All-H Analyzer Tool

Guide and Documentation

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ABBREVIATIONS AND ACRONYMS

CWT	Coded wire tag
EDT	Ecosystem Diagnosis and Treatment
HGMP	Hatchery and Genetic Management Plan
HOB	Hatchery origin broodstock
HOR	Hatchery origin return
HSRG	Hatchery Scientific Review Group
ISIT	In-Season Implementation Tool
NOB	Natural origin broodstock
NOR	Natural origin return
pHOS	Proportion of hatchery fish present on the spawning grounds
PNI	Proportionate Natural Influence
pNOB	Proportion of Natural Origin Broodstock
SAR	Smolt-to-adult survival rate

1.0   INTRODUCTION

1.1   DEVELOPMENT OF AHA

The All-H Analyzer (AHA) tool is a Microsoft Excel-based application that may be used to evaluate management options in the context of the four "Hs"—Habitat, Hydrosystem, Harvest, and Hatcheries. AHA was developed by the Hatchery Scientific Review Group (HSRG) to support its comprehensive review of more than 300 salmon and steelhead populations in the Columbia Basin (HSRG 2009). The tool integrates assumptions about the four "Hs" to estimate natural escapement and harvest of natural and hatchery origin fish. This user guide is an update and expansion of the original user guide developed by the HSRG as part of the Columbia Basin review (HSRG 2009, Appendix D).

The HSRG was established by Congress to develop recommendations for managers to help ensure hatcheries are operated consistently with goals for conservation and harvest of natural origin salmonids. It was clear from the outset that these had to be developed in close collaboration with resource co-managers. To guide this process, the HSRG arrived at a set of guiding principles (HSRG 2004). The scientific basis of the HSRG's principles and recommendations was reviewed and updated in the HSRG's *On the Science of Hatcheries* (2014) and Report to Congress (2015).

Principle 1: Develop clear, specific, quantifiable harvest and conservation goals for natural and hatchery populations within an "All H" context. (See "Program Goals" section of AHA tool). Hatcheries should be used as part of a comprehensive strategy where habitat, hatchery management, hydropower operations, and harvest are coordinated to best meet resource management goals defined for each fish population in the watershed.

Principle 2: Design and operate hatchery programs in a scientifically defensible manner. (See "Key Assumptions" sections of AHA tool). The scientific rationale for a hatchery program in terms of its benefits and risks must be formulated to explain how the program expects to achieve its goals. The strategy chosen must be consistent with current scientific knowledge.

Principle 3: Monitor, evaluate and adaptively manage hatchery programs. (See "AHA Results" and "Status and Trends" sections of AHA tool). Ecosystems affected by hatchery programs are dynamic and complex; therefore, uncertainty is unavoidable. New data and studies will change our understanding of the ecological and genetic impacts of hatchery programs, and this will likely lead to changes in hatchery operations.

The AHA tool was developed to support the interactive process with co-managers to develop programs consistent with these principles. AHA proved useful as a tool for discussing and documenting biological assumptions and evaluating the likely long-term consequences of management alternatives on conservation and harvest. Following the Columbia Basin review, the AHA tool continued to be used and refined by some funders, regulators and managers to evaluate or justify existing or proposed hatchery programs, thus becoming a management tool.

AHA is a generational model intended to simulate <u>long-term</u> effects of different management policies. It is a steady state model in the sense that management strategies are constant from year to year—e.g., harvest rates are not affected by annual variations in abundance. The HSRG has developed a life cycle model that incorporates dynamic management strategies and population age structure, the In-Season

Implementation Tool (ISIT; HSRG 2017). The ISIT model simulates year to year outcome trajectories. AHA, on the other hand, projects the average outcome after 100 generations (averaging the results from the last 80 generations), assuming the same management strategy is applied each year.

While AHA is a steady state model in terms of management of the "Hs", smolt to adult survival is applied not as a fixed rate, but is associated with user-specified variability. The user controls random variability in the smolt-to-adult survival rate (SAR) by entering a coefficient of variation, which is used to apply lognormal variation to the SAR[1]. The systematic effects of the Pacific Decadal Oscillation (PDO) are also incorporated into the SAR for natural and hatchery origin fish. Thus, each time the model is run with the same input parameters, it produces a different outcome. Running the model multiple times therefore yields a range of outcomes.

AHA calculates the long-term effects of different hatchery and harvest management strategies on natural and hatchery populations based on user-defined assumptions and hypotheses about the biology and habitat of the populations. Natural population status is expressed in terms of average spawner abundance and harvest. Natural production potential is calculated as a function of habitat quality (productivity) and quantity as well as genetic fitness of the population. Fitness is assumed to be the result of the relative magnitude of natural versus artificial selection pressures. Hatchery populations are typically assessed in terms of the average number of hatchery origin fish taken in marine and freshwater fisheries and hatchery returns. Inputs to the tool include population-specific productivity and capacity parameters, harvest rates for hatchery and natural origin fish, hydrosystem survival for adults and juveniles, and information on hatchery operations, with special emphasis on broodstock management and stray rates.

AHA estimates reflect the influence of hatchery origin fish on natural populations, measured as the percent of hatchery origin spawners (pHOS) in the natural escapement and the percent of natural origin broodstock (pNOB) incorporated into the hatchery program. The AHA tool also accounts for hatchery origin fish that stray (i.e., do not return to their hatchery of origin) and spawn with natural populations. The number of strays affects the degree of hatchery influence on natural populations receiving strays and the relative fitness of those populations. The assumptions underlying these fitness impacts are based on models developed by Ford (2002) and refined by Busack (2015).

Inputs to AHA can be derived from the results of other models, such as Ecosystem Diagnosis and Treatment (EDT) for habitat, SIMPASS or CriSP for Columbia River hydroelectric passage, and others. AHA is a relatively simple tool to help regional decision makers achieve transparency in terms of their expectations and rationale for their management choices. It can be used as an aid in discussions among co-managers to explore the impacts of different management strategies ("Hs") as well as the effects of uncertainty about biological assumptions.

Suggested Approach to Using AHA

We suggest the user start by reviewing this User Guide for an overview of the AHA tool. Following this User Guide, Appendix A provides practical guidance on how to use each of the worksheets in the AHA tool. Appendix B provides details on the inputs used in the AHA Scenario calculations, and Appendix C documents the formulas used in the AHA Scenario calculations.

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[1] See Appendix C, formula 55 for an explanation of how random variation is applied to the SAR. The degree of random variation applied to the SAR increases with the magnitude of the CV (range: 0 to 100 percent).

After reviewing the User Guide and Appendices, we suggest the user set up Scenario 1 as the 'Current Scenario' to reflect how the population is currently being managed. This is referred to as the "validation step". Once the key assumptions are entered, the AHA results should line up with current escapement, harvest and hatchery returns (on average). It is important for the user to understand that the AHA results are not expected to match actual data "to the fish," but rather fall well inside the "max-min" estimates provided by AHA.

When entering assumptions about hatchery data, we encourage the user to take advantage of the longest data sets available. Using 10-15 year averages for hatchery escapement and coded-wire tag (CWT) survival estimates is important to capture the highs and lows of survival and returns. However, this must be done with an understanding of how the individual hatchery program may have changed over those years. Large changes in the number of juveniles released, size or time of release can result in large changes to returns. This should be taken into account when selecting the range of years included in the average.

On the other hand, selecting harvest rate data (usually from CWT recoveries) should be done on a more recent time frame. As harvest rates can change dramatically from year to year (as well as change toward mark-selective-fisheries), the most recent 3-5 years of data will often provide a more realistic picture of catch.

Gathering data to populate the key assumptions and checking to make sure results line up with recent data is generally the most time consuming step in using AHA. Once the Current Scenario is set up, the user can be more confident that 'alternative' management scenarios (different numbers of hatchery releases, different harvest rates, etc.) are likely to produce realistic results.

1.2   PURPOSE OF THIS DOCUMENT

If AHA is to be used in a management decision making context, its assumptions and limitations must be clearly understood. This paper describes the analytical methods used in the AHA tool, including:

- The Beverton-Holt survival function, which is used to estimate recruitment of naturally-spawning fish.
- Calculations of broodstock composition in terms of hatchery and natural origin adults, survival of hatchery fish by life stage in nature and in the hatchery, and the fate of returning hatchery adults.
- Calculations of the mean number of fish (natural and hatchery origin) taken in the fisheries.
- Computations of ecological (density dependent) and genetic (fitness loss) interactions between natural and hatchery origin fish reproducing in the natural environment.

The AHA tool does not attempt to estimate what might happen in any particular year; rather, it projects the average outcome for the hatchery and natural population components after 100 generations.

AHA estimates juvenile and adult production and survival in nature based on the following user inputs:

- Freshwater productivity and capacity of the naturally spawning population.
- Fish passage survival (juvenile and adult).
- Harvest rates (ocean and freshwater).
- Estuarine and ocean survival conditions.

- Fitness of the natural population.
- Relative ability of hatchery fish to spawn naturally and produce adult recruits.

In addition, AHA estimates juvenile production and survival in the hatchery based on these user inputs:

- Hatchery production goals.
- Pre-spawn survival, fecundity, and sex ratio of the broodstock.
- Survival in the hatchery until release.
- Post-release survival of hatchery fish (i.e., due to fish passage survival, harvest rates, and ocean and estuarine conditions).

The AHA tool accounts for genetic interactions between natural and hatchery origin fish. Ecological interactions are not accounted for in AHA except those inherent in density-dependent interactions as expressed in the Beverton-Holt function. Ecological interactions such as predation, interspecific competition and disease are not explicitly accounted for in AHA.

Genetic interactions are expressed in terms of gene flow between natural and hatchery origin fish and depend on:

- Composition of the hatchery broodstock (percent natural origin return (NOR) and percent hatchery origin return (HOR)).
- Percentage of hatchery returns recovered at the point of release and percentage of hatchery returns that spawn in nature.
- Composition of the naturally spawning population (percent NOR and percent HOR).
- Ability of hatchery fish to spawn successfully and survival of their progeny in nature.
- Differences in selection pressure between the natural and hatchery environments.

2.0 MODELING NATURAL PRODUCTION

2.1 BEVERTON-HOLT PRODUCTION FUNCTION

The abundance of natural progeny from adults spawning in nature is computed using the multi-stage, Beverton-Holt[2] (B-H) survival function (Beverton and Holt 1957; Moussalli and Hilborn 1986). The survival function is based on life stage-specific parameters for productivity (density-independent survival) and capacity (maximum number of fish that can survive). The two-parameter B-H survival function was assumed for each of the following life stages:

1. Spawning to emergent fry
2. Emergent fry to juveniles (smolts) leaving the subbasin
3. Smolt to adult returns to the subbasin

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[2] AHA currently only supports the Beverton-Holt survival function. If evidence suggest that, e.g., a Ricker type function is more appropriate, AHA may not provide useful results. See Ricker (1975; Section 11.5) for a discussion contrasting applications of the two functions: http://www.dfo-mpo.gc.ca/Library/1485.pdf.

The B-H survival function assumed for each life stage is as follows:

$$N_{i+1} = \frac{N_i * p_i}{1 + \dfrac{N_i * p_i}{c_i}}$$

where:

N_i =	Number of fish alive at the beginning of life stage i
N_{i+1} =	Number of fish alive at end of life stage i + 1
p_i =	Density-independent survival of life stage i
c_i =	Capacity of life stage i (maximum number of fish surviving in life stage)

The abundance of hatchery origin fish spawning in nature is adjusted to account for the (hypothesized) reduced relative reproductive success of hatchery fish in nature, such that the total number of spawners, $N_{i,Total}$ is estimated as:

$$N_{i,Total} = N_{i,Nat} + N_{i,Hatch} * RRS_{i,Hatch}$$

where:

$N_{i,Nat}$ =	Number of progeny from natural origin spawners in life stage i
$N_{i,Hatch}$ =	Number of progeny from hatchery origin spawners in life stage i
$RRS_{i,Hatch}$ =	An estimate of the phenotypic impact of hatchery rearing on life stage productivity in nature for life stage i

More specifically, $RRS_{i,Hatch}$ is a user-provided estimate of the reduced reproductive success of hatchery spawners in nature. Note that in AHA, RRS is only applied to a single life stage (spawners).

