fully via the Plan Species Accounts.

Bill Gale observed that 10 years ago nearly all the same members were present, and a lot of old information had to be dredged up to better understand the BAMP. In another 10 years, there is likely to be a lot of turnover on the Committees. It is imperative this time to make a very thorough record for how recalculation was done. Hillman agreed and said he is pushing for making a robust record. The PUDs are creating the final 2021–2033 Recalculation Data Summary document with a lot of narrative that describes the approach.

Rock Island Spring Chinook Salmon NOR Spawning Escapement
Tonseth asked whether Tumwater Dam counts were used for Wenatchee spring Chinook salmon run escapement. Willard said the returns to Rock Island and Rocky Reach are done two ways. The M&E method accounts for escapement. Scott Hopkins said the NOR spawning escapement from carcass surveys was added to the NOR in the broodstock. Tonseth said the data need clarification when referencing to spawning escapement and run escapement. If using the spawning escapement, those numbers should be expanded because this would not account for pre-spawn mortality, which occurs unobserved prior to the spawning period. For the past 10 years, because of the Relative Reproductive Success study, there is a better count of NOR at Tumwater Dam compared to trying to back calculate what the proportion of NOR was from spawning surveys. Hillman said although it is not clear, it appears the NOR proportion is taken from the spawning surveys and

applied to some number that appears to be the Tumwater Dam count. Willard and Hopkins will confirm which data are shown.

Preparing to Approve in September

An extra conference call will be held to further the discussion on SAR calculations. The intent is to approve data sources in the September meeting. Murdoch said she can prioritize this work for further discussion. A meeting will be held on Tuesday, August 31, 2021, from 1pm to 4 pm.

C. Okanogan Sockeye Salmon Mitigation Obligation Statements of Agreement

The discussion was supported by a summary of the administrative history distributed by Larissa Rohrbach on Friday August 13, 2021 (Attachment E), that addresses assumptions about the original intent of the Okanagan sockeye salmon mitigation SOA (2010) related to credit for natural production.

Todd Pearsons talked about a revised version of the current draft SOA in which the background information was more clearly organized as a decision tree, showing the progression from one step to subsequent steps as identified in the 2010 SOA. Briefly, the key components describe the 12-year reintroduction program with an evaluation to occur no later than 2021. If hatchery mitigation is shown to be successful during the first 10 years, the program carries forward with hatchery propagation and associated credit for natural and hatchery production in Skaha and Okanogan lakes. If the hatchery program was not successful then habitat and flow management actions would be used for PUD mitigation. The important thing was that the 2021 evaluation was to determine what type of future mitigation and associated credit would occur. Pearsons said the mitigation agreement in 2010 was a funding agreement.

Keely Murdoch said the steps outlined in 2010 were never interpreted as credit for future mitigation or agreeing in 2010 for credit indefinitely. It was interpreted as the credit for the 10 years of mitigation within the term of the SOA. Murdoch said the Committees are now at the end of the first agreement and the program is deemed to be successful. This was a 10-year agreement that did not necessarily need to be followed by another agreement if it wasn't successful. Murdoch said the SOA limits the agreement to funding for fry produced from 2010 through 2021; there's no agreement to increase fry production.

Pearsons said there is no way the PUDs would have agreed to build a hatchery that it would not own in another country for only a 10- or 12-year period. The idea was that the PUDs would get credit for the work done and all of the NOR and hatchery fish produced. The PUD assumed there would not be many years of natural production during that first 12-year period; the focus for natural production was the out-years. The focus of the first SOA was on Skaha Lake, and it was largely unknown whether reintroduction to Okanagan Lake was even going to be possible.

Murdoch said any time you build a hatchery there would be risk, and the Committees agreed to that risk by agreeing to that natural production component to make mitigation whole. The YN is still having internal discussions about how to deal with credit for natural production. Nothing in this SOA ties the program to any commitment past 2021.

Mike Tonseth said WDFW shares a similar point of view as the YN, and this is not interpreted as fully mitigating for the term of the license with this 12-year agreement. Pearsons said they are not stating that the PUDs have met their mitigation obligation. The experimental process has been carried out through 2021 and it worked. Now we are discussing the term of credit for natural production. The last time this draft SOA was put in front of the Committees, a funding agreement was proposed for a 10-year period to release fish to Okanagan Lake to improve natural production. This is an example of the continual commitment to the program to make this reintroduction successful. The PUDs are not talking about walking away from the commitment to the hatchery and M&E work, until potentially there are very large numbers of naturally produced fish for which the PUDs receive credit.

Kirk Truscott said, in his recollection from discussions around the first SOA and his interpretation of the original SOA, if the evaluation in 2021 deemed the program to be a success, there would be an option to renew the previous SOA or an SOA that is similar to it. That is consistent with the PUDs' interpretation relative to the risk of a capital investment in a hatchery in another country. The potential upside was so large that providing NNI mitigation credit for those activities and reintroduction was worth the risk and worth acknowledging that the PUDs would get credit for naturally produced fish. Truscott sees this extending forward for at least another 10-year period.

Tonseth asked how much of the reintroduction efforts have been funded through the habitat program and how much through the hatchery side. Pearsons said he did not know. Tonseth said he wanted to clarify that his role in today's discussion is as representative on the HCP Hatchery Committee and PRCC Hatchery Subcommittee, and that both habitat and hatchery programs have contributed to the Okanagan sockeye salmon. He is not opposed to credit for naturally produced fish, but it would be a challenge to agree to credit for all-natural production. There is some natural production that was already occurring in Canadian waters, and there is now some natural production that is a result of habitat actions like reopening fish passage between lakes. Receiving credit for natural production associated with hatchery activities is reasonable but getting credit carte blanche for all-natural production may not be truly appropriate. Catherine Willard asked if Tonseth would propose a calculation to parse out the source of that natural production. Tonseth said we may not have that information to be able to attribute the amount of natural production to hatchery program activities—and would be hesitant to try to assign a number to it right now—but could support moving toward obtaining the data to better assign how much benefit is being gained by the hatchery program. The number of fry being produced is known, but it is uncertain what proportion of those fry are returning to spawn and how much of that return is being supported by the restoration projects. Willard said the concept makes sense, but she is trying to understand why it

matters because nothing would change. That is, the PUDs would continue to fund the hatchery program and M&E. If the NORs are attributed to the hatchery programs, what would it mean for this decision? Tonseth said understanding the sources of the natural production would tell you if the hatchery program is mining the natural population; sockeye salmon hatchery programs are inherently difficult (e.g., Baker Lake and Idaho programs). Willard proposed a similar 10-year check-in as the 2010 SOA to evaluate the success of the hatchery program. Tonseth said there is a need for efforts to evaluate whether those fish are returning, spawning, and contributing to natural population.

Murdoch said in both the HCPs and Priest Rapids Salmon and Steelhead Settlement agreement there are two components to meeting NNI: hatchery mitigation and funding habitat actions (7% and 2%, respectively, resulting in compensation for the total 9% unavoidable hydroproject mortality). Credit for naturally produced fish between hatchery or habitat programs gets muddled. Grant and Douglas PUDs have funded a substantial amount of restoration in Canada, and Douglas PUD's water management tool has done a substantial amount to prevent scour of those redds. The issue may be Grant and Chelan asking to get credit for natural production that is a result of Douglas PUD's habitat improvement, for example. There is a need for some sideboards and definition for where credit is due. If Grant PUD is going to continue to do habitat improvements in Canada's Okanagan Lake, but then receive hatchery credit for the naturally produced fish, it should not be funded this way, and the issue gets increasingly muddled if considering Douglas PUD's substantial funding of habitat improvements.

Pearsons said it sounds like there are substantial issues that cannot be resolved about the interpretation of the original SOA. Grant PUD's interpretation is that the PUDs receive credit for production from Skaha and Okanagan lakes. Murdoch said the YN views the last SOA as expiring in 2021 and there is a need to renew the agreement; credit for natural production is not off the table, but it is not going to be carte blanche credit forever.

Truscott said he understands the points discussed and has two observations. The two PUDs funded a large majority, if not all of the M&E activities associated with collecting and analyzing data to provide to the Provincial government to show no impacts to kokanee. Absent that work, there would be no fish passage into Skaha Lake and surely not into Lake Okanagan. While those fish passage elements were funded with habitat funds (efforts at McIntyre and Skaha Lake dams), that would not have happened without the PUD's funding of data collection and analysis within the past 12-year period to get agreement to move fish into these habitats. What is being proposed is essentially another 10-year agreement to continue the program, including M&E in Lake Okanagan, with Grant and Chelan PUDs getting credit for NNI during the next term of the SOA, not necessarily for the life of the program. There is no language to that effect in the HCPs. At the end of the next 10-year program, the agreement would be negotiated again, and all parties would agree or not agree to another agreement, as we must do now. Truscott said there should be additional monitoring to

ensure the success of the program in the face of potential changes to river conditions with climate change.

Pearsons agreed the risk assessments and mid-point studies (to confirm that negative effects on kokanee would not occur) catalyzed these other actions to happen. Grant PUD's perspective is that they would receive credit for hatchery and natural production for the duration of their license, which is through 2052. Grant PUD did not expect there would be large amounts of production for decades. Grant PUD assumed they would not reap the reward of the investment for multiple decades. Another 10-year funding agreement would describe what work would be done for the next 10-year period, at which time the Committees would then again assess whether there is a sufficient amount of natural production to potentially change operations. The initial SOA was for an experimental period primarily for reintroduction into Skaha Lake. The next SOA would be for reintroduction into Lake Okanagan, and to retain those credits through the duration of the license. The duration of the credit was not specified in the original SOA; this was the response from internal discussions within the PUD.

Murdoch said she appreciated the responses provided to her in writing. They were helpful and that they should be distributed to the Committees as final. Murdoch said she does not view anything "agreed to" in these SOAs as an agreement in perpetuity.

Tracy Hillman noted that it is clear the duration of the credit for natural production is not specified in the previous SOA nor in this draft SOA. Hillman encouraged the authors in the next draft of the SOA to include the duration of the credit and other sideboards to the degree that it can be clarified in this SOA. Pearsons and Willard said based on today's conversation, they would not be able to reconcile all issues in an SOA in a manner that could be agreeable by all parties by the September meeting.

Truscott said he views the next 10 years as Phase 2 of the program that would assess reintroduction into Lake Okanagan. Murdoch agreed to that approach to treat these as 10-year experimental blocks. There is a need to identify goals and expectations for the next 10-years. Pearsons said he agrees with the characterization of this as a 10-year experimental block. The issue of credit for natural production is unresolved. Truscott said the PUDs could get credit for natural production during the next 10 years, and natural production beyond that time period would be reserved for the next SOA. This hatchery production program only works if adults return to occupy those habitats. There is a need to understand topics like passage efficiency into Lake Okanagan. Some commitments from the PUDs to evaluate fish passage at Penticton Dam can be added as a provision to this agreement. Another potential provision could be trap-and-haul of a certain number of fish to the lower basin of Osoyoos Lake in certain years to counteract migration mortality. A sliding scale for broodstock collection should be considered if the collection to achieve 5 to 7 million eggs endangers the natural population.

