Review of the All-“H”-Analyzer Model

Introduction

The All-“H”-Analyzer (AHA) model was designed to evaluate the effects of alternative strategies for managing hatchery brood stocks on the abundance and productivity of natural populations, taking into account the productivity of the habitat and harvest management strategies. The model was the idea of scientists from the Washington Department of Fish and Wildlife (WDFW), and the Northwest Indian Fisheries Commission (NWIFC) and was developed by the Hatchery Science Review Group (HSRG) for use in a series of technical hatchery workshops held during the summer of 2004 for watersheds in Puget Sound and coastal Washington State. WDFW has also applied the model to Chinook and coho salmon populations in the Lower Columbia region and recently the model has been proposed as a decision-support tool for hatchery and recovery planning in the Columbia Basin. Results from previous applications of the model were not available for this review. A user’s manual and some related documentation were available on the Publications page of the Hatchery Reform Project web site, www.hatcheryreform.org.

Need for Review

Integration of habitat, harvest, and hatchery strategies and actions is important for federal agencies, co-managers and watershed groups developing recovery plans for listed species of salmon, trout, and bull trout under the Endangered Species Act. The Puget Sound Technical Recovery Team (TRT) organized this review with input from the Willamette/Lower Columbia TRT and the Interior Columbia TRT to provide information for policy makers on the strengths and limitations of the model and to provide constructive criticism to agencies or scientists who might want to refine the tool. The original impetus for this review came from WDFW Director Dr. Jeff Koenings. During a discussion of hatchery reform with the Shared Strategy (a coalition of tribes, state and federal agencies, local governments, and citizens that has undertaken developing recovery plans for the Puget Sound), Dr. Koenings described a potential role for the AHA model in the recovery planning process for Puget Sound Chinook salmon. The Shared Strategy subsequently requested a review of the model by the Puget Sound TRT. NOAA Fisheries Salmon Recovery Division was also interested in potential use of the model in other salmon recovery regions and supported review of the model.

Review Process

We identified reviewers from the four northwest technical recovery teams, the National Marine Fisheries Service (NMFS) Northwest Fisheries Science Center, and independent academic scientists with expertise in population dynamics and population genetics. WDFW and tribal scientists on the Puget Sound TRT who had worked with the HSRG did not review the model to minimize the perception of conflict of interest, although they participated in the joint TRT synthesis of the reviews. Each of the reviewers received a copy of Version 1.1 of the AHA Model, the User’s Guide, and the HSRG’s explanation of their “integrated hatchery” concept (“Integrated Hatchery Programs Jul04”). No written documentation of the model structure and assumptions was available at the time this review was initiated.

Each reviewer was asked to consider the following questions to guide their review:

1) Is the model consistent with viable salmon population (VSP) criteria? What are the strengths and weaknesses?

2) What are the strengths and weaknesses of the scientific assumptions of the model? Are these assumptions adequately documented or transparent in the model? Can the model be validated?

3) Does the model incorporate adequate uncertainty (e.g. environmental and demographic stochasticity) for decision making? Is it clear how uncertainty in different parameters affects the certainty of the results?

4) Is the choice and number of parameters in the model appropriate? Can the parameters be estimated from existing data or do they rely on expert opinion?

5) Is the model easy to use? Are the results easy to interpret?

Overview

Based on our analysis, the model applies basic population dynamic and genetic relationships in a Microsoft Excel© template. It provides no new theoretical modeling. The model uses sequential life-stage specific Beverton-Holt recruitment dynamics (Mousalli and Hilborn 1986) but reduces intrinsic productivity according to fitness loss predicted by Ford's (2002) model of domestication. The use of the Ford (2002) formulation for domestication refines a basic approach for incorporating hatchery effects in population recruitment models. The AHA model requires data for population dynamics at four life-stages (spawner-to-egg, egg-to-smolt, smolt-to-adult (before harvest), and adult-to-spawner (post harvest)). By varying inputs for habitat (productivity, capacity, minimum natural-origin escapement, and smolt-to-adult returns), harvest rates, and hatchery programs (brood stock number, smolts released, recruits per spawner, destination of hatchery-origin fish, and factors affecting loss of fitness), the user can calculate how many hatchery and natural-origin fish go to harvest, spawn in the wild, or return to be used at the hatchery. The program graphs the proportion of hatchery-origin fish on the spawning grounds (pHOS) and natural-origin fish in the brood stock (pNOB) compared to the HSRG's recommendation that pNOB exceed pHOS in integrated hatchery programs.

Is the model consistent with viable salmon population (VSP) criteria? What are the strengths and weaknesses?

All reviewers agreed that the strength and most attractive feature of the AHA model is the ability to incorporate information about habitat, harvest, and hatchery management in a single "what-if" analysis. The model is simple, transparent, and uses explicit mechanisms to illustrate how different levels of production, brood stock management, harvest, and management of hatchery fish can be consistent with predetermined criteria for composition of natural origin spawners given different productivity and capacity of the environment. Because of its simplicity, its strength is in illustrating the heuristic relationships between these different "H"s. This makes it very useful for identifying possible management strategies or exploring the relative merits of different types programs.

The simplicity of the model is also a weakness of the model. The reviewers agreed that the simplicity of the model, its assumptions, and the inability to actually measure many of the parameters used in the model, such as productivity, capacity, density dependence at different life-stages, and the parameters of the Ford (2002) fitness model, mean that the AHA model is best used heuristically to explore different strategies. The model should not be relied upon to allocate effects between different "H"s or decide "how much is enough", especially in the absence of supporting empirical data or independent analyses. For example, the reduction in relative fitness from antagonistic selection in the model can be seen as a surrogate for interactions between hatchery and natural fish. This would have heuristic value, but it is not realistic for predicting actual abundances or changes in productivity. The model purports to show "the degree to which the natural environment is driving the adaptation of the hatchery and natural population components." However, the model ignores relaxation of selection (sensu Lynch and O'Hely 2003) and gene flow from other stocks, which may also reduce fitness, and it does not include genetic drift or ecological interactions of hatchery and wild fish, such as intra- or interspecific competition and predation, disease transfer and amplification, or nutrient flow, which also affect productivity. Because it does not include these effects, another weakness of the model is that it cannot evaluate the risk or benefits of segregated hatchery programs or the relative merits of segregated versus integrated strategies. Because it ignores these effects, the model is not sufficient for making decisions on the integration of habitat, harvest, and hatchery actions. It seems unlikely that any single model would ever be considered scientifically sufficient by itself for making decision on the integration of habitat, harvest, and hatchery actions and that multiple tools and analyses will be necessary for making these decisions.

The model has a simple relationship to viable salmonid population (VSP) characteristics. Under the VSP concept, viability is a function of abundance, productivity, diversity, and spatial structure. The AHA model focuses on the effects of abundance given assumed changes in productivity. Users provide their own estimates of intrinsic productivity, but the program calculates potential reductions from these estimates based on the level of domestication of the population. One reviewer noted that a major deficiency of the model for recovery planning is that it does not address the question "How much reduction in fitness can a natural population sustain and still retain the ability to sustain itself in natural habitat?" The model is not (and does not pretend to be) a population viability analysis model and consequently it cannot be used to estimate the affects of different strategies on the probability that a population will be self-sustaining or go extinct. Although the model does consider changes in fitness based on whether selection in natural environments is having a greater effect than selection in the hatchery environments, simply creating the conditions where fish are more like a natural population than a hatchery adapted population does not guarantee viability of the population. Similarly, the model also does not address diversity or spatial structure, two components of viability that need to be considered in designing hatchery programs. Consideration of these viability characteristics is critically important. Achieving the diversity and spatial structure criteria outlined by McElhany et al. (2000) may be difficult in hatchery programs, as noted by two of the reviewers. Careful consideration should be given to these criteria early in the development and review of integrated hatchery programs.

What are the strengths and weaknesses of the scientific assumptions of the model? Are these assumptions adequately documented or transparent in the model? Can the model be validated?

The lack of documentation is a major weakness of the model. Without documentation describing the model and its assumptions, the model could be misused or the results could be easily misinterpreted.

The model relies on Beverton-Holt population dynamics. The assumptions, strengths and limitations of this model and the assumptions necessary to calculate estimates of intrinsic productivity or capacity are well documented and we will not repeat them here. The important point is that these parameters, which largely drive the results of the AHA model, are difficult to estimate and highly uncertain. Because these population parameters provide the only link to the habitat "H"(no habitat variables or measurements are actually included in the model) several reviewers questioned whether this should be called an all "H" analysis. Incorporating the ability to examine other population recruitment models (e.g. Ricker or "hockey-stick") to look for consistent results would greatly increase confidence in a given strategy.

Although it is relative common to incorporate hatchery affects on productivity, the AHA model uses estimates of fitness loss derived from the formulations of Ford (2002). For heuristic purposes, this assumes that overall fitness can be estimated based on the response of a single, normally distributed trait to selection in two environments (the wild and the hatchery). (In actuality fitness is based on selection at multiple loci on multiple traits, which is much more difficult to model). The strength of this approach is that it allows both domestication in the hatchery and natural selection in the wild to be incorporated in a quantitative model. The weakness of this assumption is that it is difficult to parameterize the genetic model realistically because the characteristics of such a hypothetical trait are unknown. Choice of parameter values for heritabilities of the trait in the two environments or the optimum phenotype for the hatchery environment, for example, can greatly affect the results. Using estimates from single, fitness related traits (e.g. adult return timing, fecundity, stress response) almost certainly underestimates fitness loss compared to the hypothetical trait that responds similar to multiple traits. The User's Guide provides no documentation for the parameters chosen for the model or advice to model users about alternatives.

The reviewers agreed that validating the model would be difficult. The model could be used to generate hypotheses about specific short or long-term affects of management strategies that might be tested using properly designed experiments. The lack of empirical support for the model, however, means that users should not have a high degree of confidence in the model forecasts and that they should incorporate precautionary measures in decisions based on the model. The reviewers suggested that it might be possible to "ground truth" the model by comparing the predicted fitness loss with fitness loss in programs with real data, which would at least indicate consistency. Conducting sensitivity analyses would allow users to identify parameters or assumptions that most need to be estimated or tested.

Does the model incorporate adequate uncertainty (e.g. environmental and demographic stochasticity) for decision making? Is it clear how uncertainty in different parameters affects the certainty of the results?

A major weakness of the model is that it incorporates uncertainty for only one parameter—smolt-to-adult returns (SAR) and this can be turned off by the user. The model is essentially deterministic. The model facilitates an evaluation of the effects of alternative assumptions for numerous parameters, such as population productivity, capacity, harvest rates, and composition of hatchery and natural spawners in the brood stock and the wild. Incorporating uncertainty for these and other key parameters, such as egg-to-fry survival, density dependence at different life stages, and parameters of the Ford (2002) model leading to fitness changes would greatly increase the usefulness of the model. Incorporation of uncertainty is essential for modern, well-designed decision-support tools (Clemen 1996), although it is not always easy. Rabinovich (1993) summarized the dilemma with two central tenets of such analyses: underestimating uncertainty is lying; overestimating uncertainty is cowardice. It would be scientifically irresponsible to ask decision makers to assign much weight to the model predictions for making expensive and potentially risky decisions when uncertainty could easily be incorporated in the model and displayed in the results. Programming challenges are no longer an excuse for ignoring uncertainty as modeling routines (e.g. Press et al. 1986) and add-on programs for incorporating simulations in spreadsheets are widely available.