The B-H productivity and capacity parameters are adjusted to account for the relative fitness of the natural population over the complete (adult-to-adult) life cycle. The formulas used to estimate fitness of the natural population are described in Section 5.3. The fitness multiplier is apportioned over each life stage *i* as follows:

$$f_i = Fitness^{Rel\_Loss_i}$$

where:

Fitness =	Population fitness (either Ford or Busack, selected by the user; see Section 5.3 for details)
Rel_Loss_i =	Assumed proportion of the total fitness effect occurring in life stage i

With the fitness adjustment, the Beverton-Holt survival function for life stage *i* is as follows:

$$N_{i+1,Total} = \frac{p_i * f_i * N_{i,Total}}{1 + \dfrac{p_i * f_i * N_{i,Total}}{c_i * f_i}}$$

The user supplies values for the B-H adult productivity (Prod$_{Adult}$) and capacity (Cap$_{Adult}$) assumptions. The adult productivity parameter defines the maximum adult recruitment rate (density-independent recruitment) for a population over the complete life cycle (spawner to spawner). Productivity is affected by habitat quality and population fitness. The B-H adult capacity parameter defines the maximum number of spawners (adult "carrying capacity") for a population over the complete life cycle (spawner to spawner). Adult capacity is a measure of the quantity and quality of habitat available for the adult life stage. Capacity determines the effects of density dependence on population survival.

Productivity for the spawner-to-emergence life stage is calculated as the number of eggs per spawner based on user-supplied inputs. Capacity for the spawner-to-emergence life stage is assumed to be unlimited[3] (in AHA, by default it is set to 10^{12}). Productivity for the smolt-to-adult life stage is set as the user-supplied smolt-to-adult survival rate and capacity is assumed to be unlimited (in AHA, by default it is set to 10^{12}). Given these values, productivity (*Prod$_{Em-Smolt}$*) and capacity (*Cap$_{Em-Smolt}$*) for the emergence-to-smolt life stage are calculated as follows[4]:

$$Prod_{Em-Smolt} = \frac{Prod_{Adult}}{Prod_{Spawn-Em} * Prod_{smolt-ad}}$$

and

$$Cap_{Em-Smolt} = \frac{1}{(Prod_{smolt-ad}) * \left(\dfrac{1}{Cap_{Adult}} - \dfrac{1}{Cap_{Smolt-Ad}}\right)}$$

2.2   DATA SOURCES

The cumulative B-H productivity (*P*) and capacity (*C*) parameters define the maximum adult recruitment rate (density-independent recruitment) and maximum number of spawners (adult "carrying capacity") for a population over the complete life cycle (spawner to spawner). Often, habitat-based models like EDT) are used to approximate productivity and capacity, fitting a B-H function to observed abundance data. The productivity and capacity assumptions in AHA, like other assumptions (harvest rates, SARs, etc.) have a strong influence on the model outputs.

Life stage specific parameters may be obtained from fish passage survival models, subbasin plans, evolutionarily significant unit recovery plans, and hatchery managers.

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[3] Capacity for the spawner-to-emergence and smolt-to-adult life stages are both set at default values of 10^{12}, but may be edited in the Scenario tabs (note that these cells are shaded yellow in the Scenario tabs, indicating they may be edited). We recommend that only advanced users consider altering the default assumptions. The default assumptions are obviously simplifications of reality; capacity at these life stages is not unlimited.

[4] See the Scenario 1-4 tabs, cells B8:I10, for examples of how these values are calculated.

3.0   MODELING HATCHERY PRODUCTION

3.1   KEY ASSUMPTIONS

The AHA tool is designed to allow managers to evaluate management options for both integrated and segregated hatchery programs. A hatchery program is considered segregated if no NORs are used in the hatchery broodstock (the management intent is to create a distinct population that is reproductively isolated from naturally spawning populations). A hatchery program is considered integrated if NORs are used in the hatchery broodstock (the management intent is to create a composite hatchery/natural population for which the dominant selective pressure is the natural environment). The concepts underlying the computation of net natural vs. artificial selection in integrated programs and the impact of net selective pressure on genetic fitness of the natural population are described in more detail in Section 5.3.

In some cases, more than one release strategy is used in a hatchery program. For example, some programs release both subyearlings and yearlings. In such cases, information may be entered in AHA for both release groups. The total number of hatchery juveniles produced is computed as follows:

$$HOR_{releases} = (Brood_{HOB} + Brood_{NOB} + Brood_{Imp}) * Eggs_{Spawner} * S_{Egg-Release}$$

where:

$$Eggs_{Spawner} = S_{Prespawn} * Fecund_{HOR} * \%Fem_{HOR}$$

and

$$S_{Egg-Release} = S_{Egg-smolt} * \%yearlings + S_{Egg-sub} * \%subs$$

$Brood_{NOB}$ =	Number of natural origin adults in broodstock (integrated programs)
$Brood_{HOB}$ =	Number of hatchery origin adults in broodstock (local)
$Brood_{Imp}$ =	Number of imported hatchery origin adults in broodstock
$S_{egg\text{-}smolt}$ =	Survival from egg to release for yearlings
$S_{egg\text{-}sub}$ =	Survival from egg to release for subyearlings
$\%yearlings$ =	Proportion of release comprised of yearlings
$\%subs$ =	Proportion of release comprised of subyearlings
$S_{Prespawn}$ =	Survival in hatchery of broodstock adults
$Fecund_{HOR}$ =	Average number of eggs per female in broodstock
$\%Fem_{HOR}$ =	Percent females in broodstock

The user supplies estimates of survival from release to adult return to the subbasin (SAR) for each hatchery release group. The SAR value is usually computed from coded wire tag data or other hatchery information. As with the SAR for NORs, the SAR value used for HORs in AHA is a pre-harvest SAR, i.e., does not account for harvest removals in the marine and freshwater fisheries. The SAR does account for juvenile and adult mortality in the hydrosystem (i.e., fish passage losses during outmigration of juveniles and upstream migration of adults).

The SAR for hatchery origin fish may be calculated as:

$$SAR_{HOR} = \frac{HOR_{returns}/TotExpl_{HOR}}{HOR_{releases}}$$

where:

$HOR_{returns}$ =	Number of hatchery origin adults returning to the subbasin
$TotExpl_{HOR}$ =	Total exploitation rate of HORs
$HOR_{releases}$ =	Number of hatchery origin juveniles released

If programs have more than one release strategy, the SAR should be calculated separately for each release group.

The total HOR adult run size (before harvest, adult fish passage mortality, and weir and broodstock removals) is calculated as[5]:

$$HOR_{tot} = HOR_{releases} * S_{release-adult}$$

where:

$HOR_{releases}$ =	Number of hatchery releases (i.e., subyearlings and/or yearlings)
$S_{release-adult}$ =	Survival of hatchery releases from point of release to adult life stage while still in the ocean (i.e., prior to harvest, migration back to the subbasin)

The number of hatchery adults recovered at the point of release is calculated as:

$$HOR_{Returns} = HOR_{tot} * (1 - TotExpl_{HOR}) * FPS_{Adult} - HOS_{tot} - Strays_{tot}$$

The total number of HOS on the spawning grounds in the subbasin is calculated as:

$$HOS_{tot} = HOR_{tot} * (1 - TotExpl_{HOR}) * FPS_{Adult} * (1 - \%Hatch) * (1 - \%Weir) + Strays_{tot}$$

where:

FPS_{adult} =	Adult fish passage survival rate
%Hatch =	Percent of HORs returning to the subbasin, after terminal fishery removals, that return to the hatchery. Assumption is that the remaining HORs return to the spawning grounds.
%Weir =	Percent of HORs captured in the weir
$Strays_{tot}$ =	Total strays (includes fish from in-basin segregated program that do not return to the hatchery and strays from other subbasins)

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[5] This is a simplified version of the formula. See Appendix C formula 3 for the full formula, which includes a correction factor that applies the SAR variability selected by the user.

Hatchery surplus is the number of hatchery adults collected at the point of return but not used for broodstock or exported to other programs for use as broodstock. Hatchery surplus is calculated as follows:

$$HOR_{Surplus} = HOR_{returns} - (Brood_{HOB} + HOR_{Exp})$$

Estimates of the number of hatchery strays are discussed in Section 5.1.

3.2   DATA SOURCES

Hatchery and Genetic Management Plans (HGMPs) are a major information source for hatchery programs. Although HGMPs vary in completeness, comprehensive HGMPs may include information on a wide range of parameters such as:

- Hatchery type (Segregated/Integrated)
- Broodstock target (number of fish) and hatchery/natural composition in the broodstock
- Broodstock collection procedures
- Contribution of hatchery fish to natural escapement
- Proportion of broodstock imported and/or exported
- Smolt release size and life stage
- Hatchery survival by life stage
- Hatchery return rates
- Hatchery stray rates

Hatchery managers may be personally contacted when the pertinent HGMP is out of date or lacks certain types of information.

4.0 MODELING HARVEST

4.1   KEY ASSUMPTIONS

Harvest is estimated for four major fisheries (user-defined by harvest area) as a function of user-supplied harvest rates and the estimated number of HORs and NORs available in each fishery. Mark-selective fisheries on hatchery fish are analyzed by imposing differential harvest rates on NORs and HORs. The harvest rate entered in AHA for HORs should represent the composite rate for marked and unmarked fish. See the selective harvest rate calculator at the bottom of the AHA tab for help calculating mark-selective harvest rates. The harvest analysis does not incorporate age-specific harvest rates; harvest rates represent total harvest on a brood over all ages.

The number of fish harvested in fishery 1 (typically the ocean fishery) is calculated as:

$$Harv_{F1} = HOR_{tot} * HR_{HOR,F1} + NOR_{tot} * HR_{NOR,F1}$$

The number of fish harvested in fisheries 2, 3, and 4 are then calculated sequentially with each fishery making use of the fish remaining after previous harvests.

Thus, harvest in fishery 2 is calculated as:

$$Harv_{F2} = HOR_{tot} * (1 - HR_{HOR,F1}) * HR_{HOR,F2} + NOR_{tot} * (1 - HR_{NOR,F1}) * HR_{NOR,F2}$$

Harvest in fishery 3 is calculated as:

$$Harv_{F3} = HOR_{tot} * (1 - HR_{HOR,F1}) * (1 - HR_{HOR,F2}) * HR_{HOR,F3} + NOR_{tot} \\ * (1 - HR_{NOR,F1}) * (1 - HR_{NOR,F2}) * HR_{NOR,F3}$$

Harvest in fishery 4 (terminal harvest) is calculated as follows, with adult hydrosystem mortality accounted for before the fourth (terminal) fishery:

$$Harv_{F4} = HOR_{tot} * FPS_{Adult} * (1 - HR_{HOR,F1}) * (1 - HR_{HOR,F2}) * (1 - HR_{HOR,F3}) * HR_{HOR,F4} + NOR_{tot} \\ * FPS_{Adult} * (1 - HR_{NOR,F1}) * (1 - HR_{NOR,F2}) * (1 - HR_{NOR,F3}) * HR_{NOR,F4}$$

4.2   DATA SOURCES

Since AHA simulates long-term effects; the input variables should be viewed as likely future averages. In other words inputs should be estimated from a range of years and, if possible, account for expected future trends.

Harvest rates are based on the number of fish harvested divided by the total number of fish available to the fishery. Harvest rates are taken from target harvest rates described in management plans or from CWT data on actual harvests.

5.0   MODELING STRAYS AND GENETIC INTERACTIONS

5.1   STRAYING

Hatchery returns may end up at the point of release, at a weir, on the spawning grounds within the subbasin of origin, on spawning grounds outside the subbasin of origin, or they may die after escaping the fisheries, but before spawning. In the AHA tool, all surviving hatchery adults not recovered in fisheries, at the hatchery of origin, or weirs in the subbasin of origin are considered strays. Strays are allocated to a natural population within their respective basin of origin (within-basin strays), to natural populations outside of the originating basin (out-of-basin strays), or designated as adults returning to areas with no spawning populations. The purpose of the straying component in the analysis is to account for the effect of reproductive interactions between natural populations ("recipient populations") and hatchery programs ("donor populations").