Pearsons said those are all things that can be discussed and potentially agreed to, but what happens between 2031 and 2052 for getting credit for naturally produced fish? Getting an agreement about

credit for naturally produced fish needs to be nailed down before further reintroduction occurs and also before being muddled by another 10 years of interpretation of the 2010 SOA. Truscott said this would depend on the success or lack thereof of Phase 2 of the reintroduction effort. Another 10-year funding agreement would not be novel, but achieving natural production of large numbers of fish needs discussion. There is a need to determine if putting sockeye salmon into Lake Okanagan is productive, or whether all should be placed in Skaha Lake. Truscott said there is precedence for this with the species exchange agreed to in the Rock Island Hatchery Committee for the Lake Wenatchee Sockeye Salmon program that was not working.

Tonseth said there are a number of provisions that other parties would want to include in the SOA that would be different from the original SOA. The next 10-year phase would be part of the reintroduction experiment directed toward Lake Okanagan. A provision could be included requiring assessment of whether reintroduction has been successful. If we find it is not successful in terms of natural population response, the parties will want to renew discussions on whether the natural production credit could continue into the next phase of the program.

Pearsons summarized the key points of the draft SOA:

- Agreement to another 10-year period
- Focus on Lake Okanagan reintroduction
- Inclusion of M&E of Lake Okanagan production
- Evaluation of success at the end of additional 10-year period
- Credit for natural production in Skaha and Okanogan lakes

Truscott said he was not proposing reintroduction into Lake Okanagan in lieu of Skaha Lake, but in addition to Skaha Lake. Willard agreed that fry releases into Skaha are still necessary. Truscott noted that M&E would continue in Skaha Lake; noting changing conditions with climate change make it necessary to maintain that diversity and spatial structure.

Pearsons suggested re-crafting the SOA around the points of agreement above. He is uncertain how to handle the issue of long-term credit for natural production. Tonseth said the duration of the natural production credit does not need to be the stumbling block for signing the next SOA. In a new SOA, language can address receiving credit for natural production, acknowledge differences in interpretation in the draft SOA, but reserve any agreement for later terms of the project. As long as there remains uncertainty about whether these efforts will be successful, the program is still in a feasibility assessment phase. No language would be included in the SOA that would support one or the other positions on duration of natural production credit. Pearsons and Willard agreed that this could be a workable solution.

Willard said, at the 10-year check-in, the alternative could occur that the program is deemed so successful that the hatchery program is no longer needed. This level of success is what all parties

want, and what the PUDs want. If the success is attributable to the hatchery program, the PUDs may want longer-term credit for NOR production.

Tonseth said the M&E program needs to produce data necessary to assess the success and contributions of the hatchery program on supporting natural production. Based on the information provided thus far, with a short duration and limited sample sizes, there is a need for a longer time series to ensure that the hatchery program is doing what is intended.

Murdoch said the YN would like to see the capacity of Penticton Hatchery increased to 8 million fry within the 10-year agreement. At this time, its framed as a decision to be made in the future, but the YN wants to ensure that in this SOA there is a commitment to actually achieve this. Murdoch said in order to actually release 8 million fry, there is a need to obtain approval from the Canadian Okanagan Basin Technical Working Group (COBTWG). The idea is to build out that capacity earlier so that production can be increased once that approval is obtained from COBTWG. A meeting should be had with COBTWG to understand any hesitancy for approving the increase in capacity and understand how to achieve that approval.

Murdoch said at the end of the day, all parties support this program and want to see it move forward, especially in the face of climate change, to expand sockeye salmon distribution above Osoyoos Lake. Pearsons thanked Murdoch for that affirmation.

Pearsons and Willard will revise the draft SOA for distribution along with responses to comments from the YN in preparation for the September or October meeting. This SOA is still being discussed internally at the YN.

D. Modeled Ranges for Broodstock Collection Targets

Greg Mackey shared a white paper that describes a method that could be used broadly by the hatchery programs (distributed by Larissa Rohrbach on Tuesday August 17, 2021; Attachment F *Predicting Broodstock Collection Targets: Managing Risk and Expectations in Broodstock Collection*).

At this time, to estimate the number of broodstock to be collected, several data sources are rolled up into a deterministic calculation (e.g., fecundity, green egg to eyed egg survival, etc.). Mackey briefly described the steps shown in his white paper.

Mackey said a user could choose a range of females to model. The approach works best to model a range of about 30 that includes roughly the number of females thought to be necessary. For each level, the model resamples the population 10,000 times using a Monte Carlo method, then tests at each level of number of females how often certain results occur, like meeting the program target, falling short of the program target, or achieving 110% of the program target. Mackey wrote in R code a scenario to see how often the target is met while not exceeding 110% of the program target. Shown graphically, an optimum number of broodstock to be collected is identified as well as the

probability of achieving that range around the broodstock target (the Chewuch program was shown for illustrative purposes; it is a small enough program to be sensitive to small changes in broodstock collection). Mackey showed quantile projection results that can be used like a confidence interval to show the range of smolts that are likely to be produced (95% of the time). He said this modeling approach is perhaps overkill for routine broodstock collection decisions, but over the years some programs were chronically under targets for juveniles produced and this was initially an effort to explore the factors that went into the calculation. This could be useful for small programs when NOR broodstock are in short supply to help with management expectations. This could also be used in consultation with the Services or when designing a new program. If there is a problem with a program, such as measurements that are wrong, a user could explore the sensitivity of that factor for broodstock collection. The calculation using this model typically comes out within one fish of what is calculated using the deterministic model. The intent would be to use this approach if there is a need for deeper investigation for a given population.

Mike Tonseth said larger programs also tend to be chronically over target, such as with triple digit broodstock numbers for Wells summer Chinook salmon. For programs using less than 50 females, it would serve to validate any estimate of the number of females needed, but the reality is just one female difference can shift the program above or below the target easily. Tonseth said he is curious to know how much variance this approach can eliminate within a larger program. Mackey said his initial focus was on smaller conservation programs. The quantile regression shows the data are heteroscedastic, meaning increasing variance with increasing program size. This is because a small change in early survival can cause a large change in number of juveniles produced in a larger program. Mackey said he is uncertain if this approach would be more helpful for bigger programs than for smaller. Perhaps some modest adjustments to the inputs would help the larger programs adjust for these large swings. Tonseth asked if Mackey had looked at this model for steelhead, noting the difference between 1-salt and 2-salt females can be large. Mackey said a parameter for expected number of 1-salt or 2-salt fish could be added to the model. Tonseth said there are differential fecundities used to adjust broodstock needs for the Wenatchee Steelhead program based on an in-season assessment of the number of 1-salt versus 2-salt females. Mackey said it is similar to a parameter already included for proportion of NOR or HOR broodstock that have differential fecundities; this could be done for the proportion of different ages-at-return.

E. 10-Year Comprehensive Monitoring and Evaluation Report: Review Check-in

Keely Murdoch noted that these 10-year Comprehensive Reports are meant to be an adaptive management tool, and under that pretense, the analytical framework and M&E Plan were joined into one document. The expectation for the Comprehensive Report was an analysis of the data, but the authors go one step further into recommendations for management and changes to M&E in the draft chapters. Murdoch said her understanding was the report would be a review of the data, and then it's the role of the Committees to come with recommendations.

Todd Pearsons said it's a monumental effort that the authors have been working on for a couple of years and, for the most part, all the chapters are focused on the technical aspects of M&E with recommendations toward the end of the discussion sections. One example recommendation was made regarding the use of reference streams. In the evaluation, treatment streams were compared to reference streams outside of the upper Columbia Basin. Authors found it challenging to make a definitive conclusion about the effect of the hatchery that was potentially confounded by upper Columbia Basin effects. The recommendation to use in-basin reference streams was included in the chapter because it was an observation made during the data analysis. Pearsons said he understands there is a need to avoid making value-based statements, but there are places where the data analysis informs future decisions and the ability to address the M&E objectives effectively. The authors could revise language around recommendations, so they are less value based (for example, using "if, then" statements).

Murdoch expressed a desire to be able to see other reviewer's comments to encourage more exchange of ideas. She said she is still sensitive to authors making recommendations in the documents if these are going to be presented as Committees' documents.

Pearsons said he viewed these as reports from the PUDs for approval by the Committees. The M&E Plan and Implementation Plans are the documents that really carry the weight for taking actions. Once the Comprehensive Report is completed and approved, then the process can begin to determine whether changes should be made to the M&E Plan. Changes to program responsibilities like changing the size of a hatchery program, would be codified in an Implementation Plan.

Murdoch asked if this is a PUD report in which recommendations could be made by the PUD that may not be supported or approved by the Committees. Murdoch said the M&E Plan and analytical framework are Committee documents and is not convinced the Comprehensive Report is simply a PUD document. Pearsons said this is the same approach that has been used for the annual M&E reports; there are a different suite of authors for each PUD report and the reports may be WDFW, PUD and WDFW, or a broader list of organizations. All Committees members have an opportunity to review them.

Mike Tonseth said in Section 8.87 of the Rocky Reach HCP, the 10-year Comprehensive Review is mentioned and asked if this requirement is part of the Federal Energy Regulatory Commission license agreement or part of the HCP and Settlement agreements. Greg Mackey said a 10-year Comprehensive Review is directed by the Wells HCP, but the Committees realized the 10- and 5-year reviews were too similar, so those things were rescheduled to be a 5-year statistical review and 10-year Comprehensive Report. Tonseth said the responsibility for the Comprehensive Report was changed by SOA to a 10-year interval and his interpretation is that this is not a PUD report; it should be identified as a HC report and thus any recommendations made should be Committee

recommendations. Pearsons said there may be different language in the different settlement agreements.

Tracy Hillman said the Executive Summaries for each taxon could be the core for a summary report authored by the Committees. The summary could include key findings (results) and proposed recommendations. Pearsons said the heart of the Executive Summaries would be the abstracts of each chapter and could include those recommendations in a separate section. Hillman suggested including a conclusions section that leads directly to recommendations. Tonseth, Catherine Willard, and Mackey agreed with this approach. Mackey said there are some weighty findings that will require some more in-depth thought and discussion for several objectives (particularly objectives 1, 2, and 7). He would be open to including improvements to M&E work or alternatives suggested by others.

Hillman suggested that once the chapters are finalized, authorship of the executive summary should be discussed in a future meeting.

Pearsons noted authors are currently completing draft genetics chapters.

F. Coronavirus Disease 2019 and Monitoring and Evaluation Activities

Tracy Hillman asked Committees' members to provide their monthly updates on impacts of COVID-19 restrictions on M&E activities. Delta variant cases have increased rapidly in the region.