Incorporating uncertainty in AHA, however, would strengthen the ability to examine multiple scenarios, which is one of the most attractive features of the model. By incorporating uncertainty into the model parameters and results, it will be possible for managers to identify management strategies leading to real, detectable changes. Being able to explore probability of getting detectable changes in population status before implementing potentially costly changes in hatchery infrastructure or management should greatly increase the potential for success.

Reviewers had several questions about the usefulness of the variability that could be assigned to SARs. One reviewer noted that the variance in the time series used in the model was low compared to data sets from the Columbia River and consequently might not be appropriate. The reviewers also noted that the incorporation of SAR variability followed a fixed 10-year pattern with a bit of stochasticity added to generate slightly different outputs every time the spreadsheet values were recalculated. Because of this, there was no way to examine the distribution of outputs systematically.

Documentation of the model should include a sensitivity analysis of the model results to changes in different parameters. Currently, users can not judge which parameters have the greatest impact on the results and decisions made based on the model.

Is the choice and number of parameters in the model appropriate? Can the parameters be estimated from existing data or do they rely on expert opinion?

The model relies on four sets of parameters: 1) natural population growth parameters (Beverton-Holt productivity and capacity estimates), 2) hatchery production parameters, 3) impact constraints (e.g. harvest, minimum natural-origin escapements), and 4) fitness parameters for the Ford (2002) domestication model. The ability to estimate these parameters differs among the different types.

The intrinsic productivity and capacity parameters of the Beverton-Holt population recruitment model are major drivers of the AHA model. These parameters are very difficult to estimate, although population dynamic models using these parameters provide useful hypothesis about how salmon populations will respond to different management actions. Currently there are two ways of estimating intrinsic productivity and capacity: 1) using time series data or examining relationships between habitat characteristics and productivity. The accuracy and precision of parameter estimates obtained from method 1 will vary depending on numerous factors, including the annual variability in habitat conditions, the accuracy and precision of the estimates of spawners and subsequent adult production, and the ability to incorporate variables that adjust for variations in other processes (e.g., marine survival). Uncertainty in productivity parameter estimates for salmon populations is often large. An alternative method is to use habitat-based models that relate habitat characteristics (e.g., watershed area, gradient, channel morphology, etc.) to capacity and production. One such approach, the Ecosystem Diagnosis and Treatment model (EDT) is suggested by the AHA User's Guide. The life-stage specific structure of the Beverton-Holt model used in AHA can incorporate values estimated from EDT. A number of factors raise questions about how much confidence to place in EDT derived values and review of EDT suggests that AHA analyses using EDT input should be considered highly uncertain. The results do provide a starting place for examining alternatives, however.

The rationale for including multiple life stages in the model is unclear. If the intent is for future versions of the model to incorporate additional processes (e.g., predation, competition, disease transmission) then this additional complexity may be warranted, although characterizing the interactions between these phenomena will incorporate much uncertainty. Alternatively, the transparency of the AHA model might be enhanced by incorporating a simple, single-stage Beverton-Holt function.

Reviewers also noted that estimating the parameters of the Ford equations (2002) would primarily require expert opinion, which adds to the uncertainty of the AHA model. Because of the assumption of the model, there is virtually no data for parameters such as ω^2 (strength of selection in the hatchery), θ (the optimum trait value in the hatchery), σ^2 (the variance of the trait), and h^2 (heritability of the trait in the hatchery or wild environment). The User's Guide suggests the users might want to alter θ for hatcheries based on the different environmental conditions in hatcheries, but it provides little guidance for doing this.

Is the model easy to use? Are the results easy to interpret?

Reviewers generally like the simplicity and ease of using the model and the graphical displays of results. Reviewers noted that the interaction between productivity and capacity estimates and other production parameters was difficult to follow and they often had to use trial and error to get results that made sense.

Although the model was not documented, reviewers generally liked the accessibility of the model. Because the model did not involve new theoretical development by the HSRG and it is being distributed for open use and development by the co-managers, at least one reviewer suggested the use of open source code in future development of this model. This would support future independent review and rapid evolution of the model by promoting sharing between those interested in refining the model and the general approach.

Recommendations

Based on our review, we would recommend the following use and refinements of the model

- Managers should consider the model a tool for heuristic exploration of integrated strategies for hatchery, harvest, and habitat actions rather than a quantitative predictor for specific populations

- Developers should provide documentation for the model, including the strengths and limitations of the model and sensitivity analyses;

- Users should be able to incorporate uncertainty in the parameter estimates and the model should display uncertainty of the results

- The tool should incorporate options to use multiple population recruitment models.

References

Clemen, R. T. 1996. Making hard decisions. Duxbury Press, Wadsworth Publishing Company, Belmont, CA.

Ford, M. 2002. Selection in captivity during supportive breeding may reduce fitness in the wild. Conservation Biology 16:815-825.

Lynch, M., and M.O'Hely. 2001. Captive breeding and the genetic fitness of natural populations. Conservation Genetics 2:363-378.

McElhany, P., M. H. Ruckelshaus, M. J. Ford, T. C. Wainwright, and E. P. Bjorkstedt. 2000. Viable salmonid populations and the recovery of evolutionarily significant units. Technical Memordandum NMFS-NWFSC-42. United States Department of Commerce, NOAA, Seattle, WA.

Moussali, E., and R. Hilborn. 1986. Optimal stock size and harvest rate in multistage life history models. Canadian Journal of Fisheries and Aquatic Sciences 43:135-141.

Press, W.H., B. P. Flannery, S.A. Teukolsky, and W.T. Vetterling . 1986. Numerical recipes: the art of scientific computing. Cambridge U. Press, New York, NY.

Rabinovich, S. 1993. Measurement errors: theory and practice. American Institute of Physics, New York.

Review 1: Review of the "All H Analyzer" (AHA) model.

Michael Ford

Summary: This is a useful tool for doing a "quick and dirty" analysis to determine if a particular hatchery production level is expected to meet management goals as described by numbers and proportions of hatchery and natural origin fish. Its benefits include simplicity, ease of use, and a nice "front end" for displaying model output. If its use is limited to this purpose, then I think it will prove to be very valuable at illustrating the feasibility (or not) of various hatchery/wild integration strategies.

My concern is that rather than being limited to doing rough evaluations of alternative hatchery production levels, the AHA model may be broadly used as "the tool" for evaluating alternative hatchery/harvest/habitat recovery strategies. I do not think its developers intended that the model be used in that way, but based on conversations around the region it appears that some policy makers are regarding the model in that light. <u>In my opinion, this model is NOT appropriate for conducting a comprehensive analysis of alternative recovery scenarios</u>. It will be very useful for evaluating (in a fairly gross sense) whether alternative hatchery production strategies are expected to achieve their goals.

General Comments

In evaluating the utility of any model it is important to first ask "What is the purpose of the model?" The AHA model is described as an "all H model" that can "… be used to predict the likely outcomes of different environmental conditions and fish management strategies.. " (AHA Users Guide, p. 2). I'm not sure I agree with this. Rather, I think the model as it is currently structured should primarily be regarded as a sophisticated "bookkeeping" tool for tracking the consequences of alternative hatchery production strategies. In particular, the model allows the user to determine the expected numbers of hatchery and wild fish in a population as a function of the productivity and capacity of each population, the rates of exchange between them, and the degree to which natural selection selects for different attributes in the hatchery versus natural environment. Habitat attributes enter the model only indirectly, as simple productivity and capacity parameters. Although these parameters can be varied to evaluate the effects of changing habitat conditions, any connection between the parameters and specific habitat attributes is external to the AHA model. The AHA model on its own cannot, therefore, be used to evaluate the feasibility of alternative recovery scenarios. Note that I'm sure the developers of the model never intended or claimed that should be used for that purpose, but this may not be entirely clear to policy makers.

The model is very simple – this is both a strength and a weakness. It is a strength in that allows for simple assumptions that can be clearly stated and uses only a limited number of parameters. It is a weakness in that it does not take into account a lot of uncertainty, both in the process being modeling as well as in the individual parameters describing that process. For example, the model is essentially deterministic – only one outcome is possible from a given set of inputs. The model cannot, therefore, tell a policy maker the likelihood that a particular strategy will achieve a particular goal, only whether or not goal is expected to be met under the stated set of assumptions.

Even considering only the hatchery "H", users of the model should realize that not all potential ecological or genetic interactions between hatchery and natural fish are included in the model. In particular, it is not entirely clear if ecology effects such as competition are modeled (they may be implicitly). Interspecific effects (e.g., effects of a coho hatchery on a natural chinook population) are not modeled. The model does include effects of genetic domestication, but other potential genetic effects are not included (e.g., effects on effective population size). The model is not spatially explicit, so effects on spatial structure cannot be evaluated.

Despite these limitations, I think the model is potentially extremely useful. In particular, it focuses attention squarely on the problem of how to successfully integrate (in the broad sense, not necessarily the HSRG sense) hatchery and natural production. <u>As a hatchery production planning tool, it is a HUGE step forward in that it actually models the natural population and how the hatchery interacts with it.</u> This is certainly better than the common alternative of simply ignoring the natural population. If it is used in the spirit that the HSRG intends it to be, I think it will serve a valuable role in evaluating the impacts of current and planned hatchery production levels.

Answers to specific questions:

6) Is the model consistent with viable salmon population (VSP) criteria? What are the strengths and weaknesses?

The model focuses on two of the VSP criteria: productivity and abundance. The model does not deal explicitly with either spatial structure or diversity. The model touches on diversity in its treatment of hatchery domestication, but this is largely heuristic in that it is not modeling any specific trait.

Strengths:

> Simplicity. One strength of the model is its simplicity. It has a small number of parameters which are, for the most part, easy to understand and transparent (although not always easy to estimate). The most useful aspect of the model may be that it simply forces people to state assumptions about how a hatchery and natural population are going to relate to each other, and then clearly illustrates the consequences of those assumptions.

Ease of Use

The model is very easy to use and the output is easy to understand.

Weaknesses:

> The model does not deal with all potential interactions between hatchery and natural fish. For example, it is not really clear how the model deals with ecological interactions (there is a 'competition factor' parameter, but I'm not sure what this is). It also does not deal with interspecific interactions, for example the impacts of a coho hatchery program on a natural chinook population. The model also ignores genetic interactions such as effects on effective population size. None of these are necessarily flaws (indeed, a model that tried to deal with all of these things might in fact be less useful than one that does not), but when evaluating the results of the model it is important to keep in mind the factors that it does not consider.

7) What are the strengths and weaknesses of the scientific assumptions of the model? Are these assumptions adequately documented or transparent in the model? Can the model be validated?

Strengths:

One of the strengths of the model is simply that it does keep track of natural and hatchery production in a simply and easy to understand way. If this model IS used to help plan or modify hatchery programs, this would be an improvement over the common (although not universal) practice of mostly ignoring natural populations or simply believing that the hatchery program "will work" in a certain way.

The model also allows for domestication due to hatchery production, potentially a very important factor to consider. This is done using the model described by Ford (2002), which assumes that fitness is determined by the trait value at a single normally distributed trait. This is of course completely unrealistic, since in reality many traits contribute simultaneously to an organism's fitness. Some biological details, such as phenotypic plasticity, are also not included in the model. Nonetheless, as a heuristic tool, this approach is reasonable, and certainly is far better than simply ignoring the effects of domestication. When using the model, however, it will be important to always test the sensitivity of the results to variation in the selection model's parameters. Ground truthing the model with some real data would be nice. For example, there are several empirical estimates of relative hatchery/wild fitness after a known number of generations of closed hatchery breeding. Could these be used to parameterize the domestication part of the model?