The proportion and source of hatchery strays in the natural spawning escapement is used to estimate relative genetic fitness (see following section) of recipient natural populations. The number of hatchery strays spawning in nature from the donor population p are calculated as follows, where variables are defined above in Section 3.1:

$$HOS_{Tot,p} = HOR_{tot} * (1 - TotExpl_{HOR}) * FPS_{Adult} * (1 - \%Hatch) * (1 - \%Weir)$$

The number of strays from donor hatchery *p* to a particular recipient natural population is calculated as follows:

$$Recip_{HOR,p} = HOS_{tot,p} * \%Recip$$

where *%Recip* is an estimate of the proportion of the adults that stray to the recipient natural population.

Generally the *%Recip* would sum to 100 percent for a donor population, i.e., all strays are assumed to spawn with a natural population. However, information suggests that, in some cases, a portion of the hatchery return not recovered at the hatchery does not attempt to spawn with a natural population (e.g., programs that release fish a long distance away from natural populations).

The actual number of hatchery fish spawning in a recipient natural population is the sum of hatchery fish from all donor populations:

$$Strays_{HOR} = \sum_{i=1}^{p} Recip_{HOR,p} * (1 - \%Weir)$$

where *%Weir* is the proportion of the hatchery adults destined to spawn with the natural population, but are recovered at an adult weir either below the population or within the boundaries of the natural population.

5.2   DATA SOURCES

Data on straying are typically calculated from coded wire tagged releases from the originating hatchery and adult recoveries at the originating hatchery adult trap, at other adult traps, at hatchery adult traps other than the originating hatchery, and from spawning ground surveys.

Recoveries of hatchery adults at hatchery traps other than the release hatchery were used to provide a measure of straying outside of the basin of origin. Observations of the number of hatchery adults on the spawning grounds or at weirs were used to validate or revise default assumptions. Default stray assumptions were developed using coded wire tag recovery data for several populations in the Columbia Basin.

5.3   GENETIC INTERACTIONS

The analysis of genetic interactions accounts for the long-term effects on fitness of hatchery adults spawning with natural populations. A more detailed description of the basis for these equations is described in the HSRG white paper on Fitness and Local Adaptation (HSRG 2009, Appendix B). AHA incorporates three hypotheses about the effects of fitness loss on the naturally spawning population: the Ford (2002) model, the Busack (2017) model, and no fitness loss.

The Ford (2002) model is based on gene flow between hatchery and natural fish. Two parameters represent the mean proportional genetic contributions in each generation of hatchery and natural fish to natural origin and hatchery origin progeny. The proportion of hatchery broodstock composed of natural origin adults (proportion of natural origin broodstock or pNOB) is calculated as:

$$pNOB = \frac{Brood_{NOB}}{Brood_{NOB} + Brood_{HOB}}$$

The proportion of naturally spawning fish composed of hatchery origin spawners (proportion of effective hatchery origin spawners or $pHOS_{eff}$) is calculated as:

$$pHOS_{eff} = \frac{HOS_{tot} * RRS_{HOS}}{HOS_{tot} * RRS_{HOS} + NOS}$$

where HOS_{total} and NOS are the number of natural spawning hatchery and natural adults, respectively and RRS_{HOS} accounts for the (assumed) lower reproductive success of HORs as compared to NORs. Effective hatchery spawners are those that successfully produced progeny that survived to spawn to the next generation.

The HSRG has recommended adjusting census estimates of pHOS to account for first generation differences between the genetic contributions of natural origin and hatchery origin fish spawning in the wild (known as effective pHOS). This adjustment is made using the RRS, as shown in the formula above. The HSRG's 2017 Framework Paper provided additional guidance for applying a correction factor such as RRS, noting that the reduction in spawning effectiveness of HORs is already accounted for in the Ford (2002) model. If a further discount is justified, for example due to non-genetic, spatial or temporal differences in spawn timing between fish raised in the hatchery and those raised in the wild, the additional discount or weighting scheme should be carefully considered on a population specific basis. Gene flow in a population is not a single year event in most cases and is a long-term outcome (many generations) of a broodstock management strategy. **If there is no evidence that the contribution of HORs to the spawning population should be discounted, the AHA user may set RRS to 100 percent.**

The proportional influence of the natural environment on the mean phenotypic values (and genetic constitutions) of natural and hatchery fish is referred to as PNI (proportionate natural influence). PNI is calculated as:

$$PNI = \frac{pNOB}{pNOB + pHOS_{eff}}$$

Fitness is calculated in AHA (i.e., it is not an assumption provided by the user) for each generation (g) based on pHOS and pNOB in the parent generation (g-1). The fitness value ranges from 0 to 1, but the fitness 'floor' is typically assumed to be 0.5 (i.e., the hatchery population is assumed to be at least 50 percent as fit as a fully adapted natural population). Population fitness in generation g is calculated as:

$$Fitness_g = Max\left(Fitness_{floor}, e^{-\frac{1}{2}*\left(\frac{\left(P_{Nat,g} - \theta_{Nat}\right)^2}{\omega^2 + \sigma^2}\right)}\right)$$

where:

$Fitness_{floor}$ = Minimum fitness value, typically set to 0.50

θNat = Phenotypic optimum or expected mean value of the phenotypic probability distribution for the natural population

θHatch = Phenotypic optimum or expected mean value of the phenotypic probability distribution for the hatchery population

σ^2 = Phenotypic variance for the trait in question

$\bar{P}_{Nat,g} =$ Mean phenotypic value of the natural population in generation g

$P_{Nat,g} - \theta_{Nat}=$ Deviation from the optimum phenotypic value for the natural environment

The mean phenotypic value of the natural population and hatchery population in generation *g* is calculated as:

$$\bar{P}_{Nat,g} = (1 - pHOS_{g-1}) * \left[\bar{P}_{Nat,g-1} + \left(\left(\frac{(\bar{P}_{Nat,g-1} * \omega^2 + \theta_{Nat} * \sigma^2)}{(\omega^2 + \sigma^2)}\right) - \bar{P}_{Nat,g-1}\right) * h^2\right] + (pHOS_{g-1})$$

$$* \left[\bar{P}_{Hatch,g-1} + \left(\left(\frac{(\bar{P}_{Hatch,g-1} * \omega^2 + \theta_{Nat} * \sigma^2)}{(\omega^2 + \sigma^2)}\right) - \bar{P}_{Hatch,g-1}\right) * h^2\right]$$

and:

$$\bar{P}_{Hatch,g} = (1 - pNOB_{g-1}) * \left[\bar{P}_{Hatch,g-1} + \left(\left(\frac{(\bar{P}_{Hatch,g-1} * \omega^2 + \theta_{Hatch} * \sigma^2)}{(\omega^2 + \sigma^2)}\right) - \bar{P}_{Hatch,g-1}\right) * h^2\right]$$

$$+ (pNOB_{g-1}) * \left[\bar{P}_{Nat,g-1} + \left(\left(\frac{(\bar{P}_{Nat,g-1} * \omega^2 + \theta_{Hatch} * \sigma^2)}{(\omega^2 + \sigma^2)}\right) - \bar{P}_{Nat,g-1}\right) * h^2\right]$$

where:

h^2 = Heritability

ω^2 = Measures the strength of selection in a population (selection becomes weaker as the value of ω^2 increases).

The Busack (2015) model is described in Appendix D.

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APPENDIX A - AHA MODEL STRUCTURE

The AHA tool may be used to model up to five scenarios. Scenarios 1 through 4 may be used to estimate integrated program outcomes for different management strategies. For example, Scenario 1 could be used to model the current program, and Scenarios 2 through 4 could be used to model potential future management strategies by varying the harvest rates, number of hatchery releases, pNOB goal, and so on. The fifth scenario is designated for a segregated hatchery program that is associated with an integrated program (stepping stone program) and may be left blank if the population being modeled does not have this type of program. See the 'AHA Worksheet' description below for more information on setting up segregated and stepping stone strategies.

A. SCENARIO INPUTS

The user enters Key Assumptions for each of the five AHA scenarios on 5 worksheets: the AHA, Habitat, Fitness Assumptions, Stray Assumptions and SAR worksheets, as described below. All of the inputs from the AHA, Habitat, Fitness Assumptions, and Stray Assumptions worksheets are compiled in the <u>Scenario Inputs</u> tables on each of the respective Scenario worksheets. This makes it easier for the user to see how the inputs are used in the <u>Scenario Calculations</u> shown below the Scenario Inputs. In the Scenario Inputs table, the inputs are numbered sequentially. All of the Scenario inputs are described in numerical order in **Appendix B**. The SAR Worksheet inputs are used directly in the Scenario calculations, as described below.

AHA WORKSHEET

In the AHA worksheet, the yellow cells in the **Program Background**, **Program Goals** and **Key Assumptions** tables in the upper half of the worksheet should be filled out for each of the 5 scenarios. Green cells contain formulas and cannot be edited.

The information in the **Program Background** section at the top of the AHA tab is for informational purposes only and does not affect the AHA calculations. The user may fill in the yellow cells with information about the population location (subbasin), population name, species, population designation and current program phase. Each of the Scenarios may be given a name in the yellow cells in Row 6, e.g., Current Scenario, etc.

Program Goals may differ for each scenario. The only Program Goal that 'drives' the AHA results is pNOB. The AHA calculations are set up to meet the pNOB goal entered by the user if enough NORs are available. The other goals (escapement, harvest, PNI and pHOS) are benchmarks to compare against the scenario results. **Key Assumptions** inputs are described in detail in Appendix B.

AHA results for the 5 scenarios are displayed in the tables and graphics below the Program Goals and Key Assumptions tables. The results are automatically updated/recalculated whenever the Program Goals and Key Assumptions are edited.

As noted above, Scenarios 1 through 4 are used to simulate integrated program strategies. Broodstock for integrated programs are comprised of either integrated HORs or imported brood. Scenario 5 (optional) may be used for a segregated or stepping stone program. For example, some hatchery

programs have two components: an integrated program and a segregated program associated with the same natural population. The segregated program may either use segregated HORs as brood or incorporate integrated HORs into the brood. The latter approach is called a 'stepping stone' program. To simulate a stepping stone program in AHA, the segregated scenario (#5) must be linked to an integrated scenario (e.g., #4) such that integrated HORs from Scenario 4 become part of the brood for Scenario 5[6]. This version of AHA does not accommodate integrated programs with segregated brood (integrated brood are assumed to be either integrated HORs or imported from other programs) or segregated programs with natural origin brood. This is not a serious limitation for most integrated or stepping-stone programs.

In a stepping-stone program, there are thus three spawning environments, each with three possible types of spawners. The Busack fitness option in AHA accounts for the effects of this type of program by extending the Ford fitness model to three populations. This three-population extension of the Ford model may be applied to any scenario where three populations are linked and may be extended to include even more populations. It was first developed in planning for a possible Snake River fall Chinook salmon recovery scenario featuring a hatchery, an area with numerous hatchery origin spawners, and an area with lower hatchery influence. This model appears ideally suited to development of gene flow guidelines for "stepping-stone" situations, where an integrated program operates alongside a genetically linked isolated (segregated) program, and both have some effect on a natural population through gene flow. A pertinent case in point is that of spring Chinook in the Methow basin, where an integrated supplementation program at the Methow Fish Hatchery (MFH) operates alongside an isolated safety-net program at the Winthrop National Fish Hatchery (WNFH). Returnees from both programs spawn in the wild, and the WNFH can be genetically linked to the MFH program in that all or nearly all the WNFH broodstock could consist of MFH returnees, with the remainder being WNFH returnees.

HABITAT WORKSHEET

Filling out this worksheet is optional. The Habitat worksheet is intended to help the user calculate adult or smolt productivity and capacity values, if only one or the other of these are available. In Step 1, enter the population's observed smolt-to-adult survival rate (SAR) for NORs. In Step 2, enter either the adult or smolt productivity and capacity values. The SAR entered in Step 1 is used to calculate smolt values (if adult values are entered) or adult values (if smolt values are entered). Enter the resulting adult and smolt values in the AHA tab. In Step 1, the user may also enter the baseline SAR used in EDT modeling if this differs from the observed SAR based on the most recent program data. If the baseline SAR differs from the observed SAR, AHA will automatically calculate adjusted adult productivity and capacity values. See **Appendix B**, formulas (5) and (6) for the formulas used in the adjusted productivity and capacity calculations.