- Mike Tonseth said field activities are unchanged. Office capacity is at 25%. The Governor's mandate requires State employees, including WDFW employees, to be vaccinated to stay employed. Todd Pearsons asked if this will cause problems for staffing M&E projects. Tonseth will follow up with Katy Shelby and others who manage M&E work to understand if there is an expected impact to staffing.
- Brett Farman said the federal government now requires staff to provide proof of vaccination or submit to weekly testing. Presence in the office is based on local area phase requirements. The best-case scenario is NMFS is more than 3 months out for staffing offices.
- Keely Murdoch said there are no changes for the YN at this time.
- Kirk Truscott said there are no changes for the CCT at this time. Cases are increasing in Okanogan County and on the Colville Reservation.
- Todd Pearsons said Grant PUD staff are being encouraged to work from home. People working in the office must wear masks whether or not they are vaccinated, and this is also the case for workers outside if working within 6 feet of each other or in a shared vehicle. Testing is no longer being required but is allowed. These guidelines are being reevaluated every 2 weeks. Mike Tonseth asked if there has been any discussion of impacts on the ABC fishery for fall Chinook salmon. Pearsons said he has not discussed this and expects many of the same requirements in place as last year's fishery, which was a success. Tonseth said for any

WDFW staff, contractors, and volunteers, there will be a vaccination mandate in place, which may limit participation.

- Catherine Willard said there is varied guidance on working in the office from Chelan PUD; vaccinated and unvaccinated people must wear masks in the office.
- Greg Mackey said there are no formal changes at Douglas PUD, but staff are being advised to start restricting themselves to one person per vehicle and masking requirements may be forthcoming.

III. Wells HC

A. Alternative Mating Strategies (continued)

Greg Mackey reminded the Committees of the presentation he gave last month on the mating strategy proposed for use with the Wells Hatchery summer Chinook salmon inundation program to counteract decreasing size at age based on recommendations by Hankin et al. 2009[1]. The recommendation is to pair females with a male that is larger. The program would target larger males during broodstock collection to improve the program's ability to pair females with a larger male.

Kirk Truscott asked for clarification. Mackey said it's based on heritabilities observed more predominantly in the male line. Hankin et al. 2009 modeled matings that should drive the population away from becoming younger-at-age and smaller-at-age, which is often observed in hatchery programs. Mackey noted in the July 21, 2021, meeting he presented the modeled feasibility of implementing a mating strategy where the males were larger than the females, such matings increased considerably if larger males are prioritized during broodstock collection. The method will not require additional handling of live fish prior to spawning.

Bill Gale asked if Douglas PUD is asking for approval for 1 year only, or for a longer term. Mackey said this approach could not be assessed after only 1 year, but the program can report annually on the pairings in comparison to what random pairings could have occurred. Gale said he approved the approach but would also like a report about the logistics. Keely Murdoch asked about the number of years the population would be monitored and the number of years after which monitoring results should be evaluated. Mackey said the effect is not just a family level effect, but it is a population-level effect, so it will take a long time to observe, perhaps taking at least 20 years. Murdoch said whenever a management decision is made, there should be some timeline on monitoring to avoid unanticipated adverse effects on the population. Truscott asked if the orca production program subyearling program returns could be compared to the inundation mitigation program subyearling returns. Mackey said because all summer Chinook salmon are one population, there is some mixing between groups in the broodstocks, which would confound the ability to

---

[1] Methods were first discussed in the February 20, 2020, meeting, based on those described in Hankin, D. G., J. Fitzgibbons, and Y. Chen, 2009. Unnatural random mating policies select for younger age at maturity in hatchery Chinook salmon (*Oncorhynchus tshawytscha*) populations.

compare the two groups. For evaluation purposes, Mackey suggested observing the logistics for 3 years and then revisiting the concept at that point. The adult return data would not yet be available.

All Wells HCP-HCs members approved the recommended approach to spawn males that are larger than their paired females for the Wells Hatchery summer Chinook salmon inundation program. Results from the program will be reported annually.

IV. Administrative Items

A. Next Meetings

An additional HCP-HCs and PRCC HSC meeting will be held on Tuesday, August 31, 2021, to continue discussion of Hatchery Production Recalculation Data Sources.

The next regular HCP-HCs and PRCC HSC meetings will be Wednesday, September 15, 2021; Wednesday, October 20, 2021; and Wednesday November 17, 2021, held by conference call and web-share until further notice.

There will be no U.S. Fish and Wildlife Service representation at the September 15, 2021, meeting.

V. List of Attachments

Attachment A   List of Attendees
Attachment B   Example PNI matrix
Attachment C   Multi-population PNI Modeling Questions
Attachment D   Responses to Hatchery Production Recalculation Data Summary Questions
Attachment E   Okanagan Sockeye Salmon Mitigation Administrative History
Attachment F   Predicting Broodstock Collection Targets: Managing Risk and Expectations in
                Broodstock Collection

Attachment A
List of Attendees

Name	Organization
Larissa Rohrbach	Anchor QEA, LLC
Tracy Hillman	BioAnalysts, Inc.
Scott Hopkins*	Chelan PUD
Catherine Willard*	Chelan PUD
Kirk Truscott*‡	Colville Confederated Tribes
Tom Kahler*	Douglas PUD
Greg Mackey*	Douglas PUD
Peter Graf‡	Grant PUD
Rod O'Connor	Grant PUD
Deanne Pavlik-Kunkel	Grant PUD
Todd Pearsons‡	Grant PUD
Craig Busack	National Marine Fisheries Service
Brett Farman*‡	National Marine Fisheries Service
Bill Gale*‡	U.S. Fish and Wildlife Service
Alf Haukenes	Washington Department of Fish and Wildlife
Katy Shelby	Washington Department of Fish and Wildlife
Mike Tonseth*‡	Washington Department of Fish and Wildlife
Keely Murdoch*‡	Yakama Nation

Notes:
* Denotes HCP-HCs member or alternate
‡ Denotes PRCC HSC member or alternate

Advanced Multipop PNI Matrix for Wenatchee Spring Chinook

Production Units

Spawner Composition	Chiwawa spawning gnds	Chiwawa cons program	Nason spawning gnds	Nason cons program	Nason safety net	White spawning gnds	Little Wenatchee, etc. spawning gnds	Out of basin hatchery programs
Chiwawa spawning gnds								
Chiwawa cons program								
Nason spawning gnds								
Nason cons program								
Nason safety net								
White spawning gnds								
Little Wenatchee, etc. spawning gnds								
Out of basin hatchery programs								
Total	sum(	1	1	1	1	1	1	1
Hatchery	0	1	0	1	1	0	0	1
In Model	1	1	1	1	1	1	1	1
Weights								

From:	Brett Farman - NOAA Federal
To:	Craig Busack; Mike Haggerty - NOAA Affiliate
Cc:	Tracy Hillman; Larissa Rohrbach
Subject:	Questions about Wenatchee PNI and meeting request
Date:	Wednesday, July 21, 2021 1:54:23 PM

HI Craig and Mike. It's been a while, but we'd discussed getting your input on a framework for evaluating PNI in the Wenatchee basin. At our June meeting, the Hatchery Committee narrowed down a list of questions that we were looking for input on from a genetic/modeling perspective. The questions are below:

- With the tributaries and spawning aggregates in the Upper Wenatchee River, what is the most appropriate index of domestication selection that would be appropriate above Tumwater?
- The Wenatchee is currently monitored as a two population PNI calculation (hatchery and natural). Is this an appropriate way to express PNI given the complexity of the programs and management in the basin?
- In light of the above, what "populations" should be considered for inclusion (or exclusion) in the model?
- Are "strays" to be included in a model for the Wenachee basin? Secondarily, what would be considered a "stray" in the model framework? Out of TRT population or out of spawning aggregate?
- Because of the NMFS focus on the Wenatchee as a single population, how would the model be used to show progress toward (or divergence from) recovery? Would the model results be rolled up to the TRT population, or used as is (if aggregates are used in the model) to show spawning aggregate fitness.

Craig is likely familiar (enough) to have some thoughts on this already, but Mike, you may want some more background. We can set up a separate meeting with just the three of us to dissect these in order to come up with a NOAA response.

Secondly, the group would like to have you both attend an upcoming meeting if at all possible. August 18 or September 15 are the next scheduled meetings. If possible, it would be nice to try and make the Aug. 18 meeting if we have time to discuss and provide feedback.

Thanks in advance for your help!

Brett

--

Brett Farman

Acting WCR Training Manager

And Fish Biologist

NOAA Fisheries West Coast Region

503-231-6222

Specific responses to questions about previous recalculation data summary document

1. **Highlight which methods have been modified compared to the previous recalculation effort.**
   The updated data summary includes a table that compares the previous and current methods and describes key differences.
2. **Add additional notes on how calculations were performed.**
   Additional calculation descriptions have been provided in the updated data summary. In addition, the algebra used to perform the calculations has been superimposed on the calculation figures as an appendix to the document.
3. **Matt Cooper will share the Winthrop National Fish Hatchery spring Chinook salmon spawning ground report with the PUDs for comparison to other potential adult count data sources proposed for hatchery production recalculation.**
   Data provided by Matt Cooper were incorporated into the data summary and reflected the same values as previously used
4. **Consider whether the ratio of natural-origin fish at Wells Dam (run composition) should be used to adjust calculations for unclipped hatchery summer Chinook salmon and steelhead in a similar approach for both species.**
   For summer Chinook, there are too many downstream hatchery sources and fishing impacts between Well and Rocky Reach to extrapolate Wells stock assessment data to downstream hatchery and natural origin ratios. For steelhead, it makes sense to use the Wells stock assessment data because there are no additional steelhead hatchery programs between Rocky Reach and Wells.
5. **Ensure that adjustments for fish that moved into the Wenatchee River are derived from stock assessments done at Dryden Dam for steelhead and Tumwater Dam for Spring Chinook salmon.**
   Dryden stock assessment data were obtained from WDFW and replaced the previous values from Tumwater.
6. **Verify whether adult count data for Rock Island spring Chinook salmon reflect numbers before or after adult management (fish removal) at Tumwater Dam.**
   Both methods fully account for adult management at Tumwater:

   The M&E method directly calculates natural origin fish based on escapement and broodstock collection data. The natural origin percentage from carcass data was only applied to the Wenatchee River escapement data to obtain the natural origin escapement estimate. Natural origin broodstock/removal data from Tumwater were directly added to the estimated natural origin escapement.

   The nadir method calculates the natural origin percentage based on the total spring Chinook returns to the Wenatchee river and includes all broodstock and removal activities for both hatchery and natural-origin fish.

7. **Verify whether the years identified for smolt to adult return (SAR) data are continuous and not overlapping with the years used in the previous recalculation effort.**
   The data summary document includes a narrative explanation to address this issue. The SAR data for the current recalculation period does not include any brood years from the previous recalculation effort for which returns were *complete*.   However, some brood years that had *incomplete* returns during the previous recalculation effort will overlap with the current recalculation effort because each brood year contributes to multiple return years. As long as there are multiple age classes returning from a single cohort, it is impossible to create "continuous" years of SAR estimates that will not overlap between recalculation periods (see example figure below where BY 2007 and 2008 SARs are relevant to both recalculation periods but were incomplete during the first recalculation period). It should also be noted that the availability of quality SAR data was patchy and limited in the previous recalculation effort so the number of brood years included in the analysis was also patchy and limited and reflected a negotiated outcome. The current availability of PIT and CWT data for most stocks in the current recalculation effort allows for a more systematic, defensible and repeatable process for estimating SARs that will make sense 10 years from now.