Weaknesses:

The model's simplicity is a strength, but it is also a weakness, particularly if the model is going to be used in any sort of quantitative way to attempt to determine if a particular suite of actions is likely to meet recovery goals. For example, habitat attributes in the model appear simply as the productivity and capacity terms in a Beverton-Holt production function. If the model is intended to help planners determine the effects of habitat restoration (or degradation) on future salmon population status, this will not be adequate. The model also assumes discrete generations – perfectly fine (and even desirable) if the model is going to be used as a heuristic tool to broadly explore alternative scenarios, but not adequate if it is intended to be used in a predictive fashion. The model is also essentially deterministic, so it can't really tell policy makers the probability that a particular strategy will lead to a particular outcome.

8) Does the model incorporate adequate uncertainty (e.g. environmental and demographic stochasticity) for decision making? Is it clear how uncertainty in different parameters affects the certainty of the results?

The model allows for stochastic SAR's and variable ocean regimes, but is otherwise completely deterministic. It would be useful to illustrate to decision makers the range of variation to be expected, so incorporating, for example, variation in freshwater survival/capacity would be a useful improvement. For any given model run, parameter uncertainty is not illustrated in the results – this would need to be done by manually varying the parameter values.

9) Is the choice and number of parameters in the model appropriate? Can the parameters be estimated from existing data or do they rely on expert opinion?

Natural production parameters: I was a little confused about how the model treated the natural production parameters. It allows the user to input BH productivity and capacity parameters in terms of adult recruits. It also allows the user to vary fecundity and smolt to adult survivals, as well as enter capacity parameters for eggs and adults. It then calculates egg to fry survival and smolt capacity (as far as I can tell). I found all of this to be a little confusing. For example, I tried to enter the parameter values for a population I am familiar with, and had to do a lot of fiddling with the Main Page productivity and capacity parameters to get the smolt numbers in the observed range. Rather than having the user enter production and capacity estimates in terms of adult recruits, I wonder if it would be more useful to break down the lifecycle and have the user enter these for each life stage and then have the program calculate overall values in terms of adult recruits? I'm thinking, for example, of a coho stream where density dependence occurs primarily at the fry-smolt stage – I'd like to be able to define the capacity in terms of smolts, and then let the number of adults vary as a function of the SAR's. It might be useful to make these parameters stochastic, as well. For example, the user could enter a mean and standard deviation for egg-smolt survival and smolt to adult survival, and a capacity for each.

The production and capacity parameters can in theory be estimated from data, although determining how they would change under alternative habitat scenarios is extremely non-trivial. The hatchery production parameters are usually either estimatable or are simply known values. The domestication selection parameters will not in general be estimated, but must come from expert opinion.

10) Is the model easy to use? Are the results easy to interpret?

Yes, the model is very easy to use, and the results are clearly presented.

Review 2: Reviw of AHA

Paul McElhany
January 26, 2005

Model Strengths:

A relatively simple life cycle model that partitions mortality among various factors can be an extremely useful management tool if considered in the appropriate context. In addition to providing this life stage evaluation, the model explicitly examines how hatchery management decisions affect domestication in mixed hatchery-wild populations. The model provides a compelling heuristic demonstration of the relationships between habitat, harvest, hatchery management, domestication, and stock performance. Understanding these heuristic relationships and the qualitative consequences for current and future management actions is critical. The ability to do “what if” type scenario analysis with harvest, hatcheries and habitat is a useful approach.

Model Concerns:

Documentation and Scientific Review

The model is currently undocumented, making scientific peer review impossible. Without an independent scientific review based on adequate documentation, it would be irresponsible for managers to assign much weight to the quantitative predictions of the model in making expensive and potentially risky decisions. Decisions need to based on “best available science” and current “best available” scientific practice relies on the independent review process.

The AHA Excel spreadsheet is available to reviewers and it is theoretically possible to recreate the model methods from the spreadsheet. However, this is not a practical or accepted way of documenting a model. In appendix B of this review, I include a rough start at documenting some of the model equations based on the Excel spreadsheet. Documenting the entire model in this fashion would be extremely time consuming, whereas the authors of the model could document it relatively quickly.

The model also seems to be changing fairly quickly, which is understandable and expected as the scientific process is never “done”. However, this makes review particularly challenging, since the model reviewed may not be the same model that ends up being applied. As the model evolves, it seems to be getting more complex. This make written documentation even more imperative, since evaluation of the model from the spreadsheet alone becomes increasingly problematic.

Although I have many comments on the model, I do not consider this an adequate independent review, only some thoughts based on partial information. A complete review will be required once the documentation is available.

Uncertainty

The model provides an inadequate assessment of uncertainty. Model inputs and outputs are single point estimate values that do not indicate the level of confidence associated with the model predictions. This does not represent "best available science" since contemporary methods consider the crucial issues of model uncertainty and sensitivity. This issue is particularly critical when specific model predictions are used to make management decisions about particular populations. As a heuristic tool, point estimates for input and output may be useful to describe qualitative responses (e.g. if pNOB increases, domestication increases.) However, if we want to design a hatchery program based on model outputs we need to know how much confidence to place in model results and the consequences of making an error. Again, it would be irresponsible for managers to assign much weight to the quantitative predictions of the model in making expensive and potentially risky decisions until uncertainty is incorporated into the model and sensitivity analyses have been conducted.

The model currently allows for some exploration of alternative model inputs by presenting five different scenarios. However, an approach that provides clear information on model uncertainty would be valuable. For example, inputs could be entered as distributions that represent the uncertainty in knowledge and outputs could be presented as distributions rather than "answers".

The model does contain one stochastic component. The "variable SAR" option uses randomly generated marine productivity parameters. Model results are presented one at a time and there is no way to evaluate the distribution of outputs generated by this stochastic variable. It is also baffling why this single aspect of the model is stochastic when otherwise the model is completely deterministic. Why is it useful to include stochasticity for this particular parameter and not any of the other parameters, which are also highly variable?

Model Structure

Life Cycle Model

The life-cycle model is a fairly straight forward cumulative Beverton-Holt recruitment model. There are two spawning groups that exchange migrants (the natural spawning group and the hatchery spawning group.) The model has only four basic life stages (i.e spawner->egg, egg->smolt, smolt->adult[preharvest], adult->spawner[posthavest]). Having a limited number of life stages is appropriate given there are few data to parameterize something more complex. Even with this limited number of life stages, the model can still be useful at suggesting areas of management focus (e.g. freshwater habitat vs. harvest). In looking at a preview of the January 2005 version of the AHA model, it seems that a few more life stages and mortality factors have been added compared to the September 2004 version. While the data may be available to support this increased complexity for some populations, it will be important to not over-parameterize the model as it evolves.

The variable SAR portion of the model seems extremely ridged and would benefit greatly from uncertainty/sensitivity analysis before being used for management decisions. The model only allows a singe 10 year repeating pattern of productivity. The pattern is undoubtedly more complex than this and I suspect that model predictions could vary significantly depending on marine variation assumptions.

Hatchery effects in the "All H Analyzer" are restricted to domestication affects (though the model allows some density dependent effect of hatchery fish in the ocean.). The ecological affects of hatchery fish need to be considered for the model to be truly "All H".

Fitness Model

If the "include fitness" option is not selected, the model keeps track of pNOB and pHOS but the values do not affect survival of the fish in the hatchery or wild. If the "include fitness" option is selected, the program uses an explicit genetics model to modify survivals based on pNOB and pHOS. Empirical estimates for most of the parameters in this model are sketchy at best. Although the model can serve as a useful heuristic tool for considering the consequences of pNOB and pHOS, it is problematic to use the model to identify genetically "safe" hatchery programs. For example, a lack on information on the strength of selection prevents the identification of threshold values of PNI with a low enough level of domestication that a "viable" population can be maintained (i.e. one that can persist in the wild.)

A first approach to this issue might be a sensitivity analysis exploring the consequences of alternative parameter sets. A next step might be removing the entire explicit genetic model and replace it with something simpler that relies on the qualitative conclusions of the model and empirical information without reference to the dozen or so unestimatable parameters in the explicit genetics model. Such a simpler framework could make use of empirical data on domestication effects (e.g. the Yakima project) that do not have data on all the individual parameters. For example we may be able to estimate the over all level of domestication from a particular program, but we will seldom, if ever, know omegaw.

The basic conclusion of the Ford modeling, Busack analysis, HSRG guidelines and AHA model that a population with low pHOS and high pNOB will result in less domestication in an integrated program than a population with high pHOS and low pNOB is very solid, though "how much is enough" is less clear. [This assumes a prior decision that an integrated program is appropriate and desirable.] If we focus on the basic qualitative conclusion and the need for substantial change for many hatchery programs, we should be able to make some progress, with or with out complex models.

Model Parameters

The precision with which the parameters in the model can be estimated vary greatly, again suggesting the value of considering uncertainty in interpreting results. One of the more challenging parameters to estimate is the overall preharvest productivity function of the stock. There are two basic ways this is done; from abundance time series or from habitat data. Fitting recruitment curves to empirical estimates of spawner abundance could provide the Beverton-Holt parameters used in the model. However these estimates can be highly uncertain. In an analysis of abundance time series for salmon and steelhead in the Willamette and Lower Columbia comparing different recruitment functions, we found the data contained some information on population capacity, but were in general spectacularly uninformative with regards to population productivity. The estimates of productivity are critical drivers of population response to harvest and hatchery actions in the AHA model.

The other approach to estimating over all abundance and productivity relies on inference from habitat condition. The AHA users guide suggests that EDT can be used to estimate values for AHA. The EDT model suffers to an even greater degree than AHA from a lack of documentation, a lack of independent review and a lack of sensitivity analysis. A number of factors suggest that outputs from EDT may be highly uncertain. AHA predictions based on EDT input inherit all the uncertainty that exists in EDT plus add some more uncertainty associated with the additional parameters in AHA.

Another source of uncertainty in the AHA life-cycle model involves determining which life stages are density dependent and which are density independent. The users guide does not provide suggestions on how to parameterize this. The consequences of uncertainty about this issue should be included in interpreting results.

AHA, the HSRG Guidelines and Viability

The HSRG guidelines for integrated hatcheries are focused on the issue of domestication and describe largely arbitrary thresholds for hatchery program targets (e.g. PNI >0.5 or PNI > 0.7). The guidelines do not consider thresholds for population viability, where viability is defined as a population that would persist if the hatchery were removed. In Appendix A of this review, I explore viability thresholds based only on demographic considerations (not genetic) expressed in the parameters of the HSRG guidelines (e.g. pNOB and pHOS). As indicated by these preliminary analyses and depending on the relative size of the hatchery broodstock and the natural spawning group, populations may need to have a PNI significantly higher than that suggested by the HSRG guidelines to be demonstrably self-sustaining.

The AHA model could explicitly consider viability and it would be helpful to present information on whether a population would persist if the hatchery were removed. This is the primary consideration under the ESA (at least until NOAA finalizes a hatchery listing policy.)

Open Source Modeling

This is somewhat an aside, but I urge that this and future salmon modeling be developed under the Open Source framework (http://www.opensource.org/docs/definition.php). Open Source is a software development approach that allows open access to all source code so that anyone may understand the code and make modifications that improve the project. A number of incredibly success, complicated, and critical projects have been developed under this framework including Linux, Oracle, most the internet machinery and software used for the human genome project. Open source promotes model (and software) reliability and quality by supporting independent peer review and rapid evolution of models with input from the entire modeling community. It is worth understanding how open source works before adopting a new model for wide regional application.