FITNESS WORKSHEET

The Fitness worksheet contains the standard set of default fitness assumptions used in AHA, which were developed in collaboration with Washington Department of Fish and Wildlife (Jim Scott and Craig

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[6] As AHA is currently set up, exported brood in AHA tab row 41 (Scenarios 1 through 4) are assumed to become broodstock for the segregated scenario (5). To link the segregated program to an integrated scenario (e.g., Scenario 4), the export number entered in AHA cell W41 must also be entered in AHA cell AB40.

Busack, pers. comm., 2004) and discussed in HSRG (2009). The yellow cells may be edited, but typically are not changed from the default assumptions.

STRAY ASSUMPTIONS WORKSHEET

The Stray Assumptions worksheet contains user supplied data about the total number of strays on the spawning grounds for each scenario. Section 5.1 of this document describes how stray data are used in AHA. Strays contribute to the number of hatchery origin fish on the spawning grounds in integrated populations (Scenarios 1-4 in AHA) and are accounted for in pHOS calculations. On the stray worksheet, if there is a segregated or stepping stone hatchery associated with the population, the stray data for that program are automatically loaded into the first row (green cells) for each scenario based on data entered by the user on the AHA tab for Scenario 5 if brood are exported from an integrated program (Scenarios 1-4) and imported into Scenario 5. If brood for the segregated program are not imported from an integrated program, the user will need to enter strays on the stray worksheet manually. Stray data from other programs (outside the subbasin) need to be entered manually on the stray tab by the user. Data on straying typically comes from CWT data or from genetic parentage analyses.

Data entered on the Stray Assumptions tab includes 1) the name of the donor (straying) population, 2) the total number of adult strays from each donor population, defined as the number of hatchery adults from the donor population that stray to the natural spawning grounds of any population[7], and 3) the percentage of adults from each donor population that strayed to the recipient population defined by the AHA scenario. Each row in the stray table represents a different donor population.

For example, in the table shown below, the segregated/stepping stone hatchery is linked to Naselle Scenario 1 (e.g., brood from Naselle Scenario 1 are exported to Scenario 5). Therefore, the first row in the stray assumptions tab is automatically populated with the total number of strays from the segregated population (this is the total number of HOS strays expected in Scenario 5; see AHA Scenario 5 cell AB56), shown in column 1 below. Column 2 shows the percentage of these strays that are expected to be recovered on the Naselle spawning grounds. In the second row, column 1 shows the total number of strays from hypothetical population 'XYZ'. Column 2 shows the percentage of 'XYZ' strays that are expected to be recovered on the Naselle spawning grounds. The values in Columns 3 and 4 are linked to the AHA tab – column 3 shows the percent effective spawners or RRS, and column 4 shows the percent of strays that reach the spawning grounds (i.e., are not intercepted by a weir, if present in the recipient basin). The final column is the product of columns (1) through (4). The total number of strays (56) and effective strays (45) are shown in the last row. These values are included in the total number of HOS and effective HOS shown in the Naselle Scenario 1 results and are therefore included in the pHOS and PNI calculations.

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[7] Note that stray totals entered on the stray assumption worksheet are average values, whereas AHA produces HOR and NOR values that vary across generations. This is a simplification and does not reflect the variation in stray numbers expected over time.

Naselle Scen. 1

Donor Population	Total Number adult strays (1)	Percent adults straying to recipient population (2)	Percent Effective Spawners (3)	Percent allowed to spawn naturally (4)	Effect Contrib. To Population (# HOS)
Segregated Hatchery	63	10%	80%	100%	5
Population xyz	250	20%	80%	100%	40
		0%	80%	100%	0
		0%	80%	100%	0
		0%	80%	100%	0
		0%	80%	100%	0
		0%	80%	100%	0
		0%	80%	100%	0
		0%	80%	100%	0
		0%	80%	100%	0
		Number spawn naturally:		56	45

1) Total number of adult strays is the number of hatchery adults from donor population that strayed to natural spawning grounds of any population.

2) Percent of total strays that strayed to the recipient population defined by this AHA scenario.

3) Percent effective spawners is the RRS (relative reproductive success) of HORs spawning in nature.

4) Percent allowed to spawn naturally is 1 minus the percent weir efficiency.

SAR WORKSHEET

The purpose of the SAR worksheet is to allow the user to specify how variation will be applied to the user-supplied SAR assumptions for natural origin and hatchery origin fish, depending on the option selected from the 'SAR Vary' menu on the AHA tab. If the PDO option is selected, systematic variation is applied to the SARs for naturally and hatchery produced smolts. If the PDO + Random option is selected, both systematic and lognormal random variation are applied. **See Appendix B (items 24 and 25) for more details on the 'SAR Vary' menu options and the 'SAR CV'.**

There are three user-supplied inputs on the SAR Worksheet (the yellow cells in P6:R6). The 'amplitude' controls the relative size of the PDO effect. If the amplitude is set to 100 percent, the full historical PDO variability is applied to the user-supplied SARs. If the amplitude is set to less than 100 percent or greater than 100 percent, the amount of variation applied to the SARs is reduced or increased, respectively. The user may also enter the PDO Start Year. This allows the user to select the starting point in the cycle, which corresponds to generation 21 in the AHA calculations. Finally, the user may enter the generation length (2, 3, or 4 years) for the species being modeled, which adjusts the SAR multiplier (column U) by taking the geomean of the PDO for the most recent 2, 3, or 4 years selected as the generation length.

The result of these calculations is found in SAR worksheet column V. This is a multiplier adjusted for generation length that is applied to the user supplied SARs; see the Scenario calculations, column BB (documented in Appendix C, formula 53).

AHA CONFIDENCE INTERVALS WORKSHEET

This worksheet is optional. The purpose of this worksheet is to illustrate the potential range of variation around each of the AHA Scenario outputs based on the SAR variation options selected by the user. On this worksheet, the user enters the number of model runs (up to 1,000) and clicks on the 'Run Model' button. Excel runs the model for the selected number of iterations, stores the results from each model run on the worksheet and calculates the average, standard deviation and CV for the selected number of iterations. The results table on this worksheet displays the average, CV and 'psuedo' confidence interval. The CVs and pseudo confidence intervals depend on the SAR variability inputs selected by the user (see SAR Worksheet, above, for details). The purpose of reporting the CV is to illustrate the range of values that approximately meets the NOAA CV standard (generally 15 percent) for Monitoring and Evaluation data (Rumsey and Crawford 2011).

STATUS AND TRENDS WORKSHEET

The Status and Trends worksheet is a stand-alone tab (none of the data entered here are used in the AHA calculations). This worksheet provides a place for managers to track program data and create simple graphs of harvest, escapement, etc. At a minimum, data on Terminal Harvest (columns L-N), NOR and HOR Escapement (columns O-S), and Hatchery Returns (columns T-AA) are required for the graphics to display valid results.

B. SCENARIO CALCULATIONS

There are five scenario worksheets (Scenario 1 through Scenario 5). All of the AHA results shown on the AHA tab come from calculations in the Scenario tabs. Each of the scenarios has an identical set of calculations, with one exception; the Scenario 5 (segregated program) tab does not include the Busack PNI calculations, since they apply to the affected natural population.

As noted above, in each Scenario tab, the table in the upper left portion of the tab compiles all of the inputs from other tabs (AHA, Habitat, Fitness Assumptions, and Stray Assumptions; the SAR inputs are used directly in the Scenario calculations) used in the Scenario calculations. The table in the upper right portion of the tab displays the scenario results that are also shown on the AHA tab.

The Scenario calculations are located below the Scenario Inputs and Scenario Results tables. The calculations are numbered sequentially from left to right and are described in detail (in numerical order) in **Appendix C**.

APPENDIX B - SCENARIO INPUTS

All user-supplied inputs to AHA are compiled in each Scenario tab in the **'Scenario Inputs'** table above the AHA calculations. Most inputs are entered either on the AHA tab, habitat worksheet, fitness tab, or stray assumptions tab. Some inputs are calculated based on the above user-supplied inputs. Cells containing calculated inputs are shaded green. Descriptions of each scenario input, along with formulas for calculated inputs, are listed below.

A. Natural Production (Habitat) Inputs

(1)   Prod_adult

The B-H adult productivity parameter defines the maximum adult recruitment rate (density-independent recruitment) for a population over the complete life cycle (spawner to spawner). Productivity is affected by habitat quality and population fitness.

(2)   Cap_adult

The B-H adult capacity parameter defines the maximum number of spawners (adult "carrying capacity") for a population over the complete life cycle (spawner to spawner). Adult capacity is a measure of the quantity and quality of habitat available for the adult life stage. Capacity determines the effects of density dependence on population survival.

(3)   Prod_smolt

The B-H adult productivity parameter can also be expressed in terms of smolts. Adult productivity is converted to smolt productivity simply by dividing adult productivity by the smolt-to-adult survival rate for NORs.

(4)   Cap_smolt

Smolt capacity is a measure of the quantity and quality of the habitat available for the smolt life stage. Adult capacity is converted to smolt capacity simply by dividing adult capacity by the smolt-to-adult survival rate for NORs.

(5)   Adjusted Adult Productivity (see SAR_base below (#23) for explanation)

$$AdjProd_{Adult} = Prod_{Adult} * \left(\frac{SAR_{Obs}}{SAR_{Base}} \right)$$

(6)   Adjusted Adult Capacity

$$AdjCap_{Adult} = \frac{Prod_{Em-Smolt} * SAR_{Obs}}{\frac{1}{Cap_{Spawn-Em}} + \frac{Prod_{Em-smolt}}{Cap_{Em-smolt}} + Prod_{Em-smolt} * \frac{SAR_{Obs}}{Cap_{Smolt-Ad}}}$$

(7)   Fecundity$_{NOR}$

Average number of eggs per naturally spawning female.

(8)   Percent Females (%Fem$_{NOR}$)

Percent females in the naturally-spawning population.

(9)   Spawner-Emergence Productivity

$$Prod_{spawn-em} = Fecund_{NOR} * \%Fem_{NOR}$$

(10)   Spawner-Emergence Capacity

In AHA, the default value is 1×10^{12}. Usually, there is no need to edit this value, but it can be edited on the Scenario worksheet (cell I8).

(11)   Emergence-Smolt Productivity

$$Prod_{Em-Smolt} = \frac{Prod_{Adult}}{Prod_{Spawn-Em} * Prod_{smolt-ad}}$$

(12)   Emergence-Smolt Capacity

$$Cap_{Em-Smolt} = \frac{1}{(Prod_{smolt-ad}) * \left(\frac{1}{Cap_{Adult}} - \frac{1}{Cap_{Smolt-Ad}}\right)}$$

(13)   Smolt-Adult Productivity

Either the SAR$_{obs}$ value or SAR$_{baseline}$ value, if a different baseline SAR assumption was used to estimate adult productivity and capacity.

(14)   Smolt-Adult Productivity

In AHA, the default value is 1×10^{12}. Usually, there is no need to edit this value, but it can be edited on the Scenario worksheet (cell I10).

(15)   Equilibrium Abundance of Natural origin Fish (N$_{eq}$)

The next four inputs are calculated based on the adjusted productivity and capacity values calculated above.

$$N_{eq} = Max(AdjCap_{Adult} * \left(1 - \frac{1}{AdjProd_{Adult}}\right), 0)$$

(16)   **Maximum Sustainable Yield (MSY)**

$$MSY = If(N_{eq} = 0, 0, ((\sqrt{AdjProd_{Adult}} - 1)^2) * \frac{AdjCap_{Adult}}{AdjProd_{Adult}})$$

(17)   **Escapement that Maximizes MSY (S$_{MSY}$)**

$$S_{MSY} = Max((\sqrt{AdjProd_{Adult}} - 1) * \frac{AdjCap_{Adult}}{AdjProd_{Adult}}, 0)$$

(18)   **MSY Exploitation Rate (Expl$_{MSY}$)**

$$Expl_{MSY} = \left(\frac{MSY}{MSY + S_{MSY}}\right)$$

B. Hydro and Ocean Survival Inputs

(19)   **Ocean Survival**

Survival rate during the smolt-to-adult period spent in the ocean.