	Adult Returns Recalculation Period 1			Adult Returns Recalculation Period 2		

Adult Return Year

Brood Year	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015
2004	Age 3	Age 4	Age5							
2005		Age 3	Age 4	Age5						
2006			Age 3	Age 4	Age5					
2007				Age 3	Age 4	Age5				
2008					Age 3	Age 4	Age5			
2009						Age 3	Age 4	Age5		
2010							Age 3	Age 4	Age5	
2011								Age 3	Age 4	Age5
2012									Age 3	Age 4

Overlapping Brood Years (rows 2007 and 2008)

8. **SAR data sources will be added to the data summary document.**
   The SARs have been added to the data summary.

Introduction

This document summarizes the administrative history of the Skaha program and specifically discussions confirming that 1) natural production credit was discussed multiple times and agreed to by the HC, 2) the importance of confirming natural production credit as a precursor to funding the Penticton Hatchery, 3) support of HC members for the reintroduction program and natural production credit, 4) Chelan PUDs negotiations with the HC to address contingencies related to the success of the program, and 5) the open-ended nature of the compensation commitment by Chelan PUD—specifically there was no intent by Chelan PUD to 'end' the program or abandon the compensation framework at the end of 2021.

Summary of discussions related to natural production credit

May 19, 2010, Hatchery Committee Meeting Notes (March 17, 2010 HC Meeting Date):
Chelan PUD is proposing to change the current study design to allow for a longer-term perspective, so that the focal point is natural reproduction of smolts rather than just fry survival. Chelan PUD proposes to add 10 additional years to the Hatchery Committees-approved program to fund construction of hatchery facilities and operations through 2027.

Chelan PUD is proposing that mitigation credit would be based on natural-origin smolt production. Tom Scribner asked whether Chelan PUD had contingency plans for mitigation after 2017 if reintroduction does not meet mitigation obligations. Kirk Truscott stated that he likes the innovative approach of achieving reintroduction and natural production rather than relying on hatchery production. Kris Petersen stated she does not want to forego discussion in 2017 regarding contingencies if reintroduction in Skaha Lake does not occur. Tom Scriber stated he wants to see the Hatchery Committees develop contingencies now for what to do in 2017 if reintroduction goals in Skaha Lake aren't met in 2017. The Hatchery Committees requested that Chelan PUD revise the SOA to include contingencies if the Skaha Lake reintroduction goals are not met in 2017.

July 24, 2010, Hatchery Committee Meeting Notes (June 16, 2010, Meeting Date):
Miller explained that this revised SOA provides several clarifications, including specific details of long-term funding. He explained that the SOA states that the mitigation goal is to establish self-sustaining, natural production in Skaha Lake and potentially in Okanogan Lake, with Chelan PUD receiving production credits for naturally-produced fish.

August 10, 2010, Coordinating Committee Meeting Notes (June 22, 2010, Meeting Date):
Chelan PUD has been working on a Hatchery Committees commitment on long-term goals for the Skaha sockeye program. Chelan PUD is requesting credit for natural production resulting from the reintroduction program.

Notes pertaining to discussions and approval of the 2010 Skaha SOA

September 17, 2010, Hatchery Committee Meeting Notes (August 26, 2010, Meeting Date):
Mike Schiewe opened the call by stating that the purpose of the meeting was to discuss and vote on a revised Skaha sockeye salmon program SOA (Skaha SOA). Joe Miller and Josh Murauskas (Chelan PUD) and Keely Murdock (Yakama Nation) summarized their edits to the draft version of the Skaha SOA. Truscott suggested adding language in the SOA giving credit for both fry and natural-origin fish produced in habitat previously blocked to sockeye. All members of the Rock Island and Rocky Reach Hatchery Committees present voted to approve the amended SOA as final.

November 17, 2010, Coordinating Committee Meeting Notes (October 26, 2010 Meeting Date):
Jerry Marco noted that the CCT are part of the Okanogan Nation Alliance (ONA), and support the Skaha Reintroduction Program.

Documentation of Skaha SOA contents

August 26, 2010, Hatchery Committee Statement of Agreement:

Evaluating reintroduction potential requires a larger number of sockeye fry than are currently available, and the District, in collaboration with Grant PUD, is considering funding the construction and operation of a new multimillion dollar Penticton Hatchery to meet production required for reintroduction efforts. In order for the District to proceed with

funding hatchery construction, the District needs assurance that the HC will support the annual fry plant target for the course of the experimental reintroduction program and beyond, if supported by the Canadian Okanagan Basin Technical Working Group [COBTWG; Fisheries and Oceans Canada, Okanagan Nation Alliance Fisheries Program, and the B.C. Ministry of Environment].

The "mitigation goal" of the Skaha Program is establishing natural production and significant new rearing habitats in Skaha Lake and potentially Okanogan Lake.

In the event reintroduction is successful, the District will receive NNI credit for Rocky Reach and Rock Island projects from (1) natural-origin smolts emigrating from Skaha and Okanogan lakes and (2) fry produced by the District-funded hatchery.

As a contingency for additional production at the Penticton hatchery in the future, the District will acquire the space and core infrastructure necessary to construct hatchery capacity for an 8 million egg program (i.e., 3 million more eggs than is currently approved).

If the Skaha Program is determined to be successful prior to 2021, the HC may require the District to expand the Penticton hatchery program to 8 million eggs, and reallocate all or a portion of the resulting fry production for use in Okanogan Lake until 2021, pending COBTWG approval of an Okanogan Lake reintroduction program.

November 17, 2011, Hatchery Committee Meeting Notes (October 19, 2011):
Joe Miller said that, on October 17, 2011, Chelan PUD received final approval from their Commission to move forward with the Skaha sockeye production program. Miller said that Chelan and Grant PUDs and the Okanagan Nation Alliance (ONA) Aquatic Enterprises, a subsidiary of ONA, have agreed on a long-term contract for capital and operation expenses of about $4 million for the Chelan PUD share of the program.

Slides documenting specific content during the November 17th meeting including program goals and credit expectations:

Summary

(8)

- HC has agreed to Skaha reintroduction efforts

- District needs HC support to continue program

- Critical decision point on constructing hatchery

- Questions or Comments?

Documentation of open-ended funding commitment for Skaha program to meet hatchery production requirements

April 2012, ANNUAL REPORT CALENDAR YEAR 2011 OF ACTIVITIES UNDER THE ANADROMOUS FISH AGREEMENT AND HABITAT CONSERVATION PLAN
Combined with the Rock Island HCP, the Okanogan sockeye production requirement totals 591,040 fish (production allocated between the two HCPs). By agreement of the HCP Hatchery Committee, this production requirement is satisfied for Okanogan sockeye by funding of the Okanogan Skaha sockeye reintroduction program until otherwise determined by the HCP Hatchery Committees.

Predicting Broodstock Collection Targets: Managing Risk and Expectations in Broodstock Collection

Gregory Mackey

Douglas PUD

August 17, 2021

Introduction

Broodstock collection entails collecting returning natural or hatchery origin adult salmon or steelhead at trapping facilities, or in some case by capturing fish by angling, seining, or other means. Hatchery operators and field biologists need to have collection targets in order to retain an appropriate number of broodstock to meet the program needs without producing too many or too few fish. In order to predict the number needed, a suite of variables is used to calculate the number of broodstock that are thought to be needed in the upcoming collection season to meet program targets. The suite of variables includes: desired male:female ratio in the broodstock, mean expected survival of broodstock from collection until spawning, mean expected fecundity, mean expected survival from green egg to release, and a specified over-collection target or proportion to be used a buffer against culling in case of disease (i.e., BKD, such buffers are not used for all programs). Deterministic calculation of the number of broodstock required for a program are useful for management purposes. However, program managers may gain more understanding of management decisions and expectations by using the results of a stochastic model to calculate broodstock. Both approaches can provide essentially the same point estimates, but the stochastic model provides a suite of probabilities of achieving or failing to achieve metrics of interest.

Model Description

This model uses input from monitoring and evaluation data and program operational parameters to produce sampling distributions of input variables and performs Monte Carlo simulations on ranges of broodstock numbers to estimate the number of hatchery offspring that would be produced from a given number of female broodstock and the probabilities of those outcomes. Further, the model provides the probabilities that the program will exceed or fail to meet the program production target and limits.

Model input: The hatchery program parameters and supporting biological data are housed in an MS Access database. The model is written in R.

Access Database "BroodstockParameters":
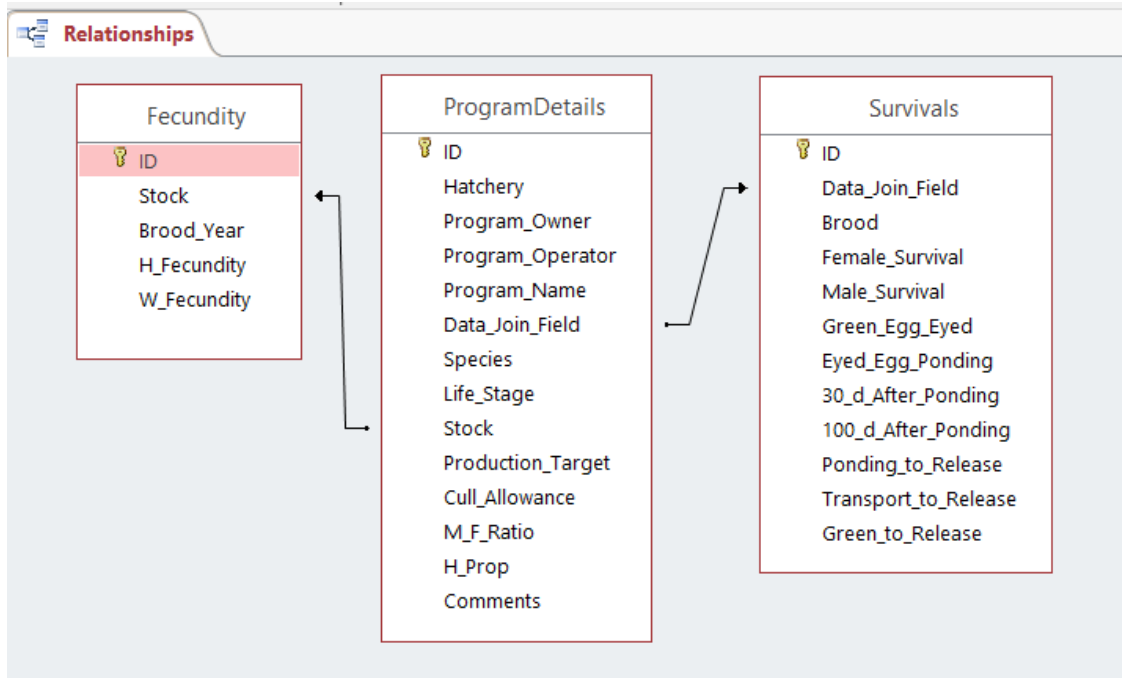
Figure 1. Database schema