So far, the AHA model source code is available in the Excel spreadsheets. This openness should be maintained and expanded on with adequate documentation and the creation of a convenient forum to allow a user community to develop and evolve the model if enough people find it valuable.

Conclusions

The AHA model has potential to help understand the basic relationships between habitat, harvest and hatcheries. It provides explicit consideration of the factors that drive domestication. However, it is premature (and indeed would be irresponsible) to apply specific quantitative results of the model to salmon management questions because the model has not been independently reviewed, and the model provides no evaluation of uncertainty in the predictions. The fact that the model will be parameterized with inputs that are known to be highly uncertain increases concern that the model point estimate predictions and conclusions may be wrong. (whereas a distribution of potential outputs considering uncertainty may be “right”)

Appendix A: Conditions for Viability in the Language of the Golden Triangle

Variable Definitions:
NOS = Natural Origin [natural] Spawners
HOS = Hatchery Origin [natural] Spawners
SOS = Size of [natural] Spawning population = NOS + HOS
pNOS = proportion of [natural] spawners that are of natural origin
pHOS = proportion of [natural] spawners that are of hatchery origin

NOB = Natural Origin [hatchery] Broodstock
HOB = Hatchery Origin [hatchery] Broodstock
SOB = Size of [hatchery] Broodstock = NOB + HOB
pNOB = proportion of [hatchery] Broodstock that are of natural origin
pHOB = proportion of [hatchery] Broodstock that are of hatchery origin

As a condition of natural self-sustainability, the number of natural origin returns needs to be greater than or equal to the total number of spawners:

$$\frac{NOS + NOB}{SOS} \geq 1 .$$

Some algebra at the viability threshold…

$$
\begin{aligned}
&SOS = NOS + NOB \\
&SOS = (pNOS * SOS) + (pNOB * SOB) \\
&SOS - (pNOS * SOS) = pNOB * SOB \\
&SOS * (1 - pNOS) = pNOB * SOB \\
&\frac{SOS}{SOB} = \frac{pNOB}{1 - pNOS} = \frac{pNOB}{pHOS} \\
&SOS * pHOS = SOB * pNOB \\
&HOS = NOB
\end{aligned}
$$

Thus the viability condition is

$$NOB \geq HOS\,.$$

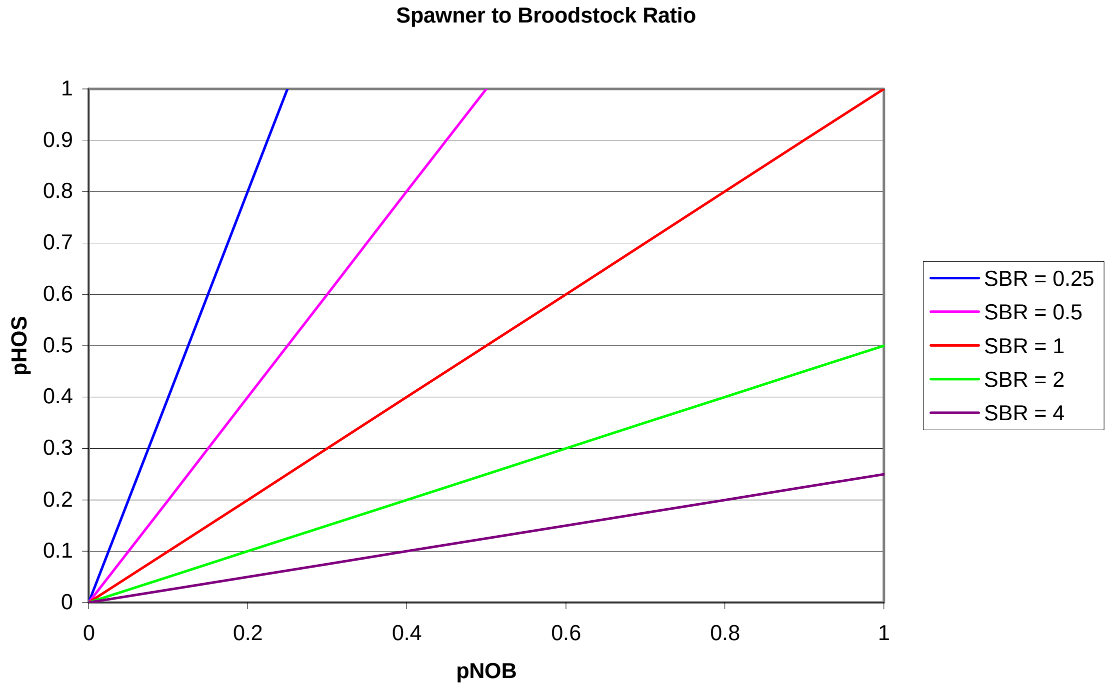
We can define a new variable to plot on the graph of the golden triangle.
SBR = Spawner to Broodstock Ratio

$$SBR = \frac{SOS}{SOB}$$

Some algebra at the viability threshold leads to the viability condition…

$$pHOS \leq \frac{pNOB}{SBR}$$

Graphed, it looks like this:



The conditions for a viable population get smaller as the spawner to hatchery broodstock ratio increases because an increase in the SBR leads to a large relative number of HOS. (You can't just increase the size of the hatchery broodstock unless you have enough natural origin fish to meet the target pNOB.)

Viability and HSRG/WDFW/NWIFC Guidelines

The HSRG et al. describe "Operational guidelines for integrated programs" (June 21, 2004). These guidelines could potentially all be met, yet the population still not meet the viability conditions described above. The HSRG et al. have four quantitative guidelines:

- Guideline #2 is pNOB>pHOS
- Guideline #3 for "significant" populations pNOB>2.3*pHOS
- Guideline #4 is pNOB >0.1
- Guideline #5 is SOB>NOS

The threshold Guideline #5 can be rewritten in terms of SBR as

$$pHOS < 1 - \frac{1}{SBR}$$

The relationship between the HSRG et al guidelines and the viability conditions for the situation where there are four times as many total spawners in the wild as there are fish in the brood stock (i.e. SBR=4) are shown in Figure 2. For the HSRG lines, the vertical part of the line is from guideline #4, the angled part of the line is from guideline #2 (or #3 for a "significant" population) and the horizontal part of the line is from guideline #5.

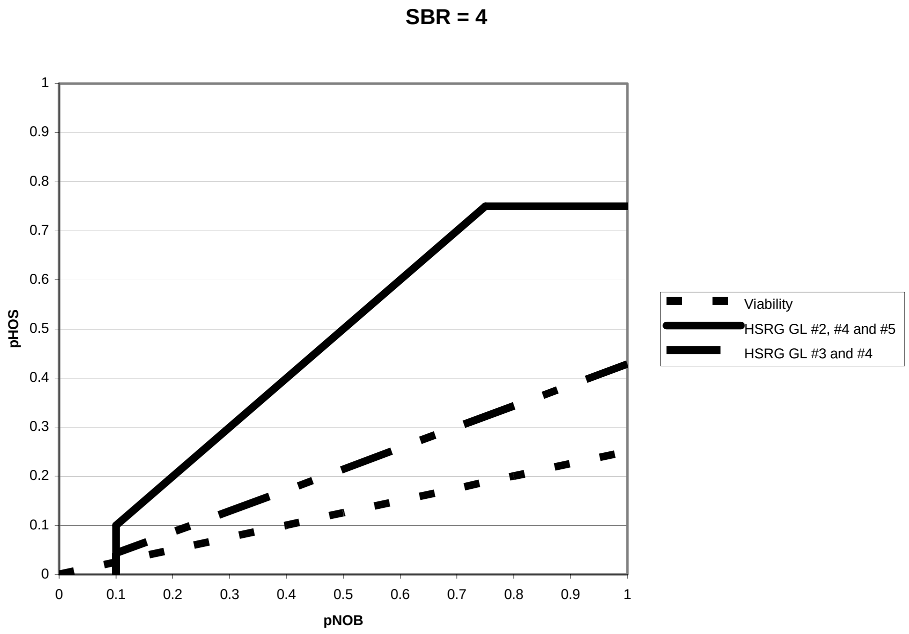


Figure 2.

Discussion:
This describes the equilibrium conditions for a demonstrably self-sustaining population. For use as a threshold condition, it is assumed that all returning natural fish not taken as brood stock are allowed to spawn in nature. This is post all mortality sources (including harvest and removal of any "surplus" fish that don't spawn anywhere.) [I'm still working on a complete list of caveats and assumptions …].

Not every population is expected to be naturally self-sustaining, so not every population would be expected to meet these conditions. However, these conditions serve as a useful reference point in determining the current status of a hatchery-natural system and for setting goals based on the HSRG et al. parameters (a.k.a. the language of the "golden triangle of genetic goodness.")

Appendix B: A Partial Field Guide to the Equations in AHA

(draft- not verified by HSRG)

Parameters:
Parameters in yellow are user inputs. The parameter symbols used in this field guide are generally made up by me, because the names in the spreadsheet are too long for tidy presentation of the equations. However, I tried to be consistent where practical. The form of the equations also may differ from that in the spreadsheet. The most convenient way to structure the spreadsheet did not always seem the clearest way to express the equations on paper. (I'm sorry that the subscripts get a little crazy, but there is a lot to keep track of.)

Natural Productivity and Capacity (parameters of Beverton-Holt function)
p_{n1} = spawner to egg productivity in the wild
p_{n2} = egg to smolt productivity in the wild
p_{n3} = smolt to spawner productivity in the wild

c_{n1} = egg capacity in the wild
c_{n2} = smolt capacity in the wild
c_{n3} = spawner capacity in the wild

P_n = total life cycle (cumulative spawner to spawner) productivity in the wild; Called "habitat productivity" in AHA
C_n = total life cycle (cumulative spawner) capacity in the wild; Called "habitat capacity" in AHA

Calculation of p_{n2} and c_{n2} is base on solving the Moussali and Hilborn (1986) cumulative Beverton-Holt equations for the egg to smolt stage given the total life cycle parameters and all the other life stage specific parameters:

$$p_{n2} = \frac{P_n}{p_{n1} * p_{n3}}$$

$$c_{n2} = \frac{1}{\frac{p_{n3}}{C_n} - \frac{1}{c_{n1} p_{n2}} - \frac{p_{n3}}{c_{n3}}}$$

If the AHA parameter "Variable SAR" is set to no ("n"), the user specified p_{n3} (in field "Smolt to Spawner" on Natural Component sheet) is used for every generation in the simulation. If the Variable SAR parameter is set to yes ("y"), the p_{n3} value varies from generation to generation in a particular pattern, which is defined as follows:
Generations are designated as either Low (L), Medium (M), or High (H) productivity.
The pattern off L, M and H generations follows a repeating 10 generation pattern of:
MHMLLLLLLLMHMLLLLLLLMHMLLLLLLLMHMLLLLLLL…
This pattern is fixed in the AHA version being evaluated.
To create a pattern of p_{n3} values that follows this general pattern with a bit of stochastic noise, a sequence of random *SARs* are generated by averaging three random lognormal values where the lognormal distribution used is a function of the whether the productivity level is L, M, or H.