(20)   **Juvenile Fish Passage Survival**

Survival of juveniles during outmigration through the hydrosystem. If there is no hydrosystem mortality, set juvenile fish passage survival rate to 100 percent.

(21)   **Adult Fish Passage Survival**

Survival of adults during outmigration through the hydrosystem. If there is no hydrosystem mortality, set adult fish passage survival rate to 100 percent.

(22)   **Observed Smolt-to-Adult Survival Rate - SAR$_{obs}$**

$$SAR_{obs} = S_{Ocean} * FPS_{juv} * FPS_{adult}$$

(23)   **Baseline Smolt-to-Adult Survival Rate - SAR$_{base}$**

SAR$_{base}$ is a value entered by the user in the Habitat Worksheet if the SAR assumption used to estimate adult productivity and capacity is different than the most recently observed SAR value. When SAR$_{base}$ differs from SAR$_{obs}$, the adjusted productivity and capacity values (formulas 5 and 6 above) are different from the user supplied productivity and capacity values.

(24)   **SAR$_{vary}$**

There are three options to select from a dropdown menu on the AHA tab: no added SAR variation ('None'), PDO, or PDO plus random variation. If 'None' is selected, no random or systematic variation is

incorporated into the SAR for naturally-spawning fish entered by the user. The SAR is applied as a fixed survival rate.

If 'PDO' is selected, the systematic effects of the Pacific Decadal Oscillation (PDO) are incorporated into the SAR for natural and hatchery origin fish. The user can edit the three inputs on the SAR tab (described in Appendix A) to determine how the PDO effects are applied.

If 'PDO + Random' is selected, both the systematic effects of the PDO and random lognormal variation are incorporated into the SAR. The user controls random variability in the SAR by entering a coefficient of variation (next input).

(25)   SAR$_{CV}$

The user may enter a value from 0-1 to add lognormal random variation to the SAR for NORs. The larger the CV, the greater the random variability incorporated into the SAR.

C. Harvest Inputs

(26)   HR$_{NOR,F1}$

Harvest rate of NORs in fishery 1 (typically the ocean fishery). In AHA, harvest rates (rather than exploitation rates) are entered for each fishery. The harvest rate is the percentage of fish harvested from the number of fish available to the fishery.

(27)   HR$_{HOR,F1}$

Harvest rate of HORs in fishery 1 (typically the ocean fishery).

(28)   HR$_{NOR,F2}$

Harvest rate of NORs in fishery 2.

(29)   HR$_{HOR,F2}$

Harvest rate of HORs in fishery 2.

(30)   HR$_{NOR,F3}$

Harvest rate of NORs in fishery 3.

(31)   HR$_{HOR,F3}$

Harvest rate of HORs in fishery 3.

(32)   HR$_{NOR,F4}$

Harvest rate of NORs in fishery 4 (typically the terminal fishery).

(33)   HR_{HOR,F4}

Harvest rate of HORs in fishery 4 (typically the terminal fishery).

(34)   TotExpl_{NOR}

Total exploitation rate of NORs in all fisheries.

$$TotExpl_{NOR} = 1 - (1 - HR_{NOR,F1}) * (1 - HR_{NOR,F2}) * (1 - HR_{NOR,F3}) * (1 - HR_{NOR,F4})$$

(35)   TotExpl_{HOR}

Total exploitation rate of HORs in all fisheries.

$$TotExpl_{HOR} = 1 - (1 - HR_{HOR,F1}) * (1 - HR_{HOR,F2}) * (1 - HR_{HOR,F3}) * (1 - HR_{HOR,F4})$$

D. Hatchery Inputs

(36)   S_{prespawn}

Prespawn survival of hatchery broodstock.

(37)   Percent Females (%Fem_{HOR})

Percent females in hatchery broodstock.

(38)   Fecund_{HOR}

Average number of eggs per female hatchery broodstock.

(39)   S_{egg-smolt}

Green egg to smolt (yearling) survival rate in the hatchery; survival rate for hatchery fish released as yearlings.

(40)   S_{egg-sub}

Green egg to subyearling survival rate in the hatchery; survival rate for hatchery fish released as subyearlings.

(41)   SAR_{yearling}

Smolt-to-adult survival of hatchery fish released as yearlings. Calculated as the number of hatchery origin adults that return to the subbasin from yearling releases, are harvested, or stray to another subbasin, divided by the number of yearlings released.

$$SAR_{yearling} = \frac{HOR_{returns,yearling}/TotExpl_{HORs}}{\#yearlings}$$

In AHA, the applied SAR for yearlings incorporates a correction factor in case SAR_{base} (used in EDT analysis, as described above in #23) differs from SAR_{obs}:

$$Applied\ SAR_{yearling} = SAR_{yearling} * \frac{SAR_{base}}{SAR_{obs}}$$

(42)   SAR$_{sub}$

Smolt-to-adult survival of hatchery fish released as subyearlings. Calculated as the number of hatchery origin adults that return to the subbasin from subyearling releases, are harvested, or stray to another subbasin, divided by the number of subyearlings released.

$$SAR_{subyearling} = \frac{HOR_{returns,subyearling}/TotExpl_{HORs}}{\#subyearlings}$$

In AHA, the applied SAR for yearlings incorporates a correction factor in case SAR_{base} (used in EDT analysis, as described above as #23) differs from SAR_{obs}:

$$Applied\ SAR_{subyearling} = SAR_{subyearling} * \frac{SAR_{base}}{SAR_{obs}}$$

(43)   RRS$_{HOS}$

Relative reproductive success of hatchery origin adults. Expressed as a percentage of the reproductive success of natural origin adults.

(44)   %Weir

Percentage of hatchery origin fish returning to the subbasin and captured in weir(s).

(45)   %Hatch

Percentage of hatchery origin fish returning to the hatchery (point of release).

(46)   %Spawn

Percentage of hatchery origin fish returning to the subbasin and returning to the spawning grounds, rather than to the hatchery.

(47)   #Yearling Releases

Target number of yearling hatchery releases.

(48)   #Subyearling Releases

Target number of subyearling hatchery releases.

(49)   **Percent Yearling Releases**

$$\%yearling = \frac{\#Yearling}{\#Yearling + \#Subyearling}$$

(50)   **Percent Subyearling Releases**

$$\%subyearling = \frac{\#Subyearling}{\#Yearling + \#Subyearling}$$

(51)   **Imported Brood**

Number of broodstock imported from outside the subbasin.

(52)   **Local Brood**

Number of local broodstock used in the hatchery program. Includes both hatchery origin broodstock (HOB) and natural origin broodstock (NOB); the proportion of NOB is determined based on the pNOB value entered by the user and the availability of NORs for brood. Calculated value based on the target number of hatchery releases, prespawning survival, percent females, fecundity of broodstock, and egg to release survival.

$$Brood_{local} = \frac{\#yearlings}{S_{prespawn} * \%Fem_{HOR} * Fecund_{HOR} * S_{egg-smolt}} + \frac{\#subs}{S_{prespawn} * \%Fem_{HOR} * Fecund_{HOR} * S_{egg-sub}}$$

(53)   **Exported Brood Goal**

Program goal for the number of broodstock to be exported from the subbasin.

(54)   **Max % NOR Run in Brood**

Maximum percentage of the NOR run to be collected for broodstock. Intended to prevent 'mining' NORs for broodstock.

(55)   **Fitness Adjustment**

The user selects from three fitness options, which determine whether the Ford or Busack fitness adjustment will be applied to the AHA estimates of natural production, or if no fitness adjustment will be applied ('None' option).

(56)   **Relative SAR of HORs**

$$SAR_{rel} = \frac{SAR_{yearling} * \%yearling + SAR_{subyearling} * \%subyearling}{Prod_{smolt-ad}}$$

(57)   Total Strays

$$Stray_{tot} = \sum_{i=1}^{n} \#strays_i * \%strays_{recip,i} * (1 - \%weir)$$

(58)   Effective Strays

$$Stray_{eff} = \sum_{i=1}^{n} \#strays_i * \%strays_{recip,i} * (1 - \%weir) * RRS_{HOS}$$

(59)   pHOS Goal

If pHOS is set to 100 percent or 0 percent, there is a simple correction to ensure the AHA calculations do not produce divide by zero errors. 100 percent is reset to 99.9999 percent; 0 percent is reset to 0.000001 percent.

(60)   pNOB Goal

If pNOB is set to 100 percent or 0 percent, there is a simple correction to ensure the AHA calculations do not produce divide by zero errors. 100 percent is reset to 99.9999 percent; 0 percent is reset to 0.000001 percent.

E. Fitness Inputs

(61)   Optimal Fitness – Nature (θ_{Nat})

Optimal fitness value for the natural population (scale of 0-100; default value in AHA is 100).

(62)   Optimal Fitness – Hatchery 1 (θ_{Hatch})

Optimal fitness value for the integrated hatchery population (scale of 0-100; default value in AHA is 80).

(63)   Optimal Fitness – Hatchery 2 (θ_{Hatch2})

Optimal fitness value for the segregated hatchery population (scale of 0-100; default value in AHA is 70).

(64)   Average Hatchery (θ_{HatAvg})

Average of θ_{Hatch} and θ_{Hatch2}

(65)   Selection Strength (SD units)

Strength of selection entered in SD units. The default value in AHA is 3. Used to calculate omega and omega-squared (formulas 79 and 80 below).

(66)   Heritability (h²)

The default assumption in AHA is 0.5. Used to calculate the natural and hatchery trait values (Appendix C, formulas 60 and 61).

(67)   Fitness Floor

Sets the minimum level for the natural and hatchery trait values. The default assumption in AHA is 0.50.

(68)   Start1

Initial population trait value for the natural population. Scale of 0-100, where 100 is a population that is fully adapted to the natural environment. Default starting value in AHA is 93.1.

(69)   Start2

Initial population trait value for the integrated hatchery population. Scale of 0-100, where 100 is a population that is fully adapted to the natural environment. Default starting value in AHA is 92.

(70)   Start3

Initial population trait value for the segregated hatchery population. Scale of 0-100, where 100 is a population that is fully adapted to the natural environment. Default starting value in AHA is 90.

(71)   Variance (O'^2)

The default assumption in AHA is 10. Used to calculate the natural and hatchery trait values and fitness (Appendix C, formulas 60, 61 and 62).

(72)   Rel_loss$_{egg}$

Distributes fitness loss over the life cycle. The sum of Rel_loss egg, fry and smolt is 1.0. The default value for Rel_loss$_{egg}$ is 0.5 in AHA.

(73)   Rel_loss$_{fry}$

Distributes fitness loss over the life cycle. The sum of Rel_loss egg, fry and smolt is 1.0. The default value for Rel_loss$_{fry}$ is 0.4 in AHA.

(74)   Rel_loss$_{smolt}$

Distributes fitness loss over the life cycle. The sum of Rel_loss egg, fry and smolt is 1.0. The default value for Rel_loss$_{smolt}$ is 0.1 in AHA.

(75)   Initial Natural Fitness (Fitness$_{initial}$)

Initial fitness level (generation 0) calculated based on the fitness value in Appendix C, formula 62.

(76) **Equilibrium Natural Fitness (Fitness_eq)**

Final fitness level (generation 100) calculated based on the fitness value in Appendix C, formula 62.

(77) **Average Natural Fitness (Fitness_average)**

Average fitness level calculated based on the fitness value in Appendix C, formula 62.

(78) **Number of Generations to Reach Average Natural Fitness**

The minimum number of generations needed to reach the Fitness_average level.

(79) **Omega**

$$\omega = SD\ units * \sqrt{O'^2}$$

(80) **Omega² (ω^2)**

The square of the value calculated in formula 79. Used to calculate the natural and hatchery trait values and fitness (Appendix C, formulas 60, 61 and 62). Measures strength of selection (larger values = weaker selection).