Figure 2. "ProgramDetails" table schema

Figure 3. "Fecundity" table schema

Figure 4. "Survivals" table schema
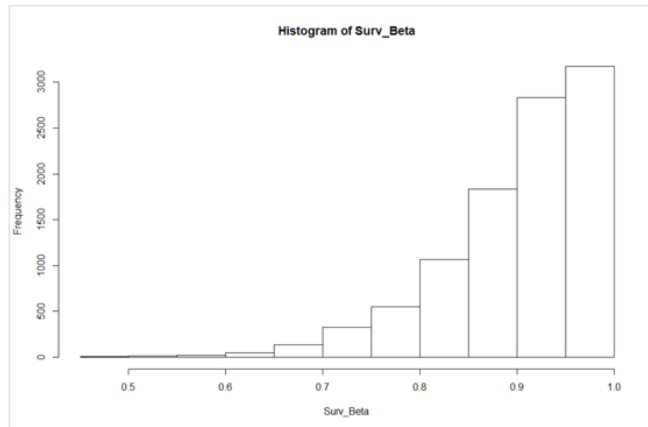
Broodstock Simulation: model in R:

1. The model extracts hatchery program parameters and biological data from the Access database.
2. The data are subsetted based on program name.
3. User specifies the range of the number of females that the model is to use to run simulations. This can be based on past experience or an estimate of the number of females that will likely be required for the hatchery program. The range should include enough females to allow the Loess function to run for graphing purposes (>=30). Modelling too large a range of females will result in long model runs with no benefit since the approximate number of females can be easily determined in advance.
4. The user specifies the increment size for female simulations (e.g., 1. Larger increments can be used if a large number of females is specified to reduce the number of separate model runs required).
5. The model calculates the acceptable range of hatchery production (e.g., +/- 10% of program target).

6. Simulated distributions are created as follows:
   a. Fecundity: a normal distribution is created for fecundity (for natural and hatchery origin females). The most recent 5 years of data are used that include numeric data. If missing values exist additional years are added until 5 years of data are attained. The model runs used geometric mean and the standard deviation to simulate a normal distribution.
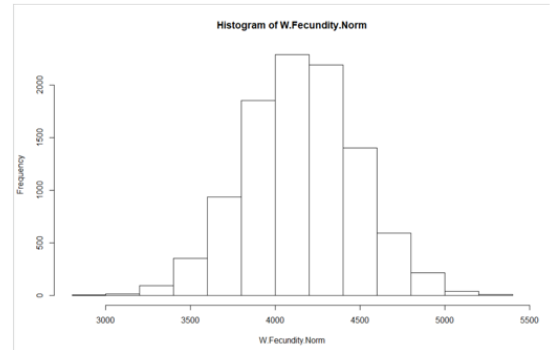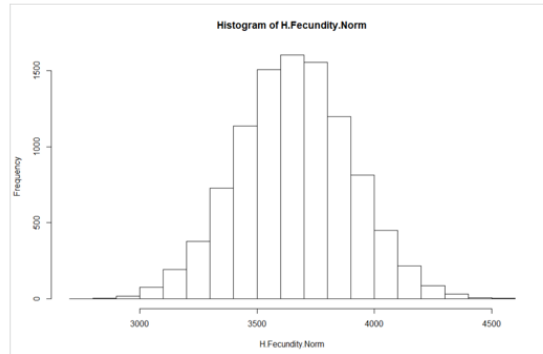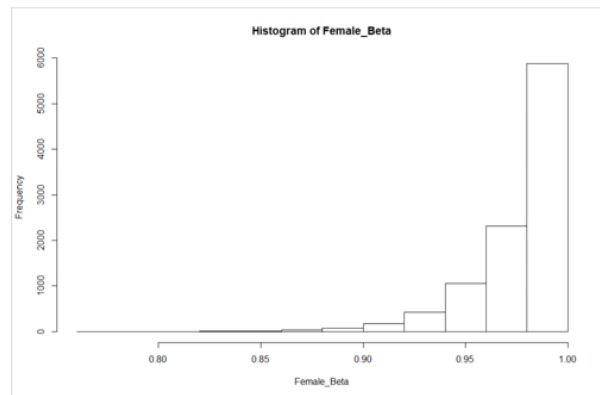

   b. Survival – green egg to release: Simulated using the beta distribution (appropriate for proportion data ranging from 0-1). Beta parameters (alpha and beta) estimated from the most recent 5 years of data that include numeric data. If missing values exist additional years are added until 5 years of data are attained.
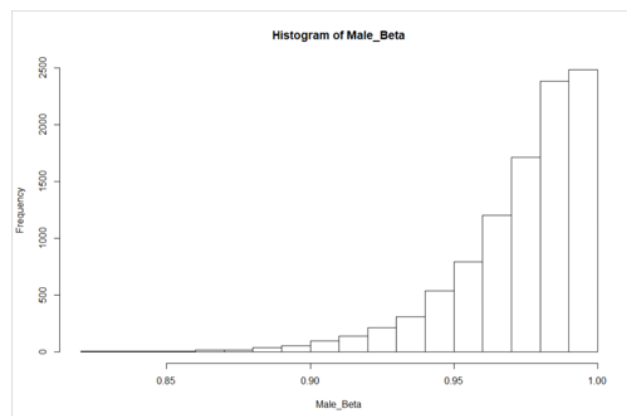

   c. Female Broodstock Survival: Survival from collection to spawning. Simulated using the beta distribution (appropriate for proportion data ranging from 0-1). Beta parameters (alpha and beta) estimated from the most recent 20 years of data are used that include numeric data. If missing values exist additional years are

added until 20 years of data are attained.

Histogram of Female_Beta

d. Male Broodstock Survival: Survival from collection to spawning. Simulated
    using the beta distribution (appropriate for proportion data ranging from 0-1).
    Beta parameters (alpha and beta) estimated from the most recent 20 years of data
    that include numeric data. If missing values exist additional years are added until
    20 years of data are attained.

Histogram of Male_Beta

e. For the standard calculation of broodstock (i.e., deterministic) fecundity uses the
    geometric mean, and all survival use the mean. Survivals are proportion data and
    are not normally distributed; therefore, the mean is not appropriate as a summary
    statistic.

7. Monte Carlo simulations are conducted by randomly drawing terms for the broodstock
    calculation from the fecundity normal distribution, and from the three survival beta
    distributions. A separate set of model iterations (number of iterations specified by user;
    e.g., 10,000) is run for each female increment (that is, for each individual female
    broodstock collection size increment (e.g., 20, 21, 22…50). For 30 increments, this
    would result in 30*10,000 = 300,000 data points.

8. Calculation of the number of broodstock and resulting eggs involves:
    a. Parsing each female increment into the specified number of broodstock by the
        program proportion of hatchery verses wild fish in the broodstock.

b. The number of female spawners is calculated by multiplying the number of female broodstock by female broodstock survival.

c. The number of male spawners is calculated by multiplying the number of female spawners by the male to female ratio for the program.

d. The number of male broodstock is created by dividing the male spawners by the male broodstock survival.

e. The male broodstock is parsed into hatchery and wild origin based on the program parameters (as per females, above).

f. The number of green eggs is calculated by multiplying the number of female broodstock by the fecundity appropriate to their origin. The total number of green eggs is then summed.

g. The hatchery production is calculated by multiplying the total green eggs by the egg to release survival.

9. The model then tests if the number of "smolts" (i.e., fish to be released) meets the following critical values:

a. Test.Target: tests if the modeled production >= program production (release) target

b. Test.Low: tests if the modeled production < program production (release) target

c. Test.VeryLow: tests if the modeled production < 90% of program production (release) target

d. Test.High: tests if the modeled production > 110% of program production (release) target

e. Test.Between: tests if the modeled production >= program production (release) target (>= 100%) and <=110% of program production (release) target

f. Test.Program: tests if the modeled production >= 90% of program production (release) target and <=110% of program production (release) target

10. The model output is collated and summarized. Search algorithms identify female broodstock numbers that meet some of the tests described above. The probabilities for successful model tests are calculated for each female increment.

11. Quantile regression is used to estimate the program production quantiles of interest (0.975, 0.500, 0.025) for the number of females that meet the Test.Target criteria.

12. Graphical analysis is provided to visual the probability response verses the number of female broodstock and the quantile response of production verses the number of female broodstock.
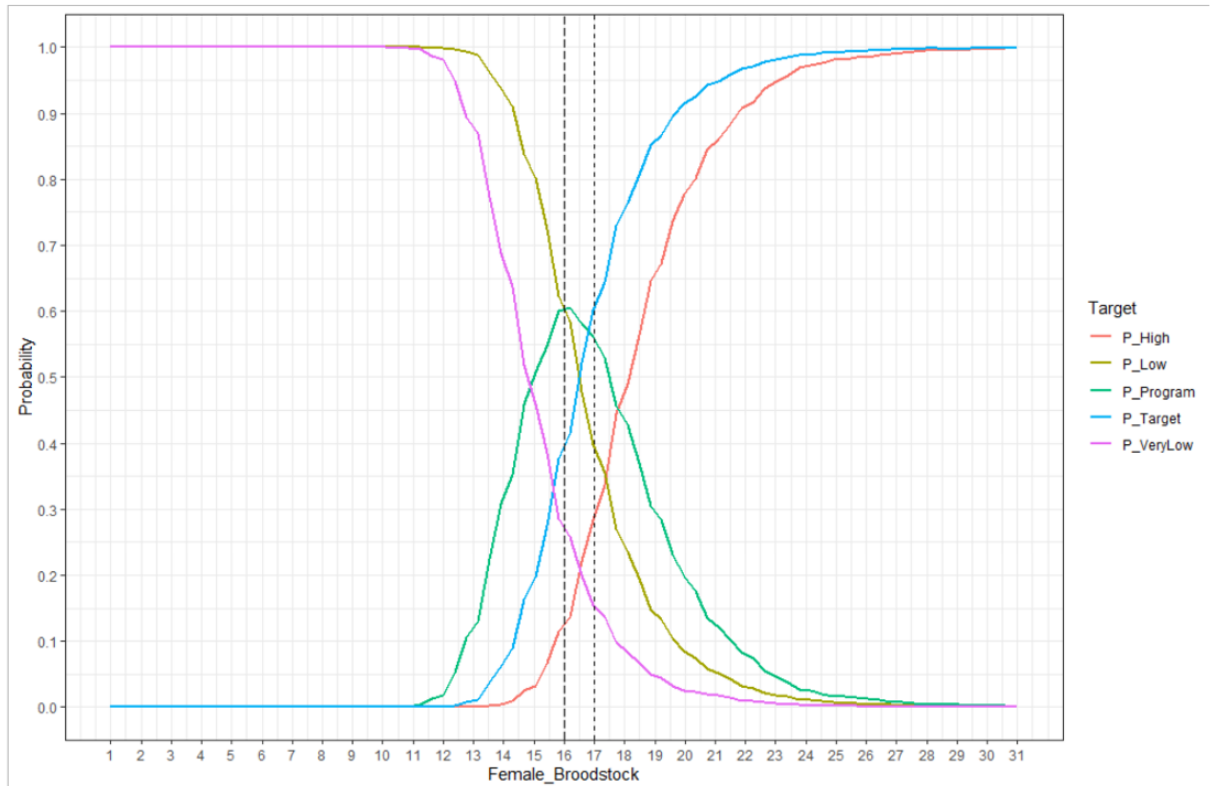
Results: Example – Chewuch Spring Chinook