	L	M	H
mean(*SAR*)	0.0056	0.0091	0.0209
var(ln(*SAR*))	0.051	0.048	0.135

For example the *SAR* in generation *i* is :

$$SAR_i = \frac{1}{3}\sum_{j=1}^{3} randLogNormal_j\left(prodLevel_i\right)$$

where $randLogNormal(prodLevel_i)$ is a random number drawn from a lognormal distribution with the parameters specified by the productivity level of generation *i*. The use of three random values has something to do with the conversion from years (units used in the original study referenced by AHA) to generations (units used in AHA).
The geometric mean value of p_{n3} is set by the user (field "Smolt to Spawner" on Natural Component sheet) and the following equation is used to obtain a sequence of p_{n3}'s that follow the SAR pattern but have the appropriate geometric mean:

$$p_{n3i} = \overline{p_{n3}} * \frac{SAR_i}{\overline{SAR}}$$

where $\overline{p_{n3}}$ is the user specified geometric mean of p_{n3} and $\overline{SAR}$ is the geometric mean of all the SAR_i values.
Because of the random values, you will get a slightly different set of outputs every time you recalculate the spreadsheet when Variable SAR is set to yes. (To recalculate all the values in an Excel spreadsheet, press CTRL-ALT-F9.)
If the model is run with variable SAR, the cumulative productivity (P_n) varies every generation:

$$P_{ni} = p_{n1i} p_{n2i} p_{n3i}$$

Except for the SAR option, the model is completely deterministic. There is no systematic way to look at the distribution of outputs caused by the stochastic inputs; you can only look at results from a particular random draw one at a time.

Hatchery Survival and Capacity

Productivity in the hatchery (spawner to egg and egg to smolt) is density independent [however, on the time series pages, there are Beverton-Holt hatchery egg and smolt capacity parameters that are never really used for anything]. Depending on the user specified parameters, density dependence could potentially affect hatchery origin adults.

p_{hh1} = spawner to egg productivity of hatchery origin fish in the hatchery = hatchery eggs per female* hatchery % female* hatchery female prespawning survival

p_{nh1} = spawner to egg productivity of natural origin fish in the hatchery = phh1 * relative productivity of eggs from natural origin fish compared to productivity of eggs from hatchery origin fish

p_{hh2} = egg to smolt survival of offspring from hatchery origin fish in the hatchery (this is incorrectly named "Fry to Smolt Surv." in the AHA spreadsheet)

p_{nh2} = egg to smolt survival of offspring from natural origin fish in the hatchery = p_{hh2} * relative egg to smolt survival of offspring from natural origin fish in the hatchery compared to egg to smolt survival of offspring from hatchery origin fish in the hatchery

p_{h3} = smolt to spawner survival of hatchery fish

P_h = spawner per spawner productivity in the hatchery ("recruits per spawner")

The smolt to spawner survival of hatchery fish is calculated by solving for p_{h3} given the other life stage survivals and the overall hatchery productivity:

$$p_{h3} = \frac{P_h}{p_{h1} * p_{h3}}$$

The relative survival of *HOR*s to *NOR*s for the smolt to spawner stage is $\frac{p_{h3}}{p_{n3}}$,

Where

HOR = preharvest hatchery origin recruits

NOR = preharvest natural origin recruits

If Variable SAR is selected, the smolt to spawner survival of hatchery origin fish follows the same relative pattern as the survival of natural origin fish, with

$p_{h3i} = \overline{p_{h3}} * \frac{SAR_i}{\overline{SAR}}$, where $\overline{p_{h3}}$ is p_{h3} calculated as described above.

If the model is run with variable SAR, the cumulative productivity of hatchery origin fish (P_h) varies every generation:

$$P_{hi} = p_{h1i} p_{h2i} p_{h3i}$$

c_{h1} = capacity of eggs in the hatchery = 10^{19} [never used in model]
c_{h2} = capacity of smolts in the hatchery = 10^{19} [never used in model]
c_{h3} = capacity of recruits of hatchery origin= capacity of recruits of natural origin = c_{n3}

N_{h2} = number of hatchery smolts = "hatchery smolt release"=$C_h p_{h1} p_{h2}$

F_{c3} = smolt to adult competition factor of HORs relative to NORs

Harvest
Harvest is set as a constant exploitation rate that can be set independently for *HOR* and *NOR*. The parameter are:
g_h = exploitation rate of HORs
g_n = exploitation rate of NORs
g_h^* = target exploitation rate of HORs
g_n^* = target exploitation rate of NORs

[the "g" symbol refers to "grilled".]

Broodstock and wild spawning composition
$pNOB_t$ = target ("goal") proportion natural origin broodstock
$pHOB_t$ = target ("goal") proportion hatchery origin broodstock = 1-pNOB_t
$pHOS_t$ = target ("goal") proportion hatchery origin wild spawners
$pNOS_t$ = target ("goal") proportion natural origin wild spawners = 1-pHOS_t

$pNOB_r$ = realized proportion natural origin broodstock
$pHOB_r$ = realized proportion hatchery origin broodstock = 1-pNOB_t
$pHOS_r$ = realized proportion hatchery origin wild spawners
$pNOS_r$ = realized proportion natural origin wild spawners = 1-pHOS_t

HOR_h = target proportion HOR destined for hatchery
HOR_n= proportion HOR destined for river = 1- HOR_h

Abundance parameters

N_{n1} = number of natural origin eggs
N_{n2} = number of natural origin smolts
N_{n3} = number of natural origin recruits
N_{n3+} = number of natural origin adults after harvest

N_{h1} = number of hatchery origin eggs
N_{h2} = number of hatchery origin smolts
N_{h3} = number of hatchery origin recruits = *HOR*
N_{n3+} = number of hatchery origin adults after harvest

G_n = number of natural origin fish harvested = N_{n3+} - N_{n3}

G_h = number of hatchery origin fish harvested = N_{h3+} - N_{h3}

NOS = S_{nn} = natural origin wild spawners
HOS = S_{hn} = hatchery origin wild spawners
SON = $S_{n\_}$ = sum of natural origin spawners = NOS+NOB
NOB = S_{nh} natural origin broodstock
HOB = S_{hh} = hatchery origin broodstock
SOB = $S_{\ h}$ = sum of broodstock = NOB+HOB
$S^*_{\_h}$ = hatchery broodstock abundance goal

X_{hh} = "surplus" (or eXtra) hatchery origin fish at the hatchery
X_{hn} = "surplus" (or eXtra) hatchery origin fish on the natural spawning grounds

$N_{h3(0)}$ = initial number of hatchery origin adults
$N_{n3(0)}$ = initial number of natural origin adults

S^*_{nn} =minimum natural origin wild spawners ("min NOR Escapement")

Model Without Fitness

$$N_{h1(i+1)} = S_{hh(i)} p_{hh1} + S_{nh(i)} p_{nh1}$$

$$N_{h2(i+1)} = S_{hh(i)} p_{hh1} p_{hh2} + S_{nh(i)} p_{nh1} p_{nh2}$$

$$N_{h3(i+1)} = \frac{p_{h3} N_{h2(i)}}{1 + \frac{p_{h3}}{c_{h3}} \left(N_{h2(i)} F_{c3} + N_{n2(i)} \right)}$$

$$G_{h(i+1)} = \max\left(g_h, \frac{G_{n(i+1)}}{N_{n3(i+1)}} \right) N_{h3+(i+1)}$$

$$N_{h3+(i+1)} = N_{h3(i+1)} - G_{h(i+1)}$$

The equation for N_{h3} is a Beverton-Holt density dependent function.
It is not clear to me why G_h is a function of G_n, it seems the appropriate equation is simply $G_h = g_h N_{h3}$.

The model allows the user to set a start generation (*hStart*) and stop generation (*hStop*) for the hatchery program. If the generation, i, is NOT $hStart <= i < hStop$, then $S_{nh(i)} = 0$. If $hStart <= i < hStop$, then there are two ways of determining $S_{nh(i)}$. If the user specifies Random Broodstock collection (*R*), the broodstock will be taken in proportion to their abundance in the return after harvest and after meeting the minimum NOR escapement constraint ($pNOB_t$ is ignored):

$$S_{nh(i)} = \min\left(\max\left(0, N_{n3+(i)} - S^*_{nn}\right), S^*_{\_h} * \frac{N_{n3+(i)}}{N_{n3+(i)} + N_{h3+(i)}} \right)$$

[Note: because of the min NOR escapement constraint, this is not always proportional to the run frequencies.]

If the Random broodstock collection option is not selected, $S_{nh(i)}$ is calculated to attain the the pNOB goal ($pNOB_t$) to the extent possible while meeting the minimum NOR escapement constraint:

$$S_{nh(i)} = \min\left(pNOB_t * S^*_{\_h}, N_{n3+(i)} - S^*_{nn}\right)$$

If $hStart <= i < hStop$ and the user selects Random Broodstock Collection, $S_{hh(i)}$ is the smaller of all hatchery origin fish after harvest or the number of hatchery origin fish needed to make the broodstock target, given the number of natural origin fish taken into the broodstock:

$$S_{hh(i)} = \min\left(S^*_{\_h} - S_{nh(i)}, N_{h3+}\right)$$

[Note: because of the min NOR escapement constraint, this is not always proportional to the run frequencies.]

If the user does not select Random Broodstock Collection, becomes a function of the target pNOB and the target HOR destined for the hatchery.

If $hStart <= i < hStop$ and the user does not select Random Broodstock Collection, and the target $pNOB_t > 0$, $S_{hh(i)}$ is:

$$S_{hh(i)} = \min\left(\max\left(0, \min\left(\frac{S_{nh(i)}}{pNOB_t}, S^*_{\_h}, N_{h3+(i)}\right) - S_{nh(i)}\right), HOR_h * N_{h3+(i)}\right)$$

[this equation could use some explanation.]

If $hStart <= i < hStop$ and the user does not select Random Broodstock Collection, and the target $pNOB_t = 0$, $S_{hh(i)}$ is:

$$S_{hh(i)} = \min\left(\max\left(0, \min\left(S^*_{\_h}, N_{h3+(i)}\right) - S_{nh(i)}\right), HOR_h * N_{h3+(i)}\right)$$

The "surplus" hatchery fish returning to the hatchery is

$$X_{hh(i)} = \max\left(0, N_{h3+(i)} - S_{hh(i)} - S_{hn(i)} - X_{hn(i)}\right)$$

The realized exploitation rate for hatchery fish is

$$g_{h(i)} = \max\left(g^*_h, \frac{G_{n(i)}}{N_{n3(i)}}\right)$$

[Not sure why this is a function of the natural origin fish]

with the number of harvested hatchery origin fish being

$$G_{h(i)} = g_{h(i)} * N_{h3(i)}$$

This is as far as I got…

Review 3: Comments on the AHA model and associated documents

Robin Waples

I have not tried to work through the model or the spreadsheets, so I can't comment on how user friendly it is. However, I am familiar with characteristics of the hatchery-wild fitness module so will focus my comments on that, as well as on some potential uses (and misuses) of the AHA model. The model has some attractive features that suggest it might be able to provide useful insights into some difficult problems in salmon management. On the other hand, it has some limitations that should be understood. Failure to properly consider these limitations could lead to inappropriate uses of the model with potentially far-ranging consequences for natural populations. These points are discussed in more detail below.

Useful features of the AHA model

The most attractive feature of this model is that it can incorporate information relevant to three of the Hs. Hatchery, harvest, and habitat issues are closely related, and analyses that consider them separately or only in pairs will generally be incomplete. The model should allow managers to gain insights into the tradeoffs involved in trying to manage complex systems, and could help guide some tentative conclusions about relative merits of different types of management programs.