(81) **A**

Used in Busack PNI calculations (Appendix C, formulas 81, 82 and 83).

$$A = 1 - \frac{h^2 * O'^2}{\omega^2 + O'^2}$$

APPENDIX C - SCENARIO CALCULATIONS

I. Hatchery Calculations

(1) HOR$_{fry}$

The total number of hatchery fry produced is calculated as follows:

$$HOR_{fry.g} = \left(Brood_{HOB,g-1} + Brood_{NOB,g-1} + Brood_{Imp}\right) * Eggs_{Spawner,g-1}$$

(2) HOR$_{releases}$

The total number of hatchery juveniles released is c calculated as follows:

$$HOR_{Releases,g} = \left(Brood_{HOB,g-1} + Brood_{NOB,g-1} + Brood_{Imp}\right) * Eggs_{Spawner,g-1} \\ * S_{Egg-Release,g-1}$$

(3) HOR$_{adults}$

The total number of hatchery adults present in the ocean, prior to ocean and freshwater harvest and prior to any adult fish passage mortality during upstream migration back to the subbasin is calculated as:

$$HOR_{tot,g} \\ = \frac{HOR_{releases,g} * S_{release-adult,g-1}}{1 + \left(\dfrac{\left(\left(HOR_{releases,g} * S_{release-adult,g-1}\right) + Smolt_{total,g} * SAR_{appl,g-1} * FPS_{juv}\right)}{Cap_{smolt-adult,g-1}}\right)}$$

where the denominator applies any random or systematic variation to the SAR selected in the SAR Vary option (see Appendix B, #24).

(4) Eggs$_{spawner}$

$$S_{Spawn-Egg,g} = S_{Prespawn} * Fecund_{HOR} * \%Fem_{HOR}$$

(5) S$_{egg-release}$

$$S_{Egg-Release,g} = S_{Egg-smolt} * \%Yearlings + S_{Egg-sub} * \%Subs$$

(6) S$_{release-adult}$

$$S_{release-adult,g} = SAR_{applied,g} * SAR_{rel} * FPS_{juv}$$

(7) Cap$_{smolt-adult}$

Set equal to the Cap$_{smolt-adult}$ value for each generation, g, calculated in formula 51.

---

(8) Brood_{NOB}

NOB is calculated as the minimum of the user-defined pNOB level multiplied by the number of local brood needed for a full hatchery program, or the user-defined maximum percentage of NORs collected for brood multiplied by the number of adults returning to the subbasin minus terminal harvest of NORs. In either case, at least one returning NOR will be allowed to escape to the spawning grounds.

$$
\begin{aligned}
Brood_{NOB,g} \\
&= Rounddown(If\big((NOR_{tot,g} - Harv_{NOR,F1,g} - Harv_{NOR,F2,g} - Harv_{NOR,F3,g} \\
&\quad - Harv_{NOR,F4,g}) > 1, \\
&\quad Min(pNOB * Brood_{local}, \%NOR_{max} \\
&\quad * \big(NOR_{tot,g} - Harv_{NOR,F1,g} - Harv_{NOR,F2,g} - Harv_{NOR,F3,g} - Harv_{NOR,F4,g} \\
&\quad - 1\big)),0), 1)
\end{aligned}
$$

(9) Brood_{HOB}

Although this formula looks complicated, generally the number of HOB is the number of local brood required for a full program minus the number of NOB calculated in formula (8) above. If there are not enough returning HORs to support a full program (in combination with NOB collected), an alternative calculation is used based on the formula below.

$$
\begin{aligned}
Brood_{HOB,g} \\
&= Min(Max\left(0, If(pNOB_{goal} > 0.000001,\right. \\
&\quad Max\left(Brood_{local}, Min\left(\frac{Brood_{NOB,g}}{pNOB}, Brood_{local}, HOR_{tot,g}\right.\right. \\
&\quad \left.\left.- Harv_{HOR,F1,g} - Harv_{HOR,F2,g} - Harv_{HOR,F3,g} - Harv_{HOR,F4,g}\right)\right) - Brood_{NOB,g}\right), \\
&\quad Min\big(Brood_{local}, HOR_{tot,g} \\
&\quad - Harv_{HOR,F1,g} - Harv_{HOR,F2,g} - Harv_{HOR,F3,g} - Harv_{HOR,F4,g}\big)), (1 - \%Spawn) \\
&\quad * (HOR_{tot,g} - Harv_{HOR,F1,g} - Harv_{HOR,F2,g} - Harv_{HOR,F3,g} - Harv_{HOR,F4,g})
\end{aligned}
$$

(10) HOR_{returns}

The number of hatchery adults recovered at the point of release is calculated as:

$$
\begin{aligned}
HOR_{Returns,g} &= Max(0, (HOR_{tot,g} * \left(1 - TotExpl_{HOR}\right) * FPS_{Adult}) \\
&\quad - (HOS_{tot,g} - \frac{SAR_{appl,g-1}}{SAR_{appl-avg}} * Strays_{tot}))
\end{aligned}
$$

(11)   HOR_{surplus+export}

$$HOR_{Surplus+Export,g} = Max(0,(HOR_{tot,g} * (1 - TotExpl_{HOR}) * FPS_{Adult}) - (HOS_{tot,g} - \frac{SAR_{appl,g-1}}{SAR_{appl-avg}} * Strays_{tot}) - Brood_{HOB,g})$$

(12)   HOR_{surplus}

$$HOR_{Surplus+Export,g} = Max(0,(HOR_{tot,g} * (1 - TotExpl_{HOR}) * FPS_{Adult} - (HOS_{tot,g} - \frac{SAR_{appl,g-1}}{SAR_{appl-avg}} * Strays_{tot}) - Brood_{HOB,g} - HOR_{exp,g}))$$

(13)   HOR_{export}

$$HOR_{Returns,g} = Max(Min(Brood_{exp,goal}, HOR_{Surplus+Export,g}),0)$$

II.   Harvest Calculations

(14)   Harv_{NOR,F1}

The number of NORs harvested in fishery 1 is calculated as:

$$Harv_{NOR,F1,g} = NOR_{tot,g} * HR_{NOR,F1}$$

(15)   Harv_{NOR,F2}

The number of fish harvested in fisheries 2, 3, and 4 are then calculated sequentially with each fishery making use of the fish remaining after previous harvests.

Thus, harvest of NORs in fishery 2 is calculated as:

$$Harv_{NOR,F2,g} = NOR_{tot,g} * (1 - HR_{NOR,F1}) * HR_{NOR,F2}$$

(16)   Harv_{NOR,F3}

Harvest of NORs in fishery 3 is calculated as:

$$Harv_{NOR,F3,g} = NOR_{tot,g} * (1 - HR_{NOR,F1}) * (1 - HR_{NOR,F2}) * HR_{NOR,F3}$$

(17)   FPS_{Adult, NOR}

$$FPS_{Adult,NOR,g} = (NOR_{tot,g} - (Harv_{NOR,F1,g} + Harv_{NOR,F2,g} + Harv_{NOR,F3,g})) * (1 - FPS_{Adult})$$

(18)   Harv$_{NOR,F4}$

Harvest of NORs in fishery 4 is calculated as follows, with the result ensuring that not all NORs are harvested (at least one NOR returns to the spawning grounds):

$$
\begin{aligned}
Harv_{NOR,F4,g} \\
= Min(NOR_{tot,g} \\
* FPS_{Adult} * \left(1 - HR_{NOR,F1}\right) * \left(1 - HR_{NOR,F2}\right) * \left(1 - HR_{NOR,F3}\right) \\
* HR_{NOR,F4}, Max(0, NOR_{tot,g} * \left(1 - HR_{NOR,F1}\right) \\
* \left(1 - HR_{NOR,F2}\right) * \left(1 - HR_{NOR,F3}\right) - 1))
\end{aligned}
$$

(19)   Harv$_{HOR,F1}$

The number of HORs harvested in fishery 1 is calculated as:

$$Harv_{HOR,F1,g} = HOR_{tot,g} * HR_{HOR,F1}$$

(20)   Harv$_{HOR,F2}$

The number of HORs harvested in fishery 2 is calculated as:

$$Harv_{HOR,F2,g} = HOR_{tot,g} * \left(1 - HR_{HOR,F1}\right) * HR_{HOR,F2}$$

(21)   Harv$_{HOR,F3}$

Harvest of HORs in fishery 3 is calculated as:

$$Harv_{HOR,F3,g} = HOR_{tot,g} * \left(1 - HR_{HOR,F1}\right) * \left(1 - HR_{HOR,F2}\right) * HR_{HOR,F3}$$

(22)   FPS$_{Adult, HOR}$

$$
\begin{aligned}
FPS_{Adult,HOR,g} = (HOR_{tot,g} - (Harv_{HOR,F1,g} + Harv_{HOR,F2,g} + Harv_{HOR,F3,g})) \\
* (1 - FPS_{Adult})
\end{aligned}
$$

(23)   Harv$_{HOR,F4}$

Harvest of NORs in fishery 4 is calculated as:

$$
\begin{aligned}
Harv_{HOR,F4,g} = HOR_{tot,g} \\
* FPS_{Adult} * \left(1 - HR_{HOR,F1}\right) * \left(1 - HR_{HOR,F2}\right) * \left(1 - HR_{HOR,F3}\right) \\
* HR_{HOR,F4}
\end{aligned}
$$

(24)   Harv$_{total}$

Sum of HOR and NOR harvests in fisheries 1 through 4.

(25) **Exploitation Rate as Percentage of Harvestable Surplus**

$$Harv_{perc.g} = Min\left(1, Max\left(0, TotExpl_{NOR} * \frac{NOR_{tot,g}}{NOR_{tot,g} - S_{MSY}}\right)\right)$$

III. Natural Production Calculations

(26) HOS$_{total}$

The total number of HOS on the spawning grounds in the subbasin is calculated as:

$$HOS_{Tot,g} = Rounddown(0, Max(0, HOR_{tot,g} * (1 - TotExpl_{HOR}) * FPS_{Adult}$$
$$* \%spawn), 0) * (1 - \%Weir) + \frac{SAR_{appl,g-1}}{SAR_{appl-avg}} * Strays_{tot}$$

(27) HOS$_{effective}$

The effective number of HOS on the spawning grounds in the subbasin accounts for the assumed RRS of HORs and is calculated as:

$$HOS_{eff,g} = Rounddown(Max(0, HOR_{tot,g} * (1 - TotExpl_{HOR}) * FPS_{Adult} *$$
$$\%spawn), 0) * (1 - \%Weir) * RRS_{HOR} + \frac{SAR_{appl,g-1}}{SAR_{appl-avg}} * Strays_{eff}$$

(28) HOS$_{goal}$

The number of HOS on the spawning grounds that would allow the user-defined pHOS goal to be met is calculated as:

$$HOS_{goal,g} = Min\left(HOS_{Tot,g}, NOS_g * \frac{pHOS_{goal}}{(1-pHOS_{goal})}\right)$$

(29) HOS$_{surplus}$

Hatchery surplus is the number of hatchery adults collected at the point of return but not used for broodstock or exported to other programs for use as broodstock. Hatchery surplus is calculated as follows:

$$HOS_{Surplus,g} = HOS_{total,g} - HOS_{goal,g}$$

(30) NOR$_{esc}$

The number of NOR reaching the subbasin after adult fish passage mortality and harvest are accounted for:

$$NOR_{esc,g} = FPS_{Adult} * (1 - HR_{NOR,F3}) * (1 - HR_{NOR,F2}) * (1 - HR_{NOR,F1}) * NOR_{tot,g}$$
$$- Harv_{NOR,F4,g}$$

(31)   NOS

The number of natural origin fish reaching the spawning grounds, after NOB are collected:

$$NOS_g = Max(NOR_{esc,g} - Brood_{NOB,g}, 0)$$

(32)   NOS + HOS$_{total}$

The sum of formulas 26 and 31 (**HOS$_{tot}$** and **NOS**)

(33)   Fry$_{total}$

The sum of formulas 34 and 35 (**Fry$_{HOS}$** and **Fry$_{NOS}$**).