Figure 5. Model results showing all probability curves output. Long dashed verticle line indicates the number of female broodstock needed to achive production being between 90% and 110% of program target. Short dashed verticle line indictes the number of female broodstock needed to achive maximum probability of production being between 90% and 110% of program target.
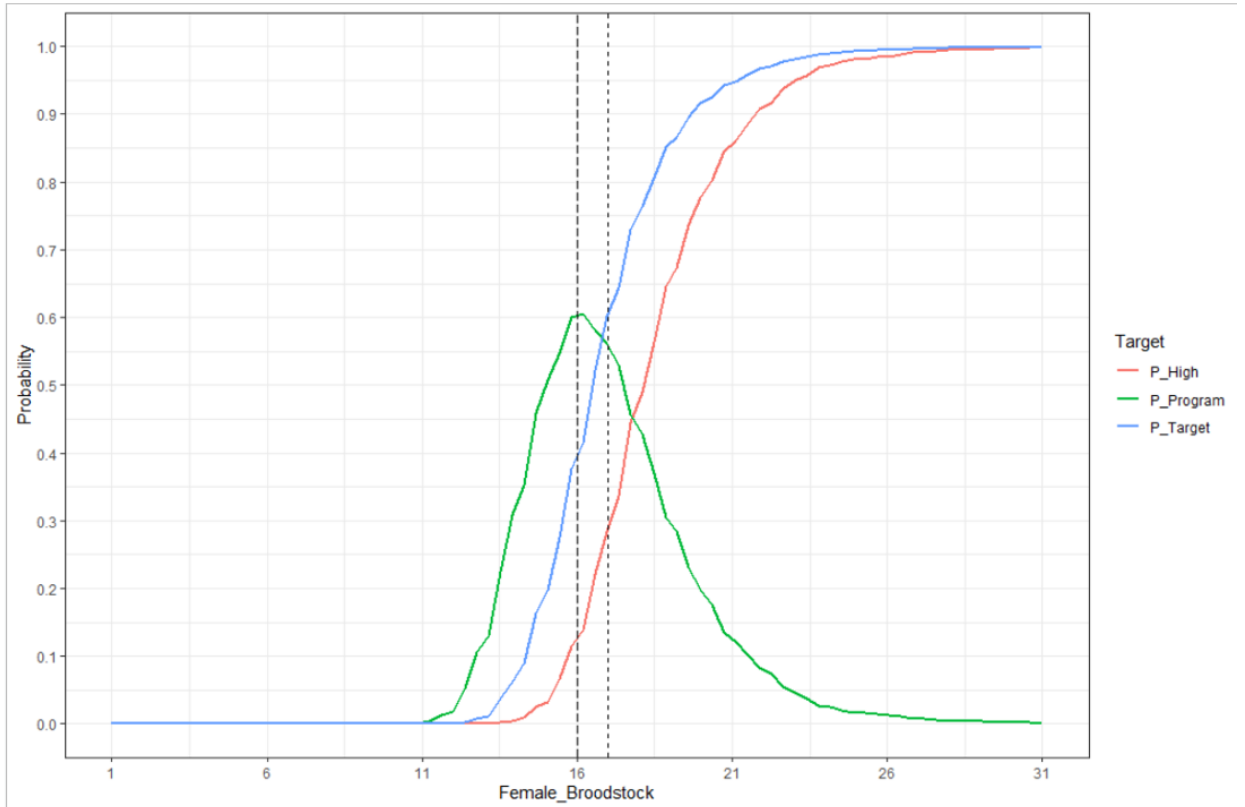
Figure 6. Model results showing probability curves of exceeding 110% of program (P_High), probability of being between 90% and 110% of program (P_Program), and probability of at least meeting 100% of program (P_Target). Long dashed verticle line indicates the number of female broodstock needed to achive production being between 90% and 110% of program target. Short dashed verticle line indictes the number of female broodstock needed to achive maximum probability of production being between 100% and 110% of program target.
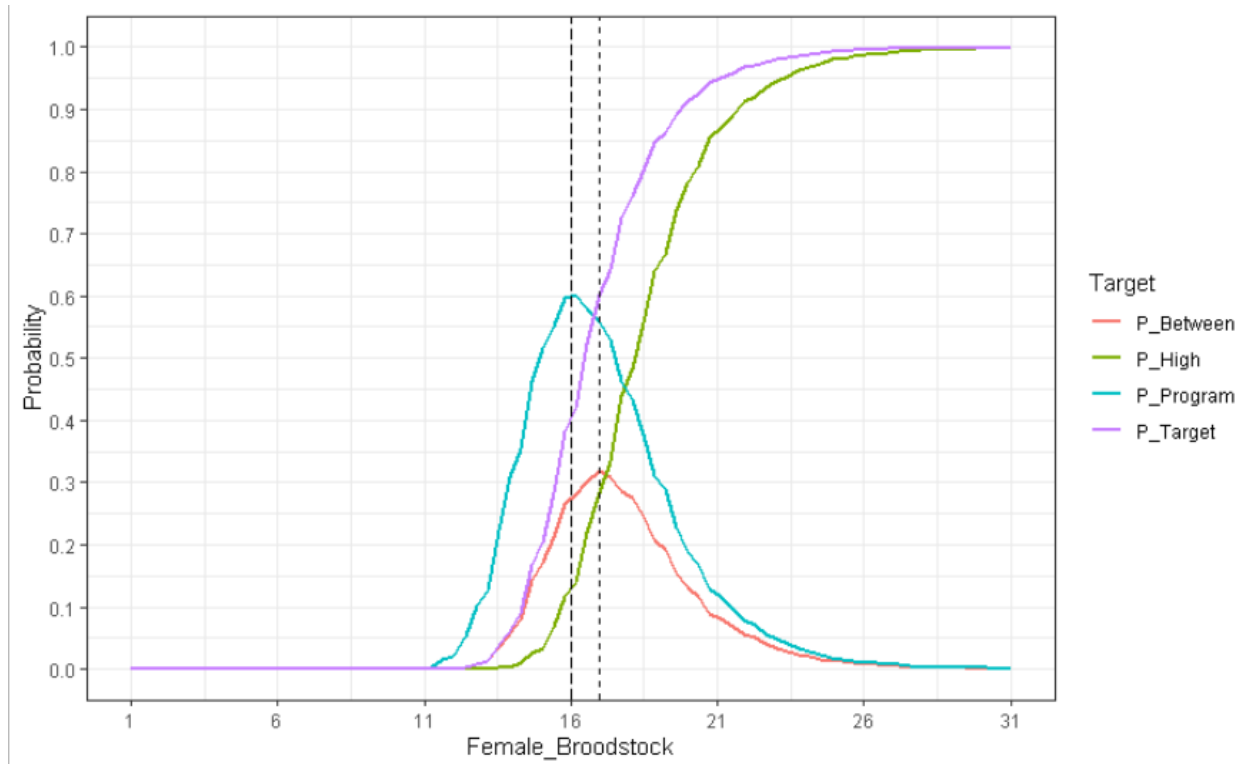
Figure 7. Model results showing probability curves of exceeding 110% of program (P_High), probability of being between 90% and 110% of program (P_Program), probability of at least meeting 100% of program (P_Target), and probability of being between 100% and 110% of program (P_Program). Long dashed verticle line indicates the number of female broodstock needed to achive production being between 90% and 110% of program target.. Short dashed verticle line indictes the number of female broodstock needed to achive maximum probability of production being between 100% and 110% of program target.
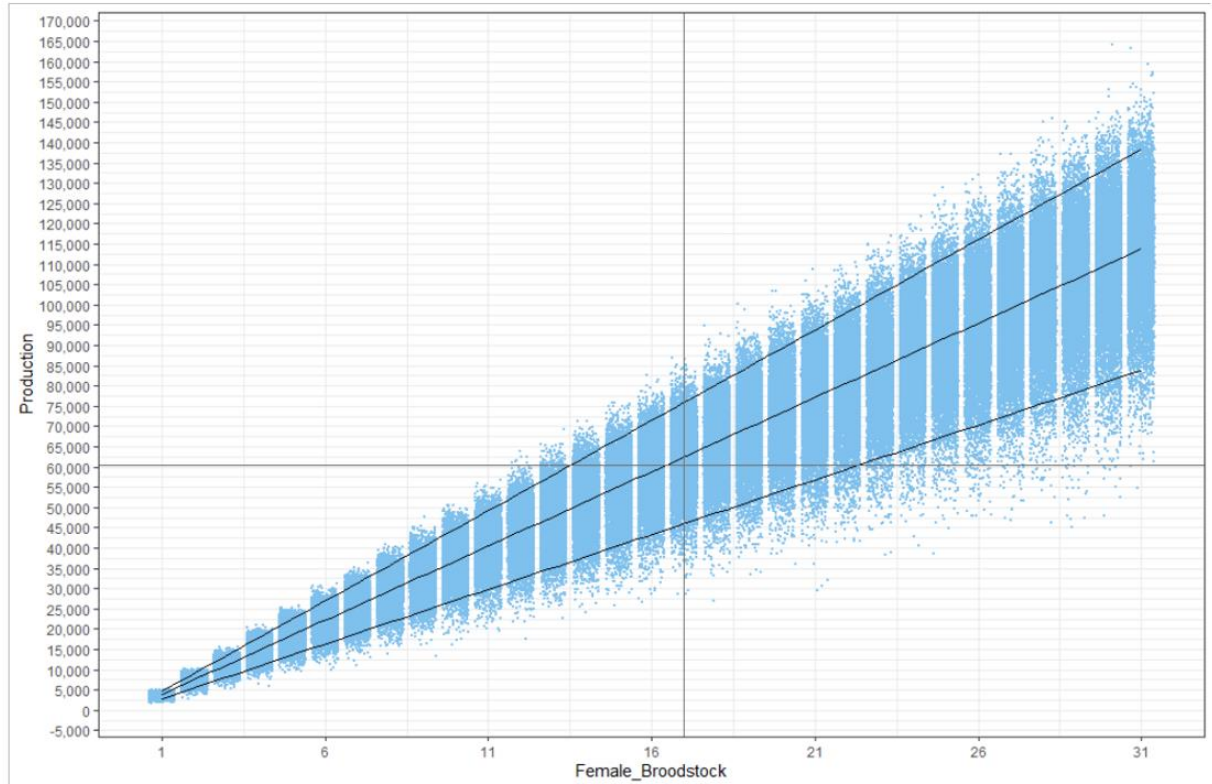
Figure 8. Quantile regression plot of modeled output. Lines represent the 97.5th, 50th, and 2.5th quantiles (i.e. 95% of observations are captured between the 97.5th and 2.5th lines). Horizontal line represent the program production target. Vertical line represents the number of female broodstock needed to achieve the maximum probability of producing between 100% and 110% of program target.