Caveats regarding AHA

The major caveat is that this is only a model. Like all models, it tries to capture some essential elements of a very complex reality within a finite number of parameters. This of necessity involves major assumptions and simplifications to make the model tractable. Because this model tries to capture some very complex interactions, the necessary assumptions and simplifications are substantial. As a consequence, it will require extensive ground-truthing to determine whether the outputs of the model are an accurate prediction of reality. To do this validation process properly would be a very major effort that could not be accomplished anytime in the near future. Some of the strictly demographic predictions might be able to be validated relatively soon, but conclusions about effects on long-term fitness and viability cannot. A major danger is that these caveats and this factual reality will be ignored by those who would like to use the model now to help make management decisions.

This module does take advantage of recent published literature, esp the "Ford" model and related papers. The Ford model is useful for evaluating effects of selection in two different environments on a fitness trait. However, this model makes a rather large number of assumptions that are obviously not met in the real world. It might be argued that violation of these assumptions will not dramatically alter results of the model, but at this point whether that is indeed the case cannot be known with any certainty. Therefore, this model should be viewed as one (of potentially very many) hypothesis about how selection might operate in hatchery-wild systems. In theory, testing this model with empirical data is possible, but it is hard to see how that can be done with any rigor without a major, long-term effort.

In my opinion, a major deficiency of the existing AHA model and documentation is the absence of meaningful consideration of the question, "*How much reduction in fitness can a natural population sustain and still retain the ability to sustain itself (without hatchery influence) in natural habitat?*" This is absolutely THE most important question from the perspective of wild salmon conservation. Instead of focusing on this question, the AHA model focuses on reaching a point at which the natural environment is expected to dominate selection of the combined system, which according to the model occurs when the ratio pNOB/(pHOS+pNOB) > 0.5. Even if this actually turns out to be true in reality (which has not been demonstrated), achieving a ratio > 0.5 simply would mean that the equilibrium fitness optimum for the hatchery-wild system is closer to the wild optimum than to the hatchery optimum. This would in no way guarantee that the fitness of the combined population would be sufficient to sustain itself naturally if the hatchery were terminated. Even requiring that the ratio exceed an arbitrary higher value (e.g., 0.7 as proposed) would not guarantee viability; substantial losses of fitness compared to the pristine unsupplemented condition can be expected even with pNOB/(pHOS+pNOB) = 0.7.

Integrated and segregated programs

In general it is reasonable to recognize two general classes of hatchery programs--integrated and segregated. The AHA model and other review documents focus heavily on integrated hatchery programs, so I will make some general comments about this issue here, followed by some more specific comments below.

In the last decade, and especially in the last 5 years, managers in the Pacific Northwest have moved strongly toward integrated programs as a solution to management and conservation problems. Integrated programs have definite benefits under some scenarios, but, in my opinion, this approach is being uncritically endorsed for a wide range of scenarios for which it is not appropriate.

The only scenario for which an integrated program is clearly superior to a segregated program is the following:

Scenario 1. A natural population faces high short-term risk and hatchery supplementation is the most feasible short-term conservation measure. All hatchery programs, regardless how enlightened, entail a high degree of uncertainty and a high degree of risk to natural populations. If the natural population is already at high risk, the potential benefits of hatchery supplementation may outweigh the potentially deleterious effects. Whether this is likely to be the case should be evaluated after conducting a comprehensive risk-benefit analysis. If it is decided to use supplementation, then an integrated program is the only reasonable approach to take.

The only scenario for which a segregated program is clearly superior to an integrated program is the following:

Scenario 2. A hatchery program designed for mitigation and/or fishery enhancement can effectively accomplish these goals with little or no interaction with nearby wild populations, including both direct effects such as interbreeding, competition, and predation, and indirect effects such as overharvest of wild fish in mixed-stock fisheries targeting hatchery fish. This type of program has little or no potential benefit for the wild population, so integration has little to recommend it.

Neither of these two scenarios is common, although examples of both kinds can be found. Most situations involve some sort of combination of these scenarios. Some of these are discussed below.

The above considerations have some important implications for appropriate (and inappropriate) uses of the AHA model. Below I outline what, in my opinion, are appropriate and inappropriate uses.

Appropriate uses of AHA

This model clearly has potential usefulness as a heuristic tool to evaluate the relative merits of different management scenarios. Specifically, this model could be used to generate hypotheses about short-term and long-term effects of specific management regimes. These hypotheses could be tested empirically with properly designed experiments. This would best be viewed as a long-term process in which the model is periodically refined and updated based on empirical data.

The lack of empirical testing of this model means that one cannot have a high degree of confidence that predictions of the model will be even approximately correct. Therefore, as discussed below, this model should not be used as an excuse to avoid a precautionary approach to resource management. However, it seems reasonable that this model might provide useful, real-time guidance under one scenario. In this scenario (Scenario #1, above), the wild population is at substantial short-term risk of extinction and it is not feasible or possible to sufficiently alleviate the risk factors in the short term. In this case, a risk-benefit analysis might indicate that hatchery supplementation is a reasonable strategy to try. Assuming such a risk analysis has been conducted and a conclusion has been reached to supplement, it seems reasonable that results of this model can be effectively used in an adaptive management framework to help manage the program. Although the many uncertainties would remain, a program that is implemented has to be managed in some way, and this model could help guide that management.

Uses of AHA that would increase risk to natural populations

It is not hard to envision this model being used in ways that would increase, not reduce, overall risks to natural populations. For example, if managers were to conclude that a hatchery program has little or no effect on natural population fitness as long as pNOB/(pHOS+pNOB) > 0.5 or 0.7, it might lead managers to initiate new integrated programs or transform existing, largely segregated programs into integrated programs. In my opinion, this could be disastrous for the natural populations for several reasons.

1) There is virtually no empirical record demonstrating that hatchery supplementation is consistent with long-term viability of the supplemented population. The only proven template for long-term sustainability of salmon populations is an adequate supply of high quality habitat and suitable environmental conditions.
2) On the other hand, there is a substantial body of empirical evidence demonstrating lower fitness of hatchery-origin fish in the wild. Given the widespread concern for the status of natural salmon populations in the Pacific Northwest, it seems likely that few can afford the reduction in fitness that is inevitably associated with hatchery supplementation.

3) Given #1 and #2, it is apparent that widespread implementation of integrated hatchery programs, with or without use of the AHA model, would pose major risks to long-term sustainability of salmon resources in the Pacific Northwest. Given all the uncertainties about risks as well as benefits, it is reasonable, however, to consider implementing integrated supplementation programs on an experimental basis in a limited number of systems. This overall effort should be coordinated across regions and species to maximize the value of adaptive management information. The AHA model could play a role in helping to design individual programs and in the design of an overall, regionally-coordinated effort to experimentally evaluate salmon supplementation.

An important and common scenario to consider with respect to use of the AHA model is that of a failed segregated program (that is, a program that is designed to be segregated but which has failed to keep hatchery fish from interacting with wild fish). In many such programs, pNOB/(pNOB + pHOS) <<< 0.5. Assuming that changes are desired, what options should be considered and what role might the AHA model play in evaluating options? Some important considerations:

1) From the point of view of conservation of the wild population, in most cases the optimal solution would be to terminate the hatchery program. This type of program has no tangible benefits for the wild population, and if it cannot be effectively segregated, the only option to stop the deleterious effects is termination.
2) In some cases a risk-benefit analysis might indicate that developing a new, integrated program is the preferred option. This corresponds to Scenario 1, above, and the AHA model and other information could help guide program design.
3) In many cases, it will have already been decided, based on societal goals, that a hatchery program will continue to exist in the basin, even though it increases overall risks to the wild population. The question then becomes, how best to manage it? Some key elements to consider are:
    a) Integrated programs reduce genetic divergence between hatchery and natural fish, so genetic interactions that do occur will be less detrimental (on a per-interaction basis);
    b) Integrated programs generally will create more opportunities for both genetic and ecological interactions between hatchery and wild fish.

   Many managers throughout the Pacific Northwest seem to have gravitated toward integrated programs, which are justified biologically primarily on the basis of point a). In contrast, little attention has been paid to point b). However, the total effect of all hatchery-wild interactions is a function of the product of the number of interactions and the severity of each. A typical integrated program will have more interactions (both genetic and ecological) than a segregated program, but on average, each interaction will be less severe. A large number of people seem to have concluded that the net effects will be less in an integrated program, but I have never seen this addressed rigorously. It is easy to identify plausible scenarios under which a segregated program poses much less risk to a natural population than an integrated program. For example, assume a failed segregated

> program with pNOB/(pNOB + pHOS) <<< 0.5, as above, but also assume pNOB ~ 0 and pHOS ~ 10%. This program has no wild fish in its broodstock but leaks enough that about 10% of spawners are hatchery escapees. Assume now that this program were repackaged as a "conservation" hatchery with pNOB/(pNOB + pHOS) > 0.7 and about half the natural spawners being hatchery fish (pNOB ~ 0.5). Would this be better for the long-term health of the wild population? The documentation for the AHA model and the Integrated Hatchery Programs documents would suggest that the integrated program is better because the pNOB/(pNOB + pHOS) ratio is higher. However, the true answer is, NOBODY KNOWS WHICH SCENARIO WOULD BE BETTER; the outcome depends on too many poorly understood parameters. The AHA model cannot reliably answer this question.

Thus, an integrated program is not necessarily better or more conservation oriented than a segregated program. And in many (perhaps most) cases of failed segregated programs, the optimal solution from the point of conservation of wild populations is termination of the hatchery program. In this context, neither a segregated nor an integrated program represents a true conservation option; they are only more or less bad compared to the real optimal solution. The AHA model has some potential to help identify options that are less detrimental than others, but the model also has some limitations in this regard.

Relationship to VSP criteria

The review package asked for comments on consistency of the AHA model with VSP criteria. This can be evaluated both at the level of the population and the ESU as a whole.

At the population level, the model has little relevance to VSP criteria, which focus on self-sustainability of the natural population. As discussed above, the AHA model is largely silent on the absolute fitness of the natural population, focusing instead on relative fitness of the hatchery-wild system compared to the wild optimum. At this point there is no way to relate this relative value to absolute fitness or long-term viability. More generally, integrated hatchery-wild systems present severe challenges to evaluating sustainability in the absence of hatchery supplementation; they require one to consider a hypothetical scenario under which the unsupplemented population might be self-sustaining. The AHA model can be used in a general way to suggest which types of programs would be of relatively high or relatively low concern, but results of the model cannot reliably be used to demonstrate than any given program is consistent with wild population viability.

Most salmon ESUs contain multiple populations and allow, at least in theory, multiple scenarios that could lead to whole-ESU viability. Most or all viable-ESU scenarios might involve at least some populations at below VSP levels. Some of these might be sub-viable because of hatchery effects. The AHA model, in conjunction with other models and information, could help to rank in a rough way the relative viabilities of populations with hatchery influence, which would help facilitate "rolling up" population viability to the ESU level.

Comments on HSRG et al. Paper #1: Integrated Hatchery Programs

This document was provided along with the AHA model and deals with closely related issues, so I have provided some comments on it as well. A key omission is lack of a definition of or rationale for a segregated program. This makes it difficult to compare the relative merits of integrated and segregated programs. The definition of an integrated program is based on intent of the program rather than reality. This seems odd and could easily lead to an oxymoron is there is a disconnect between intent and reality.