(34)   Fry$_{HOS}$

$$Fry_{HOS,g} = \frac{HOS_{eff,g-1} * FitProd_{sp-em,g-1}}{1 + \left(\dfrac{FitProd_{sp-em,g-1} * (HOS_{eff,g-1} + NOS_{g-1})}{FitCap_{sp-em,g-1}}\right)}$$

(35)   Fry$_{NOS}$

$$Fry_{NOS,g} = \frac{NOS_{g-1} * FitProd_{sp-em,g-1}}{1 + \left(\dfrac{FitProd_{sp-em,g-1} * (HOS_{eff,g-1} + NOS_{g-1})}{FitCap_{sp-em,g-1}}\right)}$$

(36)   Smolt$_{total}$

The sum of formulas 37 and 38.

(37)   Smolt$_{HOS}$

$$Smolt_{HOS,g} = \frac{Fry_{HOS,g} * FitProd_{em-smolt,g-1}}{1 + \left(\dfrac{FitProd_{em-smolt,g-1} * (Fry_{NOS,g} + Fry_{HOS,g})}{FitCap_{em-smolt,g-1}}\right)}$$

(38)   Smolt$_{NOS}$

$$Smolt_{NOS,g} = \frac{Fry_{NOS,g} * FitProd_{em-smolt,g-1}}{1 + \left(\dfrac{FitProd_{em-smolt,g-1} * (Fry_{NOS,g} + Fry_{HOS,g})}{FitCap_{em-smolt,g-1}}\right)}$$

(39)   Adult$_{total}$

The sum of formulas 40 and 41.

(40)   Adult$_{HOS}$

$$Adult_{HOS,g} = \frac{Smolt_{HOS,g} * FitProd_{smolt-ad,g-1}}{1 + \left(\dfrac{FitProd_{smolt-ad,g-1} * (Smolt_{NOS,g} + Smolt_{HOS,g} + HOR_{releases,g})}{FitCap_{smolt-ad,g-1}}\right)}$$

(41)   Adult$_{NOS}$

$$Adult_{NOS,g} = \frac{Smolt_{NOS,g} * FitProd_{smolt-ad,g-1}}{1 + \left(\dfrac{FitProd_{smolt-ad,g-1} * (Smolt_{NOS,g} + Smolt_{HOS,g} + HOR_{releases,g})}{FitCap_{smolt-ad,g-1}}\right)}$$

(42)   Fitness$_{sp-egg}$

$$Fitness_{egg.g} = Fitness_g \,^\wedge Rel\_loss_{egg}$$

(43)   Fitness$_{egg-smolt}$

$$Fitness_{fry.g} = Fitness_g \,^\wedge Rel\_loss_{fry}$$

(44)   Fitness$_{smolt-ad}$

$$Fitness_{fry.g} = Fitness_g \,^\wedge Rel\_loss_{smolt}$$

(45)   FitProd$_{sp-em}$

$$FitProdf_{sp-em,g} = Prod_{sp-em,g} * Fitness_{egg,g}$$

(46)   FitProd$_{em-smolt}$

$$FitProdf_{em-smolt,g} = Prod_{em-smolt,g} * Fitness_{fry,g}$$

(47)   FitProd$_{smolt-ad}$

$$FitProd_{smolt-ad,g} = FPS_{juv} * SAR_{applied,g} * Fitness_{smolt,g}$$

(48)   FitProd$_{cum}$

$$FitProd_{cum,g} = FitProd_{sp-em,g} * FitProd_{em-smolt,g} * FitProd_{smolt-ad,g}$$

(49)   FitCap$_{sp-emerg}$

$$FitCapf_{sp-em,g} = Cap_{sp-em,g} * Fitness_{egg,g}$$

(50)   FitCap$_{em-smolt}$

$$FitCapf_{em-smolt,g} = Cap_{em-smolt,g} * Fitness_{fry,g}$$

(51)   FitCap$_{smolt-ad}$

$$FitCap_{smolt-ad,g} = Cap_{smolt-ad,g} * Fitness_{smolt,g}$$

(52)   FitCap$_{cum}$

$$FitCap_{cum,g} = \frac{FitProd_{cum,g}}{\frac{FitProd_{sp-em,g}}{FitCap_{sp-em,g}} + \frac{FitProd_{sp-em,g} * FitProd_{em-smolt,g}}{FitCap_{em-smolt,g}} + \frac{FitProd_{sp-em,g} * FitProd_{em-smolt,g} * FitProd_{smolt-ad,g}}{FitCap_{smolt-ad,g}}}$$

(53)   SAR$_{PDO}$

Applies systematic variation of the PDO to the ocean survival assumption entered on the AHA tab. See the SAR tab for calculations producing the SAR multiplier in SAR column V.

$$SAR_{PDO,g} = S_{Ocean} * SAR!V^8_g$$

(54)   SAR$_{applied}$

Applies systematic variation of the PDO (formula 53) and/or random variation (formula 55) to the SARs for natural and hatchery origin fish.

$$SAR_{applied,g} = If(SAR_{vary} = "PDO", \ SAR_{PDO,g}, \ If(SAR_{vary} = "None", SAR_{obs}, SAR_{rand,g}))$$

(55)   SAR$_{rand}$

Applies lognormal random variation to the SAR$_{PDO}$ calculated in formula 53 above. In Excel, the loginv function takes 3 arguments: a probability, the mean, and the standard deviation, in the format: Loginv(probability, mean, SD). The function returns the inverse of the lognormal cumulative distribution function of x, where ln(x) is normally distributed with parameters mean and SD.

$$SAR_{Rand,g} = Min(LogInv(Rand(), Ln(SAR_{PDO,g}),$$
$$Max\left(\frac{\ln(2 * SAR_{CV} + 1)}{2}, 0.00000001\right)), 0.99999)$$

---

[8] Values are from SAR tab, column V.

IV. FORD FITNESS CALCULATIONS

(56) Max$_{gen}$

Identifies the generation in which the population reaches average fitness, Fitness$_g$, as calculated in formula 62 (below).

(57) Generation

Numbered from 0 to 100 in the calculations.

(58) 1-pHOS

$$1 - pHOS_g = \frac{NOS_g}{NOS_g + HOS_{eff,g}}$$

(59) 1-pNOB

$$1 - pNOB_g = If(Brood_{HOB,g} + Brood_{NOB,g} + Brood_{imp} > 0,$$
$$\frac{Brood_{HOB,g} + Brood_{imp}}{Brood_{HOB,g} + Brood_{NOB,g} + Brood_{imp}}, If(Strays_{tot} > 0, 1, 0))$$

(60) Natural Trait Value

$$\bar{P}_{Nat,g} = \left(1 - pHOS_{g-1}\right) * \left[\bar{P}_{Nat,g-1} + \left(\left(\frac{\left(\bar{P}_{Nat,g-1} * \omega^2 + \theta_{Nat} * \sigma^2\right)}{(\omega^2 + \sigma^2)}\right) - \bar{P}_{Nat,g-1}\right) * h^2\right] + (pHOS_{g-1})$$

$$* \left[\bar{P}_{Hatch,g-1} + \left(\left(\frac{\left(\bar{P}_{Hatch,g-1} * \omega^2 + \theta_{Nat} * \sigma^2\right)}{(\omega^2 + \sigma^2)}\right) - \bar{P}_{Hatch,g-1}\right) * h^2\right]$$

(61) Hatchery Trait Value

$$\bar{P}_{Hatch,g} = \left(1 - pNOB_{g-1}\right) * \left[\bar{P}_{Hatch,g-1} + \left(\left(\frac{\left(\bar{P}_{Hatch,g-1} * \omega^2 + \theta_{Hatch} * \sigma^2\right)}{(\omega^2 + \sigma^2)}\right) - \bar{P}_{Hatch,g-1}\right) * h^2\right]$$

$$+ (pNOB_{g-1}) * \left[\bar{P}_{Nat,g-1} + \left(\left(\frac{\left(\bar{P}_{Nat,g-1} * \omega^2 + \theta_{Hatch} * \sigma^2\right)}{(\omega^2 + \sigma^2)}\right) - \bar{P}_{Nat,g-1}\right) * h^2\right]$$

(62) **Fitness$_g$**

$$Fitness_g = If(FitnessAdj = \text{"Ford"}, Max(Fitness_{floor}, e^{-\frac{1}{2}*\left(\frac{(P_{Nat,g} - \theta_{Nat})^2}{\omega^2 + O^2}\right)}), If(FitnessAdj = \text{"Busack"}, PNI_{Busack}, 1))$$

V.   BUSACK FITNESS CALCULATIONS

Values for Natural Spawning Population

(63) **NOS**

The NOS value in formula 31 (above).

(64) **HOS$_{int}$**

$$HOS_{int,g} = HOS_{tot,g} - HOS_{seg,g}$$

(65) **HOS$_{seg}$**

$$HOS_{seg,g} = \frac{SAR_{appl,g-1}}{SAR_{appl-avg}} * Strays_{tot}$$

Values for Integrated Hatchery Program

(66) **NOB$_{int}$**

$$NOB_{int,g} = Max(Brood_{NOB,g}, 1)$$

(67) **HOB$_{int,1}$**

$$HOB_{int,1,g} = Brood_{HOB,g}$$

(68) **HOB$_{seg,1}$**

Set to 0 (assumes 0 segregated brood used for the integrated program).

Values for Segregated Hatchery Program

(69) **NOB$_{seg}$**

Set to 0 (assumes 0 NOB used for the segregated program).

(70) **HOB$_{int,2}$**

Assumes exported HORs are used for the segregated program.

$$HOB_{int,2,g} = Max(HOR_{exp,g}, 1)$$

(71) **HOB$_{seg,2}$**

In Scenarios 1-4, these values are taken from Scenario 5, which models the segregated program:

$$HOB_{seg,2,g} = Scenario\ 5!\ Brood_{HOB,g}$$

(72) **P$_{11}$ (pNOS)**

$$pNOS_g = \frac{NOS_g}{NOS_g + RRS_{HOR} * (HOS_{int,g} + HOS_{seg,g})}$$

(73) **P$_{21}$ (pHOS$_{int}$)**

$$pHOS_{int,g} = \frac{HOS_{int,g} * RRS_{HOR}}{NOS_g + RRS_{HOR} * (HOS_{int,g} + HOS_{seg,g})}$$

(74) **P$_{31}$ (pHOS$_{seg}$)**

$$pHOS_{seg,g} = \frac{HOS_{seg,g} * RRS_{HOR}}{NOS_g + RRS_{HOR} * (HOS_{int,g} + HOS_{seg,g})}$$

(75) **P$_{12}$ (pNOB$_1$)**

$$pNOB_{1,g} = \frac{NOB_{int,g}}{NOB_{int,g} + HOB_{int,1,g} + HOB_{seg,1,g}}$$

(76) **P$_{22}$ (pNOB$_{int,1}$)**

$$pHOB_{int,1,g} = \frac{HOB_{int,1,g}}{NOB_{int,g} + HOB_{int,1,g} + HOB_{seg,1,g}}$$

(77) **P$_{32}$ (pNOB$_{seg,1}$)**

$$pHOB_{seg,1,g} = \frac{HOB_{seg,1,g}}{NOB_{int,g} + HOB_{int,1,g} + HOB_{seg,1,g}}$$

(78)   P$_{13}$ (pNOB$_2$)

$$pNOB_{g,2} = \frac{NOB_{seg,g}}{NOB_{seg,g} + HOB_{int,2,g} + HOB_{seg,2,g}}$$

(79)   P$_{23}$ (pNOB$_{int,2}$)

$$pHOB_{int,2,g} = \frac{HOB_{int,2,g}}{NOB_{seg,g} + HOB_{int,2,g} + HOB_{seg,2,g}}$$

(80)   P$_{32}$ (pNOB$_{seg,2}$)

$$pHOB_{seg,2,g} = \frac{HOB_{seg,2,g}}{NOB_{seg,g} + HOB_{int,2,g} + HOB_{seg,2,g}}$$

(81)   Z-value – Pop1

Initial value (generation 0) is Start1

Subsequent values (generation 1 on) are calculated as follows:

$$Z_{Pop1,g} = A * (pNOS_{g-1} * (Z_{Pop1,g-1} - \theta_{Nat}) + pHOS_{int,g-1} * (Z_{Pop2,g-1} - \theta_{Nat}) + pHOS_{seg,g-1} * (Z_{Pop3,g-1} - \theta_{Nat})) + \theta_{Nat}$$

(82)   Z-value – Pop2

Initial value (generation 0) is Start2

Subsequent values (generation 1 on) are calculated as follows:

$$Z_{Pop2,g} = A * (pNOS_{g-1} * (Z_{Pop1,g-1} - \theta_{Hatch}) + pHOS_{int,g-1} * (Z_{Pop2,g-1} - \theta_{Hatch}) + pHOS_{seg,g-1} * (Z_{Pop3,g-1} - \theta_{Hatch})) + \theta_{Hatch}$$

(83)   Z-value – Pop3

Initial value (generation 0) is Start3

Subsequent values (generation 1 on) are calculated as follows:

$$Z_{Pop3,g} = A * (pNOS_{g-1} * (Z_{Pop1,g-1} - \theta_{Hatch2}) + pHOS_{int,g-1} * (Z_{Pop2,g-1} - \theta_{Hatch2}) + pHOS_{seg,g-1} * (Z_{Pop3,g-1} - \theta_{Hatch2})) + \theta_{Hatch2}$$

(84)   Busack PNI

$$PNI_{Busack,g} = \frac{Abs(Z_{Pop1,g} - \theta_{HatAvg})}{Abs(\theta_{Nat} - \theta_{HatAvg})}$$

APPENDIX D - EXTENDING THE FORD MODEL TO THREE OR MORE POPULATIONS

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The commonly cited HSRG guidelines for integrated hatchery programs are based on a model developed by Mike Ford (NMFS-NWFSC) and published in Conservation Biology in 2002 (Ford 2002). The purpose of this paper is to explain how the model can be extended to additional populations, and demonstrate the value of this approach.