Discussion

This modeling approach provides managers with an estimate of the number of broodstock to collect to meet program objectives. It also provides probabilistic output describing the likelihood of meeting, failing to meet, or exceeding program objectives. For programs that are particularly sensitive to the number of broodstock collected due to limitations of natural origin broodstock availability, small program size, or challenges in fish husbandry, this model may allow managers to make more informed decisions, and will also provide context for expected results.

The R Code:

```
library(MonteCarlo)
library(dplyr)
library(ggplot2)
library(truncnorm)
library(readxl)
library(tidyr)
library(scales)
library(openxlsx)
library(RODBC)
library(EnvStats)
library(WriteXLS)
library(quantreg)


#############################Broodstock Analysis###########################

#Get Survival Data for Analysis of Distribution Types and Parameters

setwd("S:\\GregM\\Broodstock\\Broodstock_R_Code")
list.files()
#Connect via ODBC to the Access database.  Set the Access DB ODBC DNS name using
#C:\Windows\SysWOW64\odbcad32.exe
#Parameters
Parameters<-odbcConnect("BroodstockParameters")
#Extract the table or query of interest
ProgramDetails<-sqlQuery(Parameters,paste("select * from ProgramDetails"))
#Show table
ProgramDetails


Survivals<-sqlQuery(Parameters,paste("select * from qrySurvivals"))
#Show table
Survivals

Fecundity<-sqlQuery(Parameters,paste("select * from qryFecundity"))
#Show table
Fecundity

#List fields and properties
str(ProgramDetails)
str(Survivals)
str(Fecundity)


#Subset Dataframe for the species and program of interest using dplyr

############Enter the program and species name here

ProgramName<-"Methow Steelhead Conservation"  #from the Access database - refer to dataset to get the correct program name

Program<-ProgramDetails %>% filter(Program_Name==ProgramName)  #subsets data by Program
Program  #check to make sure Program is properly defined


#######################Input Data###############################

#Return the Number of smolts in program

Smolt_Target<-Program$Production_Target #The program fish production target
```

```r
Smolt_Target
Smolt_Min<-Smolt_Target*0.90 #Minimum bound for smolt production (e.g., -10%)
Smolt_Min
Smolt_Max<-Smolt_Target*1.10 #Maximum bound for smolt production (e.g., +10%)
Smolt_Max

Cull_Allowance<-Program$Cull_Allowance#The percentage added post hoc to the smolt_target for expected [BKD] culling
Cull_Allowance

#Male:Female Ratio

MF_Ratio<-Program$M_F_Ratio #Desired male to female ratio in the broodstock


H_Prop<-Program$H_Prop #The target proportion of hatchery-origin fish to be used in the broodstock
W_Prop<-1-H_Prop #The target proportion of wild-origin fish to be used in the broodstock
W_Prop

#Enter Number of Female Broodstock (the Range) you Want to Simulate (ex: 100-201), by the step (e.g., 2), so you get seq(100,201,2)

Females_Min = 1
Females_Max = 31

Increment = 1

Females<-seq(Females_Min,Females_Max,Increment) #sets range and number of females and step increment for number of females
Females
CountFemales<-length(Females) #The number of females chose to include in the simulation
CountFemales
H_Females<-floor(Females*H_Prop) #"floor" rounds down - calculates the number of hatchery females
W_Females<-floor(Females*W_Prop) #"floor" rounds down - calculates the number of wild females
H_Females
W_Females

###########################End Input Data###############################

BroodS1<-Survivals %>%  #Groups survival data by program name, removes any NAs, returns the last 5 records (years) of data for each group
  group_by(Program_Name)%>%
  drop_na(Green_to_Release)%>%
  slice(tail(row_number(),5))

BroodSurvivals<-BroodS1 %>% filter(Program_Name==ProgramName) #subsets data by Program and Species
BroodSurvivals


FemaleS1<-Survivals %>%  #Groups Female survival data by program name, removes any NAs, returns the last 5 records (years) of data for each group
  group_by(Program_Name)%>%
  drop_na(Female_Survival)%>%
  slice(tail(row_number(),20))

FemaleSurvivals<-FemaleS1 %>% filter(Program_Name==ProgramName) #subsets Female survival data by Program and Species
FemaleSurvivals

MaleS1<-Survivals %>%  #Groups Male survival data by program name, removes any NAs, returns the last 5 records (years) of data for each group
  group_by(Program_Name)%>%
  drop_na(Male_Survival)%>%
  slice(tail(row_number(),20))

MaleSurvivals<-MaleS1 %>% filter(Program_Name==ProgramName) #subsets Male survival data by Program and Species
```

MaleSurvivals

FecundityH1<-Fecundity %>% #Groups H fecundity data by program name, removes any NAs, returns the last 5 records (years) of data for each group

    group_by(Program_Name)%>%

    drop_na(H_Fecundity)%>%

    slice(tail(row_number(),5))

FecundityH<-FecundityH1 %>% filter(Program_Name==ProgramName) #subsets data by Program and Species

FecundityH

FecundityW1<-Fecundity %>% #Groups W fecundity data by program name, removes any NAs, returns the last 5 records (years) of data for each group
  group_by(Program_Name)%>%
  drop_na(W_Fecundity)%>%
  slice(tail(row_number(),5))

FecundityW<-FecundityW1 %>% filter(Program_Name==ProgramName) #subsets W Fecundity data by Program and Species
FecundityW

#################Create Simulated Distributions###

Female_Param<-ebeta(FemaleSurvivals$Female_Survival)
Fem_Par_1<-Female_Param$parameters[1]
Fem_Par_2<-Female_Param$parameters[2]
Female.mean<-rbeta(1, shape1=Female_Param$parameters[1], shape2=Female_Param$parameters[2])
Female_Beta<-rbeta(10000, shape1=Female_Param$parameters[1], shape2=Female_Param$parameters[2])
hist(Female_Beta)
FemaleBetaMean<-mean(Female_Beta)
FemaleBetaMean
Female.mean
Female_Survival<-mean(FemaleSurvivals$Female_Survival) #for the standard broodstock calculation
Female_Survival   #for the standard broodstock calculation

Male_Param<-ebeta(MaleSurvivals$Male_Survival)
Mal_Par_1<-Male_Param$parameters[1]
Mal_Par_2<-Male_Param$parameters[2]
Male.mean<-rbeta(1, shape1=Male_Param$parameters[1], shape2=Male_Param$parameters[2])
Male_Beta<-rbeta(10000, shape1=Male_Param$parameters[1], shape2=Male_Param$parameters[2])
hist(Male_Beta)
MaleBetaMean<-mean(Male_Beta)
MaleBetaMean
Male.mean
Male_Survival<-mean(MaleSurvivals$Male_Survival) #for the standard broodstock calculation
Male_Survival   #for the standard broodstock calculation