Operational guidelines

#4 The scenario considered here, requiring 10% pNOB even when pHOS = 0, does not describe an integrated program. A program like this, which produces zero natural spawners, also has no potential benefit for the natural population. From this perspective, it is clear that requiring hatchery managers to mine the wild population to make up 10% of their hatchery broodstock is NOT a conservation measure. In this situation, the best scenario from the perspective of viability of the wild population would be to terminate the hatchery program so that no diversion of wild fish into the hatchery is necessary. In any case, it should be noted that 10% wild fish in the broodstock will not "avoid" divergence of that hatchery program from the wild fish, it will only reduce such divergence to some (poorly understood and not quantified) level.

#6 All of these hatchery practices are reasonable and can help reduce domestication effects. However, it must be remembered that the whole purpose of a salmon hatchery is to produce more adults than would be produced in the wild. If this is accomplished, genetic change compared to the pristine wild population is inevitable. Creating more natural conditions in the hatchery cannot eliminate domestication unless the hatchery is made identical to the wild, in which case there is no point to having a hatchery.

A key question for supplementation is whether naturally spawning hatchery fish "confer a net benefit." To whom does this benefit relate? The natural population, or society?

I don't understand how a supplementation program can be segregated, if the term supplementation implies that hatchery fish spawn in the wild. Perhaps this refers to a fishery enhancement program? Another reason to define what a segregated program is.

Conspicuously absent from the list of scenarios considered is any discussion of what should be the first step, which involves asking the following questions: What are the goal or goals for this population? Will starting a new integrated program (or transitioning from a segregated program) help to accomplish these goals? Since these topics are not considered in any detail in this document, the importance of this step should be emphasized here, and the reader should be directed to a document where they are discussed at length.

Does the guideline that effective size should be 500 or larger refer to Ne per generation or Nb per year? Where did the values 10% and ratio = .7 come from?

The creation of a single quasi-panmictic population undermining of structure and diversity can be visualized in Figure 3 (from McElhany et al. 2000) below.

Review 4: Some Comments Relating to the AHA Model

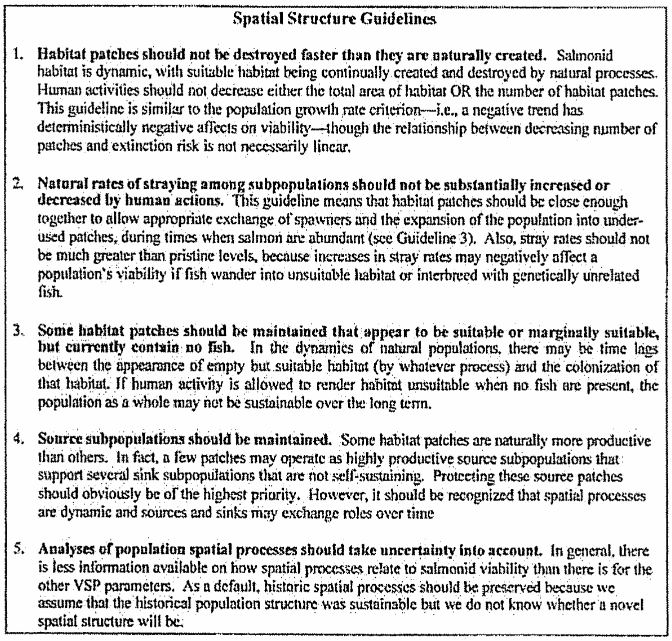
Fred Utter

Some Comments relating to the AHA Model

Given the apparently prominent role of integrated hatchery programs in the model, I have a few concerns that I need to pass on. Specifically, I address "the consistency of the model with recovery planning under the VSP concept" (from **Guide for Reviewers,** PSTRT 2005) as it relates to integrated hatchery programs.

A viable salmonid population (VSP) adequately meets four criteria – (1) abundance, (2) population growth rate, (3) population spatial structure , and (4) diversity (McElhany et al. 2000). By creating "..a composite population of fish that spawns both in a hatchery and in the wild.." (Discussion Paper #1, HSRG 2004), an integrated hatchery program cannot fulfill criteria (3) and (4) for any population having inherent spatial structure or diversity under the guidelines of figures 1 and 2 (from McElhany et al. 2000).

Figure 1



Spatial Structure Guidelines

1. **Habitat patches should not be destroyed faster than they are naturally created.** Salmonid habitat is dynamic, with suitable habitat being continually created and destroyed by natural processes. Human activities should not decrease either the total area of habitat OR the number of habitat patches. This guideline is similar to the population growth rate criterion—i.e., a negative trend has deterministically negative affects on viability—though the relationship between decreasing number of patches and extinction risk is not necessarily linear.

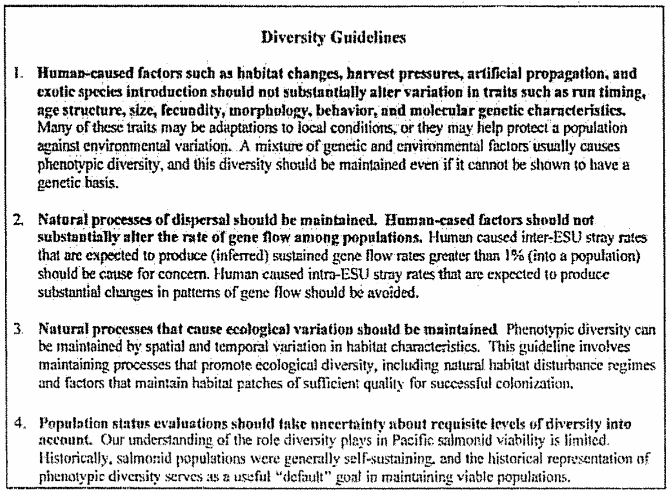
2. **Natural rates of straying among subpopulations should not be substantially increased or decreased by human actions.** This guideline means that habitat patches should be close enough together to allow appropriate exchange of spawners and the expansion of the population into under-used patches, during times when salmon are abundant (see Guideline 3). Also, stray rates should not be much greater than pristine levels, because increases in stray rates may negatively affect a population's viability if fish wander into unsuitable habitat or interbreed with genetically unrelated fish.

3. **Some habitat patches should be maintained that appear to be suitable or marginally suitable, but currently contain no fish.** In the dynamics of natural populations, there may be time lags between the appearance of empty but suitable habitat (by whatever process) and the colonization of that habitat. If human activity is allowed to render habitat unsuitable when no fish are present, the population as a whole may not be sustainable over the long term.

4. **Source subpopulations should be maintained.** Some habitat patches are naturally more productive than others. In fact, a few patches may operate as highly productive source subpopulations that support several sink subpopulations that are not self-sustaining. Protecting these source patches should obviously be of the highest priority. However, it should be recognized that spatial processes are dynamic and sources and sinks may exchange roles over time

5. **Analyses of population spatial processes should take uncertainty into account.** In general, there is less information available on how spatial processes relate to salmonid viability than there is for the other VSP parameters. As a default, historic spatial processes should be preserved because we assume that the historical population structure was sustainable but we do not know whether a novel spatial structure will be.

Figure 2



Diversity Guidelines

1. **Human-caused factors such as habitat changes, harvest pressures, artificial propagation, and exotic species introduction should not substantially alter variation in traits such as run timing, age structure, size, fecundity, morphology, behavior, and molecular genetic characteristics.** Many of these traits may be adaptations to local conditions, or they may help protect a population against environmental variation. A mixture of genetic and environmental factors usually causes phenotypic diversity, and this diversity should be maintained even if it cannot be shown to have a genetic basis.

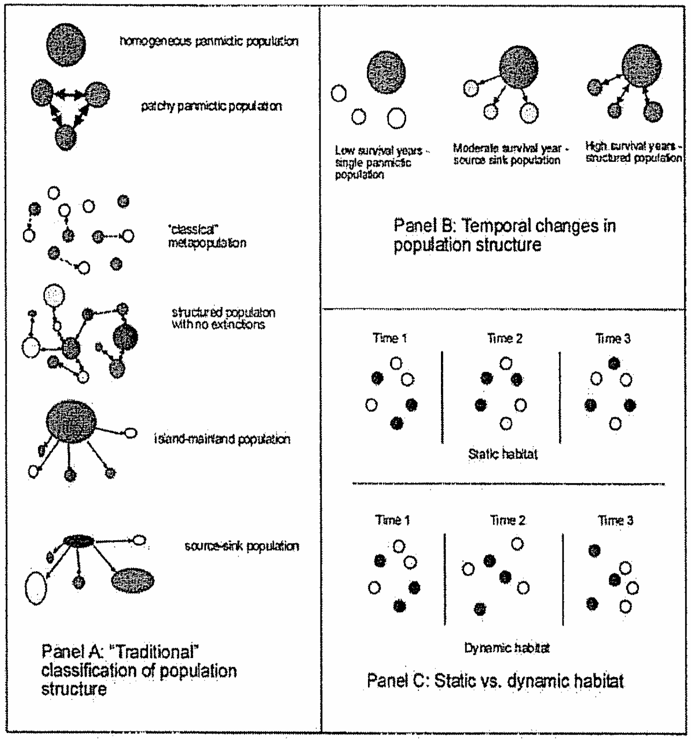
2. **Natural processes of dispersal should be maintained. Human-cased factors should not substantially alter the rate of gene flow among populations.** Human caused inter-ESU stray rates that are expected to produce (inferred) sustained gene flow rates greater than 1% (into a population) should be cause for concern. Human caused intra-ESU stray rates that are expected to produce substantial changes in patterns of gene flow should be avoided.

3. **Natural processes that cause ecological variation should be maintained** Phenotypic diversity can be maintained by spatial and temporal variation in habitat characteristics. This guideline involves maintaining processes that promote ecological diversity, including natural habitat disturbance regimes and factors that maintain habitat patches of sufficient quality for successful colonization.

4. **Population status evaluations should take uncertainty about requisite levels of diversity into account.** Our understanding of the role diversity plays in Pacific salmonid viability is limited. Historically, salmonid populations were generally self-sustaining, and the historical representation of phenotypic diversity serves as a useful "default" goal in maintaining viable populations.

The creation of a single quasi-panmictic population undermining of structure and diversity can be visualized in Figure 3 (from McElhany et al. 2000) below.

Figure 3



. Theoretical types of spatially structured populations. Panel A shows a "traditional" type classification scheme that does not consider correlated environmental effects that impact all subpopulations nor does it explicitly consider the physical dynamics of the habitat patches themselves. The circles indicate habitat patches, with the size of the circle indicating the size or capacity of the patch, and the degree of shading indicating the density of the subpopulation—white indicating an empty patch and black indicating a high density patch. The arrows indicate levels of migration, with thick arrows indicating high migration; thin arrows moderate migration, and dashed arrows indicating intermittent migration. Panel B shows how spatial structure may oscillate over time as a result of correlated environmental changes in survival or productivity among subpopulations. Correlated environmental changes might result, for example, from annual variation in ocean survival that affects all subpopulations. Panel C shows two potential habitat patterns. In a static habitat, the location of suitable patches remains constant over time, though patches may or may not always be occupied. In a dynamic habitat, the location of suitable habitat continually changes, and so the location of subpopulations must also change.

By definition, the composite hatchery-wild integrated population becomes homogenized, as depicted in the upper population depicted in Panel A of Figure 3. Based on ongoing considerations of the Interior Columbia Basins Technical Recovery Team, populations of anadromous salmonids commonly appear to be spatially and temporally structured as depicted elsewhere in this figure.

The loss of structure and diversity in an integrated population precludes fulfillment of criteria outlined in Figures 1 (notably items 2, 4 and 5) and 2 (notably items 1, 2 and 4). The consistent increase of effective straying above natural levels breaks down existing structure in a complex population and prevents its reformation. This action explicitly violates the guideline "…human caused intra-ESU stray rates that are expected to produce substantial changes in patterns of gene flow should be avoided…" (Figure 2-2).