The Ford model assumes a normally distributed trait with heritability h^2, variance σ^2 and phenotypic means $\bar{z}_w$ and $\bar{z}_c$ in the natural (wild) and hatchery (captive) environments, respectively. The trait is under Gaussian stabilizing selection with fitness functions having optima θ_w and θ_c, and selection strengths ω_w and ω_c in the natural and hatchery environments, respectively. The recursion equations for changes (Ford's equations 5 and 6) in the mean trait values in the two environments are:

$$\bar{z}_w^{'} = p_w\left[\bar{z}_w + \left(\frac{\bar{z}_w\omega_w^2 + \theta_w\sigma^2}{\omega_w^2 + \sigma^2} - \bar{z}_w\right)h^2\right] + \left(1 - p_w\right)\left[\bar{z}_c + \left(\frac{\bar{z}_c\omega_w^2 + \theta_w\sigma^2}{\omega_w^2 + \sigma^2} - \bar{z}_c\right)h^2\right] \qquad (1)$$

$$\bar{z}_c^{'} = p_c\left[\bar{z}_c + \left(\frac{\bar{z}_c\omega_c^2 + \theta_c\sigma^2}{\omega_c^2 + \sigma^2} - \bar{z}_c\right)h^2\right] + \left(1 - p_c\right)\left[\bar{z}_w + \left(\frac{\bar{z}_w\omega_c^2 + \theta_c\sigma^2}{\omega_c^2 + \sigma^2} - \bar{z}_w\right)h^2\right] \qquad (2)$$

where p_w is the proportion of individuals spawning naturally that are natural origin fish, and p_c is the proportion of individuals in the hatchery broodstock that are hatchery origin fish. Although equilibrium values for natural origin and hatchery origin fish could be generated by iterating these equations until the solutions did not change, Ford also developed equations for the equilibrium trait values. For natural origin fish, for example, the equilibrium point is given by:

$$\hat{z}_w = \frac{\sigma^2((1 + p_c(h^2 - 1))\theta_w + (h^2 - 1)(p_w - 1)\theta_c + \theta_c(\omega_w^2 - \omega_w^2 p_w) - \theta_w\omega_c^2(p_c - 1)}{\sigma^2(2 - p_w - p_c + h^2(p_w + p_c - 1)) + \omega_w^2(1 - p_w) + \omega_c^2(1 - p_c)} \qquad (3)$$

These equations could in theory be used for an actual trait, provided the heritability, selection strength, an optima were known, but it is debatable that these are known for any trait in salmon or steelhead. The equations' purpose in the paper was to demonstrate the relative importance of the various parameters in the equation in determining genetic change, and for the range of parameter values that Ford explored, the most important by far were the gene flow rates from natural to hatchery and vice versa. The HSRG concluded that a useful statistic would be *proportionate natural influence* or *PNI*, the position of the natural population equilibrium point relative to the two optima. Substituting the expressions pNOB and pHOS for Ford's $(1 - p_c)$ and $(1 - p_w)$, respectively, the HSRG also presented a simple equation that approximates PNI:

$PNI \approx pNOB/(pNOB + pHOS)$. Although the PNI approximation equation is commonly used as a performance metric, it is important to keep in mind that it is not an instantaneous measure of population condition, but an approximation of the equilibrium point at which the population would arrive after many generations.

In extending the Ford equations to additional populations it is useful to use an alternative form of his equations, one based on Lande's (1976) equation: $\quad \bar{x}' = \left(1 - \dfrac{h^2\sigma^2}{\omega^2 + \sigma^2}\right)\bar{x} \qquad (4)$, where $\bar{x}$ is the deviation of the population trait mean from the optimum. Ford's equation 1 can then be rewritten as:

$$(\bar{z}_w{}' - \theta_w) = \left(1 - \frac{h_w^2\sigma^2}{\omega_w^2 + \sigma^2}\right)\left(p_w(\bar{z}_w - \theta_w) + (1 - p_w)(\bar{z}_c - \theta_w)\right) \qquad (5)$$

Although the particular situation Ford was considering was gene flow between a hatchery population and a natural population, there is nothing in the equations that strictly applies to either a hatchery or a natural population. The equations simply describe the effect of gene flow between two populations[9]. Equations 1 and 2 can be rewritten as:

$$(\bar{z}_1{}' - \theta_1) = \left(1 - \frac{h^2\sigma^2}{\omega_1^2 + \sigma^2}\right)\left(p_{11}(\bar{z}_1 - \theta_1) + p_{21}(\bar{z}_2 - \theta_1)\right) \qquad (6)$$

$$(\bar{z}_2{}' - \theta_2) = \left(1 - \frac{h^2\sigma^2}{\omega_2^2 + \sigma^2}\right)\left(p_{12}(\bar{z}_1 - \theta_2) + p_{22}(\bar{z}_2 - \theta_2)\right) \qquad (7),$$

where p_{ij} is the proportion of spawners in population j that originated from population i.

Extension to three populations is now straightforward:

$$(\bar{z}_1{}' - \theta_1) = \left(1 - \frac{h^2\sigma^2}{\omega_1^2 + \sigma^2}\right)\left(p_{11}(\bar{z}_1 - \theta_1) + p_{21}(\bar{z}_2 - \theta_1) + p_{31}(\bar{z}_3 - \theta_1)\right) \qquad (8)$$

$$(\bar{z}_2{}' - \theta_2) = \left(1 - \frac{h^2\sigma^2}{\omega_2^2 + \sigma^2}\right)\left(p_{12}(\bar{z}_1 - \theta_2) + p_{22}(\bar{z}_2 - \theta_2) + p_{32}(\bar{z}_3 - \theta_2)\right) \qquad (9)$$

$$(\bar{z}_3{}' - \theta_3) = \left(1 - \frac{h^2\sigma^2}{\omega_3^2 + \sigma^2}\right)\left(p_{13}(\bar{z}_1 - \theta_3) + p_{23}(\bar{z}_2 - \theta_3) + p_{33}(\bar{z}_3 - \theta_3)\right) \qquad (10)$$

Derivation of equilibrium equations from equations 8-10 is also straightforward, but is messy and not necessary at this point, so is left to the adventurous reader.

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[9] Throughout this document the term population is used simply to denote a group of fish spawning together, not a population defined for recovery purposes.

This three-population extension of the Ford model can be applied to any scenario where three populations are linked, and obviously be extended to include even more populations. It was first developed in planning for a possible Snake River fall Chinook salmon recovery scenario featuring a hatchery, an area with a large number of hatchery origin spawners, and an area with lower hatchery influence, but appears ideally suited to development of gene flow guidelines for "stepping-stone" situations, where an integrated program operates alongside a genetically linked isolated program, and both have some effect on a natural population through gene flow. A pertinent case in point is that of spring Chinook in the Methow basin, where an integrated supplementation program at the Methow Fish Hatchery (MFH) operates alongside an isolated safety-net program at the Winthrop National Fish Hatchery (WNFH)[10]. Returnees from both programs spawn in the wild, and the WNFH can be genetically linked to the MFH program in that all or nearly all the WNFH broodstock could consist of MFH returnees, with the remainder being WNFH returnees. I will develop this example in detail below.

Let:

Population 1= natural spawners in Methow basin
Population 2=MFH broodstock
Population 3=WNFH broodstock

Assume that optima for both hatcheries are the same, and are different from the optimum for the natural spawning population. Further assume that selection strength is the same everywhere, and assume a reasonable heritability (e.g., 0.5). All these are routine assumptions that were used in application of the Ford model to develop HSRG guidelines.

Let P be the matrix of spawning proportions (=gene flow surrogates).

P_{11} Proportion of natural spawners that are natural origin fish	P_{12} Proportion of MFH broodstock that are natural origin fish	P_{13} Proportion of WNFH broodstock that are natural origin fish
P_{21} Proportion of natural spawners that are MFH returnees	P_{22} Proportion of MFH broodstock that are MFH returnees	P_{23} Proportion of WNFH broodstock that are MFH returnees
P_{31} Proportion of natural spawners that are WNFH returnees	P_{32} Proportion of MFH broodstock that are WNFH returnees	P_{33} Proportion of WNFH broodstock that are WNFH returnees

Set starting points for z values. These can be arbitrary. But I recommend values between the optima. Then run the equations recursively until the z values equilibrate, and calculate PNI for the natural population as percentage of the distance between the optima[11]. Different combinations of P values can be used to simulate different situations. The lack of equilibrium equations is annoying, but simulating to equilibrium points, which may require hundreds of generations, can be done very easily in a spreadsheet or with a simple R script.

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[10] Although these are real hatchery programs, the gene flow values used in the example are meant to be illustrative, not necessarily accurate depictions of current or proposed true values for these programs.

[11] This PNI value is the true PNI, in contrast to the simple approximation equation for two populations. It may be possible to develop an approximation equation for this situation, but it is unclear how useful this would be.

The following tables demonstrate use of the concept[12]. First assume that 50 percent of the fish on the spawning grounds are of natural origin, 30 percent are MFH returnees, and 20 percent are WNFH returnees; that the MFH program broodstock is 80 percent natural origin fish and 20 percent MFH returnees; and finally that the WNFH program broodstock is completely isolated. Without the multi-population stepping stone approach, there is no adequate way to compute PNI. If you chose to ignore the source of the hatchery fish on the spawning grounds and just assume a pHOS of 0.5, calculating PNI using the familiar equation, you would get 0.63, which seems (and is) way too high because so many of the hatchery origin spawners are not part of the integrated program. Using the stepping stone model, however, you get a PNI value of 0.19, demonstrating the huge load on PNI originating from the fish on the spawning grounds from the isolated program (if all the hatchery origin spawners were WNFH returnees, the PNI value would be 0.10).

Spawners/Broodstock

Sources	Natural Population	MFH Program	WNFH Program
Natural	0.5	0.8	0
MFH Program Returnees	0.3	0.2	0
WNFH Program Returnees	0.2	0	1

Now consider linking the WNFH program to the MFH program by using surplus MFH returnees as broodstock. Suppose 80 percent of WNFH broodstock needs can be met this way. The gene-flow matrix is shown to the left. This scenario yields a PNI of 0.55, a big improvement over 0.19.

By investigating the consequences of a series of realistic gene flow matrices, gene flow objectives for both programs can be developed that will result in a specified PNI.

[12] In the example I used a selection strength of 3 sd and a heritability of 0.5.

Spawners/Broodstock

Sources	Natural Population	PUD Program	WNFH Program
Natural	0.5	0.8	0
PUD Program Returnees	0.3	0.2	0.8
WNFH Program Returnees	0.2	0	0.2

Literature Cited

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