Surv_Param<-ebeta(BroodSurvivals$Green_to_Release)
Sur_Par_1<-Surv_Param$parameters[1]
Sur_Par_2<-Surv_Param$parameters[2]
EggToRelease.mean<-rbeta(1, shape1=Surv_Param$parameters[1], shape2=Surv_Param$parameters[2])
Surv_Beta<-rbeta(10000, shape1=Surv_Param$parameters[1], shape2=Surv_Param$parameters[2])

```
hist(Surv_Beta)
SurvBetaMean<-mean(Surv_Beta)
SurvBetaMean
EggToRelease<-mean(BroodSurvivals$Green_to_Release) #for the standard broodstock calculation
EggToRelease                        #for the standard broodstock calculation

H.Fecundity.sd<-sd(FecundityH$H_Fecundity, na.rm=TRUE) #Hatchery origin fecundity standard deviation
H.Fecundity.mean<-geoMean(FecundityH$H_Fecundity, na.rm=TRUE)#Hatchery origin fecundity mean
H.Fecundity.Norm<-rtruncnorm(10000,a=0,b=Inf, H.Fecundity.mean,H.Fecundity.sd)#create normal distribution of hatchery origin fecundity
plot(H.Fecundity.Norm)
hist(H.Fecundity.Norm)
H.Fecundity.Norm
H.Fecundity.mean
H.Fecundity.sd


W.Fecundity.sd<-sd(FecundityW$W_Fecundity, na.rm=TRUE)#Wild origin fecundity standard deviation
W.Fecundity.mean<-geoMean(FecundityW$W_Fecundity, na.rm=TRUE)#wild origin fecundity mean
W.Fecundity.Norm<-rtruncnorm(10000,a=0,b=Inf, W.Fecundity.mean,W.Fecundity.sd) #create normal distribution of wild origin fecundity
plot(W.Fecundity.Norm)
hist(W.Fecundity.Norm)
W.Fecundity.Norm
W.Fecundity.mean
W.Fecundity.sd




#################Monte Carlo##############################################
# collect parameter grids in list for the Monte Carlo Package (see help for this package):
#param_list=list("Females"=Females, "W.Fecundity.mean"=W.Fecundity.mean, "W.Fecundity.sd"=W.Fecundity.sd,
"EggToRelease.mean"=EggToRelease.mean, "EggToRelease.sd"=EggToRelease.sd,"Smolt_Target"=Smolt_Target )

# collect parameter grids in list (for Monte Carlo Package):

paramlist=list("Females"=Females, "H_Prop"=H_Prop, "W_Prop"=W_Prop, "MF_Ratio"=MF_Ratio,
        "Smolt_Target"=Smolt_Target, "Smolt_Max"=Smolt_Max,"Smolt_Min"=Smolt_Min,
        "W.Fecundity.mean"=W.Fecundity.mean, "H.Fecundity.mean"=H.Fecundity.mean,
        "Female.mean"=Female.mean, "Male.mean"=Male.mean, "EggToRelease.mean"=EggToRelease.mean )


sim=10000 #number of iterations to run in Monte Carlo

##########################################################################

broodtest<-function(Females, MF_Ratio, H_Prop, W_Prop,
            W.Fecundity.mean, H.Fecundity.mean, Smolt_Target, Smolt_Min,
            Smolt_Max, Female.mean, Male.mean, EggToRelease.mean)
{

  Female_mean<-rbeta(1, shape1=Female_Param$parameters[1], shape2=Female_Param$parameters[2])
  Male_mean<-rbeta(1, shape1=Male_Param$parameters[1], shape2=Male_Param$parameters[2])

  H.Fecundity_Norm<-rtruncnorm(1,a=0,b=Inf, W.Fecundity.mean,W.Fecundity.sd)  #Hatchery origin fecundity mean #draw hatchery fecundity
from normal distribution
  W.Fecundity_Norm<-rtruncnorm(1,a=0,b=Inf, W.Fecundity.mean,W.Fecundity.sd) #draw wild fecundity from normal distribution
  EggToRelease_Beta<-rbeta(1, shape1=Surv_Param$parameters[1], shape2=Surv_Param$parameters[2]) #draw egg to release survival from
Beta distribution

  #Calculate number of broodstock collected and number of spawners
  Female_Broodstock=Females
```

```r
  H.Female_Broodstock<-round(Females*H_Prop)   #Parse Females into Hatchery Female broodstock
  W.Female_Broodstock<-round(Females*W_Prop)   #Parse Females into Wild Females broodstock

  H.Female_Spawners<-round(H.Female_Broodstock*Female_mean)   #Parse Females into Hatchery Female spawners
  W.Female_Spawners<-round(W.Female_Broodstock*Male_mean)   #Parse Females into Wild Female spawners
  Female_Spawners = H.Female_Spawners+W.Female_Spawners

  Male_Spawners=round((H.Female_Spawners+W.Female_Spawners)*MF_Ratio)
  H.Male.Spawners=round(Male_Spawners*H_Prop)   #Parse Male_Spawners into Hatchery Male Spawners
  W.Male.Spawners=round(Male_Spawners*W_Prop)   #Parse Male Spawners into Wild Male Spawners

  Male_Broodstock=round(Male_Spawners/Male.mean)   #Create number of males broodstock based on number of females, sex ratio, male
survival
  H.Male_Broodstock<-round(Male_Broodstock*H_Prop)     #Create number of H males based on number of females, sex ratio
  W.Male_Broodstock<-round(Male_Broodstock*W_Prop)     #Create number of W males based on number of females, sex ratio

  # calculate production estimates
  H.Eggs<-H.Female_Spawners*H.Fecundity_Norm #Hatchery eggs
  W.Eggs<-W.Female_Spawners*W.Fecundity_Norm #Wild eggs
  Total.Eggs<-H.Eggs+W.Eggs #Hatchery+Wild eggs = Total Eggs

  # calculate test statistic:
  Production<-Total.Eggs*EggToRelease_Beta #Calculate total program production

  # get test decisions:
  Test.Target<-ifelse (Production>=Smolt_Target,1,0)#test if production >= program target
  Test.Low<-ifelse (Production<Smolt_Target,1,0) #test if production < program target
  Test.VeryLow<-ifelse (Production<Smolt_Min,1,0) #test if production < program minimum
  Test.High<-ifelse (Production>=Smolt_Max,1,0) #test if production >= program maximum
  Test.Between<-ifelse(Production>=Smolt_Target & Production<=Smolt_Max,1,0) #test if production is between program target and maximum
  Test.Program<-ifelse(Production>=Smolt_Min & Production<=Smolt_Max,1,0) #test if production is between program minimum and
maximum

  # return result (for Monte Carlo Package):
  return(list("Female_Broodstock"=Female_Broodstock, "H.Female_Broodstock"=H.Female_Broodstock,
"W.Female_Broodstock"=W.Female_Broodstock,
          "Male_Broodstock"=Male_Broodstock,"H.Male_Broodstock"=H.Male_Broodstock, "W.Male_Broodstock"=W.Male_Broodstock,
          "Female_Spawners"=Female_Spawners, "H.Female_Spawners"=H.Female_Spawners, "W.Female_Spawners"= W.Female_Spawners,
          "Male_Spawners"=Male_Spawners, "H.Male.Spawners"=H.Male.Spawners, "W.Male.Spawners"=W.Male.Spawners,
          "MF_Ratio"=MF_Ratio, "Production"=Production, "Test.Target"=Test.Target,"Test.Low"=Test.Low,"Test.High"=Test.High,
          "Test.VeryLow"=Test.VeryLow,"Test.Between"=Test.Between,"Test.Program"=Test.Program,
          "H.Fecundity.Norm"=H.Fecundity_Norm, "W.Fecundity.Norm"=W.Fecundity_Norm,
          "EggToRelease.Beta"=EggToRelease_Beta, "Female_Survival"=Female_mean, "Male_Survival"=Male_mean,
"Green_Eggs"=Total.Eggs))
}

MonteCarlo_Result<-MonteCarlo(func=broodtest, nrep=sim, param_list=paramlist) #Inputs to run monte carlo simulation from package

summary(MonteCarlo_Result)#Monte Carlo simulation summary output
df<-MakeFrame(MonteCarlo_Result)
head(df)
df

#Summarize the results of the Monte Carlo Simulation by grouping by the number of females
summary_df<-dplyr::group_by(df, Female_Broodstock)%>% summarise(H.Female_Broodstock=mean(H.Female_Broodstock),
          W.Female_Broodstock=mean(W.Female_Broodstock), Male_Broodstock=mean( Male_Broodstock),
H.Male_Broodstock=mean(H.Male_Broodstock),
          W.Male_Broodstock=mean(W.Male_Broodstock), Female_Spawners=mean(Female_Spawners),
H.Female_Spawners=mean(H.Female_Spawners),
          W.Female_Spawners= mean(W.Female_Spawners), Male_Spawners=mean(Male_Spawners),
H.Male.Spawners=mean(H.Male.Spawners),
```

```
        W.Male.Spawners=mean(W.Male.Spawners), P_Target=sum(Test.Target)/sim, P_Low=sum(Test.Low)/sim,
        P_High=sum(Test.High)/sim, P_VeryLow=sum(Test.VeryLow)/sim,
        P_Between=sum(Test.Between)/sim, P_Program=sum(Test.Program)/sim, Smolts=mean(Production),
Female.Survival=mean(Female_Survival),
        Male.Survival=mean(Male_Survival), EggToRelease=mean(EggToRelease.Beta), Total_Eggs=mean(Green_Eggs))


summary_df #short tibble summary
print(summary_df, n=NULL) #full summary table with all females, sized by number of females used in model run
write.csv(summary_df, "C:\\Users\\GregM\\Desktop\\summary_df.csv") #export csv of the summary_df dataframe to the desktop


############Calculate the number of brood needed the "Old Way"
GreenEggsNeeded<-Smolt_Target/EggToRelease
HatcheryFemaleSpawners<-GreenEggsNeeded/H.Fecundity.mean*H_Prop
WildFemaleSpawners<-GreenEggsNeeded/W.Fecundity.mean*W_Prop
HatcheryFemaleBrood<-HatcheryFemaleSpawners/Female_Survival
WildFemaleBrood<-WildFemaleSpawners/Female_Survival
TotalFemaleBrood<-HatcheryFemaleBrood+WildFemaleBrood
HatcheryMaleBrood<-HatcheryFemaleBrood*MF_Ratio
WildMaleBrood<-WildFemaleBrood*MF_Ratio
TotalMaleBrood<-HatcheryMaleBrood+WildMaleBrood


GreenEggsNeeded
HatcheryFemaleSpawners
WildFemaleSpawners
HatcheryFemaleBrood
WildFemaleBrood
TotalFemaleBrood
HatcheryMaleBrood
WildMaleBrood
TotalMaleBrood


#melt dataframe summary_df into long format for ggplot2 using tidyr.

summary_df.melted<-summary_df%>%gather(P_Target,P_Low,P_High, P_VeryLow, P_Program, key="Target",value="Probability")
summary_df.melted

maxF<-summary_df[which.max(summary_df$P_Program),] #find the row withe max "Between" probability
maxF     #Returns the number of females for the max Between probability - for graph reference line

TargetF<-summary_df[min(which(summary_df$Smolts>=Smolt_Target)),] #find number of females that just meet program target
TargetF   #Returns the number of females to meet program target - for graph reference line

########Quantile Regression from df of Female_Broodstock verses Production

qs<-c(0.975, 0.50, 0.025)

quantiles<-rq(Production ~ Female_Broodstock, data = df, tau=qs)
summary(quantiles)
c1<-coef(quantiles)
c1

##Extract coefficients for each tao (quantile)
bUpper<-c1[1,1]
aUpper<-c1[2,1]

bMedian<-c1[1,2]
aMedian<-c1[2,2]

bLower<-c1[1,3]
```

```
aLower<-c1[2,3]

ResponseUpper<-TargetF$Female_Broodstock*aUpper + bUpper
ResponseUpper

ResponseMedian<-TargetF$Female_Broodstock*aMedian + bMedian
ResponseMedian

ResponseLower<-TargetF$Female_Broodstock*aLower + bLower
ResponseLower

###########End Quantile Regression


ggplot(data=summary_df.melted, aes(x=Female_Broodstock,y=Probability, color=Target))+
  geom_smooth(se=FALSE, method= "loess", span=0.1)+scale_y_continuous(breaks = seq(0,1,by=0.1))+
  scale_x_continuous(breaks = seq(Females_Min,Females_Max,by=1)) + geom_vline(xintercept=maxF$Female_Broodstock,
linetype="longdash") +
  geom_vline(xintercept=TargetF$Female_Broodstock, linetype="dashed")+
  theme_bw()

summary_df1.melted<-summary_df%>%gather(P_Target,P_High,P_Program, key="Target",value="Probability")
summary_df1.melted

ggplot(data=summary_df1.melted, aes(x=Female_Broodstock,y=Probability, color=Target))+
  geom_smooth(se=FALSE, method= "loess", span = 0.1)+scale_y_continuous(breaks = seq(0,1,by=0.1))+
  scale_x_continuous(breaks = seq(Females_Min,Females_Max,by=5)) + geom_vline(aes(xintercept=maxF$Female_Broodstock),
linetype="longdash") +
  geom_vline(aes(xintercept=TargetF$Female_Broodstock), linetype="dashed") +
  theme_bw()

p <- ggplot(data=summary_df, aes(x=Female_Broodstock,y=Smolts))+geom_smooth()+ theme_bw() + geom_hline(yintercept=Smolt_Target) +
geom_vline(xintercept=TargetF$Female_Broodstock)+
  scale_x_continuous(breaks = seq(Females_Min,Females_Max,by=5)) + scale_y_continuous(breaks = scales::pretty_breaks(n=30), labels =
scales::comma)#create basic graph
p

ggplot(data=df, aes(x=Female_Broodstock,y=Production))+ geom_jitter(size = 0.25, color="skyblue2")+ geom_quantile(quantiles=c(0.025, 0.5,
0.975), color="black") + theme_bw() +
  geom_hline(color = "grey45", yintercept=Smolt_Target) + geom_vline(color = "grey45", xintercept=TargetF$Female_Broodstock)
+scale_x_continuous(breaks = seq(Females_Min,Females_Max,by=5)) +
  scale_y_continuous(breaks = scales::pretty_breaks(n=30), labels = scales::comma) #create graph of females vs hatchery production
```