An integrated wild-hatchery population can fulfill VSP guidelines for abundance and productivity. Furthermore, this process is designed to reduce "domestication" (Waples 1999). However, for the above reasons, the integrated hatchery concept directly violates VSP guidelines and thus prevents rather than promotes a population's recovery. This restriction is consistent with a widely accepted principle for hatchery-wild interactions that "..programs that produce fish for release into the wild should strive to maintain the genetic variation of the original wild population.." (Allendorf and Ryman 1987). These authors also noted the difficulties in incorporating different management goals (e.g., supplementation and conservation) into a single hatchery program. The integrated hatchery concept typifies this problem. I have discussed these concerns in greater detail elsewhere (Utter in press) and raise them here, at least as a basis for further discussion and clarification.

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References.

Allendorf., F.W. and Ryman, N. 1987. Genetic management of hatchery stocks. In: Ryman, N. and Utter, F. (eds.) Population Genetics and Fishery Management. University of Washington Press, Seattle, WA pp. 141-159.

HSRG (HSRG/WDFW/NWIFC) 2004. Technical Discussion Paper #1: Integrated Hatchery Programs. June 21.

McElhany, P., Ruckelshaus, M.H., Ford, M.J., Wainwright, T.C. and Bjorkstedt, E.P. 2000. Viable salmonid populations and the recovery of evolutionarily significant units. Technical Memorandum NMFS-NWFSC-42. United States Department of Commerce, NOAA, Seattle, WA.

PSTRT (Puget Sound Technical Recovery Team). 2005. Guide for Reviewers. January.

Utter, F.M. In press. Point of view - populations genetics, conservation and evolution in salmonids and other wisely cultured fishes: some perspectives over six decades.

Waples, R.S. 1999. Dispelling some myths about hatcheries. Fisheries 24(2):12-21.

Review 5: Comments on AHA Model

Tom Cooney

Context for the following comments was the request for the PSTRT to "..review the All "H" Analysis (AHA) model because tools for exploring integrated effects of hatcheries, harvest and habitat actions are needed for recovery planning." I didn't have time to 'test' the model by systematically varying outputs, etc, the following are initial comments based on reviewing the documentation and code.

Summary:

It is extremely important to recognize up front that the AHA model was designed as a tool for use in hatchery reform efforts - not as a generalized recovery planning model. As I understand it, the AHA model was specifically designed to be applied in situations where a decision has been made to use hatchery production, either in an integrated approach or a segregated approach. Recovery planning, following VSP guidelines, should focus on restoring some minimum number of populations within a listed salmonid ESU to self sustaining levels. The AHA model may be a useful tool for application to those populations designated for Integrated or Segregated hatchery programs, but it is not designed to do all H analyses on populations designated for wild production.

The AHA model can provide useful, but limited, insights regarding the design of hatchery programs in the context of natural production objectives. Strength of the model is that it quantitatively links broodstock removal rates and hatchery contribution rates and capacity assumptions with natural survival rates and capacity estimates- therefore providing insights into program levels that would be required to meet particular broodstocking/impact guidelines (proportion natural in hatchery broodstock, allowable contribution rates on natural spawning grounds). It is important to note that the AHA model itself does not determine acceptable levels of integration between natural and hatchery production elements for a given population or subbasin area - its most useful application would be in evaluating potential performance relative to criteria that are established independent of the model. VSP guidelines recognize that the long-term resilience of an ESU depends not only on current abundance and productivity, but on the adaptive potential fostered by natural spawning processes. The AHA model is not designed to cover all of these considerations.

The documentation of the model does not provide explicit guidance for key input parameters or driving elements (e.g., fitness model parameters), other than the advice to use output from production models and to compare results (average spawning levels, harvest levels, hatchery/wild proportions??) against current conditions. There is a brief reference to setting PNI objectives relative to a populations biological significance (page 12 of the AHA document) - the benefit/risk tool appendix referred to has some good elements, but would need to be expanded to cover TRT criteria. More explicit guidance on inputs, or a more specific framework for justifying values used, should be developed if this model is going to be used to complement recovery planning analyses.

The documentation for the AHA model implies that it is a tool for application to specific population/hatchery combinations. Given the relatively simplistic nature of the model, the lack of specific information for each unique setting, the most appropriate use of the model may be to evaluate risks of different levels of integration/segregation under a set of population scenarios chosen to represent the range likely to be encountered within a particular ESU. This type of approach would lend itself to relatively simple sensitivity analyses designed to demonstrate effects of variation or bias in input parameters/assumptions. It would be helpful if the TRTs provided guidance on the role of different available or potential models (not just AHA) in analyzing recovery planning scenarios - what level of modeling is most appropriate for what types of questions, etc.?

Specific responses to review questions:

11) Is the model consistent with viable salmon population (VSP) criteria? What are the strengths and weaknesses?
    a. The model is coded to use generations as a time step and is basically an equilibrium model set up to demonstrate the implications of different combinations of relative capacity/survival improvements, brood stocking 'rules', general harvest rates on average adult production.
    b. The simple genetic selection model incorporated into AHA was developed (Ford 2002) to "..gain some insight into the possible effects of artificial or natural selection on supportive breeding and to determine the sensitivity of these potential effects to the different parameters of the model." not intended as a detailed, realistic model of actual fitness relationships for a particular population/hatchery combination.
    c. The model does contain simple, explicit mechanisms relating production assumptions (hatchery and natural) to one another - e.g., natural broodstock removals explicit, accounted for in allocation of returning adults.
    d. Strengths - the model can be used to illustrate general combinations of production levels, broodstocking controls and harvest that are consistent with predetermined broodstocking/straying criteria (pNOR and pHOR).
    e. Weaknesses - the model is not designed to directly simulate quasi-extinction risks or within population level interactions between hatchery and natural production. The simple genetic impacts mechanism incorporated into the model is limited in scope- does not address the potential impact of multiple genetic factors, differences in phenotypic characteristics such as adult spawn timing, etc.
    f. The model is NOT a stand alone approach for evaluating performance against VSP criteria. When combined with 1)a clear idea of the policy objectives for a particular setting (integrated or separated program, degree of desired separation between hatchery/natural production components within the general strategy AND at least a crude understanding of key production parameters for the situation (e.g., SARs (including relative rates for hatchery and natural origin components), straying rates, etc), the model can give general insight into the level of program appropriate for a particular situation.

I believe that it is inappropriate to call this version of the model an ALL H tool - it simply doesn't have the level of detail in key parameters to serve that function across the range of situations involving populations of listed ESUs.

12) What are the strengths and weaknesses of the scientific assumptions of the model? Are these assumptions adequately documented or transparent in the model? Can the model be validated?
    a. Although the driving assumptions in the model are not really systematically described in the documentation, the coding of the model as an excel spreadsheet makes it pretty transparent. Could use a written narrative explaining key choices, etc. Model assumes a simple Beverton Holt stock production function describes natural production. Natural production is treated as a panmictic population, the current version does not allow for simulating geographic segregation of hatchery impacts WITHIN a population.
    b. SARs drawn from HI, MED, LOW distributions, but category assigned to a given out year is fixed. Harvest impacts are limited to a constant exploitation rate. Brood stocking assumed to be random from across the runs (I think).
    c. Define validated. The documentation suggests that the user compare results from runs using 'current' parameters to recent observed escapements, harvests and hatchery production levels. While that confirms consistency, it doesn't really fully validate the model for use in projecting response to changes in elements. It would be helpful if the documentation stressed that the AHA model is a planning tool - outputs are dependent upon input assumptions. Actions based on results from any such models should be accompanied by evaluation efforts aimed at confirming key assumptions, tracking early signs of response consistent with projections, etc.
    d. Priority need - a lot more justification/rationale/qualifications on the fitness component of the model. Clear statements about what it does represent and what it does not represent.

13) Does the model incorporate adequate uncertainty (e.g. environmental and demographic stochasticity) for decision making? Is it clear how uncertainty in different parameters affects the certainty of the results?
    a. The model does incorporate a mechanism for generating some level of environmental variation through SARs. The option can be switched on or off through an entry on the main page. This simple mechanism basically relies on a table of annual hatchery SARs incorporated into the SAR page. For a given scenario, the sequence of values in that table drives year to year variations. The table values were generated by assigning each brood year to a survival category (high, med, low), then generating a value for that brood year by averaging three draws from a lognormal distribution specified for that particular category. Natural return rates are driven off of the values generated for hatchery return rates using relative survivals from the input pages.

   b. Given that the model is set up with generational time steps, I am not sure how to judge the value of having a stochastic SAR mechanism. I think the main value of the model is in displaying average hatchery production levels consistent with NOR and HOS objectives for selected populations. The model does not directly incorporate uncertainties in parameter estimates - it would be relatively straight forward to set up a structured sensitivity analysis, varying individual parameters from input values. This would require changing the output mechanisms of the model to summarize across variable parameter run sets, not trivial but certainly doable.
   c. I am not that familiar with hatchery sar time series for Puget Sound, but the lnnormal variance in the series incorporated into the model is pretty low in comparison to time series for Col. River stocks.

14) Is the choice and number of parameters in the model appropriate? Can the parameters be estimated from existing data or do they rely on expert opinion?
   a. The model relies on three sets of parameter estimates 1) natural population production characteristics (expressed as adult Beverton Holt productivity and capacity parameters), 2) hatchery program production parameters 3)impact constraints (optional minimum natural escapements, hatchery capacity ceilng on broodstocking) and 3)optional yes or no on fitness loss parameter. The model has default parameters from Ford (2002), but they can be changed by the user. There is no guidance/rationale for particular choices of these parameters - or sideboards for reasonable variations, adaptations to particular circumstances, etc.
   b. The model is currently coded as a Beverton Holt model, defined by productivity and capacity parameters expressed in terms of adult spawners. It was designed to run off values generated by EDT. The spreadsheet can incorporate Beverton Holt parameter estimates generated by other habitat/production model frameworks. The model assumes that a user would input productivity and capacity estimates reflecting current status, historical status (for reference) and for specified alternative scenarios. Use of the model as an aid to recovery planning would require some standards/guidelines for generating appropriate parameter sets.
   c. Hatchery parameters - the model requires estimation of a standard set of program parameters (broodstock targets and smolt release levels). It allows for setting a lower limit on broodstocking in terms of impacts on natural spawning numbers (NOR) - can be set as low as 1, covering scenarios where there are virtually no constraints on the number of broodstcok extracted from a natural spawning population.
   d. Harvest - limited to simple exploitation rates - although you can set different rates on hatchery and non-marked (presumably wild) production.
   e. Fitness parameters - The model includes the option of using simple fitness equations taken from Ford 2002. The documentation also suggests one can ‘fine tune’ the fitness parameters in the model. No specific guidance was provided in the materials distributed for review on adjusting the fitness parameters.

15) Is the model easy to use? Are the results easy to interpret? The model is easy to use, needs a lot more guidance on how to interpret. At a minimum, needs a disclaimer about the strengths of these types of models are in projecting relative differences between major action scenarios - not in projecting specific numbers. This is especially true given the simple AHA output graphs depicting average escapement (natural and hatchery) and harvest levels. Need to clearly recognize that average escapement and harvest levels should best be interpreted in a relative sense, and that year to year variations in survival are the reality - be careful interpreting projected averages as realities for any given year. (If it isn't obvious, I ran out of time to work on response).