ECOSYSTEM DIAGNOSIS AND TREATMENT PLANNING MODEL AS APPLIED TO SUPPLEMENTATION

Model Description, User Guide, and Theoretical Documentation for the Model Introduced in the Summary Report Series on Supplementation in the Columbia Basin

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ABSTRACT

This document describes the formulation and operation of a model designed to assist in planning supplementation projects. It also has application in examining, a broader, array of questions related to natural production and stock restoration. The model is referred to as the Ecosystem Diagnosis and Treatment (EDT) Model because of its utility in helping to diagnose and identity possible treatments to be applied to natural production problems for salmonids. It was developed through the Regional Assessment of Supplementation Project (RASP), which was an initiative to help coordinate supplementation planning in the Columbia' Basin. The model is operated within the spreadsheet environment' of Quattro Pro using a system of customized menus. No experience with spreadsheet macros is required to operate it. As currently configured, the model should only be applied to spring chinook; modifications are required to apply it to fall chinook and other species.

The purpose of the model is to enable managers to consider possible outcomes of supplementation under different sets of assumptions about the natural production system and the integration of supplementation fish into that system. It was designed to help assess uncertainty and the relative risks and benefits of alternative supplementation strategies. The model is a tool to facilitate both -planning and learning; it is not a predictive model. Modeling in this sense is meant to be a catalyst for thinking and helps to ensure accountability to the planning process. Hypotheses, rationale, and expectation for a project are clarified and refined through this process. In helping to assess uncertainty and risks, it can also be an aid in identifying and prioritizing elements to. be addressed through the monitoring and evaluation phases of a project.

This document consists of three principal parts. Part I provides a description of the model. Part II is a guide to running the model. Part III provides theoretical documentation. In addition, a sensitivity analysis of many of the model's parameters is provided in the appendix. This analysis was used to test whether the model produces consistent and reasonable results and to assess the relative effects of specific parameter inputs on outcome.

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ECOSYSTEM DIAGNOSIS AND TREATMENT MODEL AS APPLIED TO SUPPLEMENTATION

GENE-L INTRODUCTION

Ecosystem Diagnosis and Treatment (EDT) Model' is a tool to assist in the planning of supplementation projects, though its structure provides a way to examine other types of natural production improvement measures. It was developed through the Regional Assessment. of Supplementation Project (RASP), which was an initiative to help coordinate supplementation planning in the Columbia Basin. The objectives of RASP included the development of tools to help assess the relative risks and benefits of alternative supplementation strategies and to help prioritize uncertainties requiring attention. The EDT model is one tool produced through that work. RASP (1992) summarizes the **findings** and products of that coordination initiative and describes an earlier version of the model in Part IV of that report. A broader application of those findings and tools to ecosystem planning can be found in Lichatowich et **al.** ***(in press).***

This document provides complete and up-to-date documentation for the model and its use. Since the publication of RASP (1992), the model has been revised to correct errors that have been detected and to update certain, components to improve the model's usefulness. These revisions have been incorporated here. The model is currently configured to be applied only to chinook populations that smolt as yearlings (e.g. spring chin&k populations east of the Cascade Crest). Modifications are required to apply it to fall chinook and steelhead.

This document consists of three parts, not counting this general introduction or 'the appendices. Part I gives an updated description of the model and its application. The purpose of this part is to provide a general description of the model's intended application, model components, and model operation, and to give a simple, yet practical example **of** applying the model.

Part II is a user guide for model operation. This part describes how to prepare the Quattro Pro software for using the model; the model's menu system, and how to initiate model runs: No experience with modeling, complex spreadsheets, or spreadsheet macros is' needed 'to follow this guide and run the model.

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1 Assessment of relative risks and benefits of supplementation requires, comparison with non-supplementation methods to meet restoration objectives. **The EDT model can be adapted to** examine alternative habitat improvement strategies (Lestelle et al. 1993).

Part III presents the theoretical documentation for the model. Formulas for all but the most trivial calculations in the model are provided. Since the distribution of RASP (1992), several requests have been received to provide more detailed documentation than what was given in that earlier report. We found, however, that these pieces were often linked to others, making it difficult to document only selected portions. Part III satisfies the need for full documentation. We recognize that the numerous formulas given here may be intimidating and 'of little value to many model users; they are provided to ensure full accountability for all parts of the model. We expect that Part III will be of most use to individuals wanting to customize the model, use portions of it in other modeling tasks, or to better understand a particular set of computations.

Appendix A provides a sensitivity analysis of a select set of parameters within the model. The purpose of this analysis was twofold. First, it was used to assess the relative effects of specific parameter inputs on outcome; this helped us to consider ranges of values that produce results that might be considered appropriate as management strategies. Secondly, the analysis enabled us to corroborate model design and how various elements were coded. The analysis in this sense provides a test of whether the model is producing consistent and reasonable results.

Working copies of the EDT model can be obtained by contacting Tom Vogel at the Bonneville Power Administration (BPA), (503) 230-5201, or from BPA's Public Information Office, l-800-622-4520.

ECOSYSTEM DIAGNOSIS AND TREATMENT MODEL AS APPLIED TO SUPPLEMENTATION

PART I
MODEL DESCRIPTION

1. INTRODUCTION

Part I provides a foundation for understanding the purpose and application of the model, its general structure, and its operation. We encourage, individuals interested in running the model to not move too quickly over the following sections. The section on purpose and application, especially important to individuals not familiar with modeling, is designed to promote learning.

The Ecosystem Diagnosis and Treatment (EDT) Model is a spreadsheet model developed with Quattro Pro version 4.0 for DOS. Modifications to the spreadsheet are required to run it properly with Quattro Pro for Windows. Versions to be operated through Lotus l-2-3 or Excel have not been developed.

We developed the model within the spreadsheet environment in the hope that it would be more widely used than if it had been "hardened" in Basic or Fortran. Our perception is that' many project biologists are more comfortable -working with spreadsheets than they are with the standard computer languages. Because the model is meant to be a learning tool, we intended it to be highly interactive with the user. Besides being interactive in its operation, it can be readily modified by knowledgeable spreadsheet users for other applications besides supplementation planning. One example of this can be-found in Lestelle et al. (1993). In that case, the model was modified to gain a clearer understanding about the likely nature of habitat-fish production relationships. That version is being used by management biologists to help assess the role of habitat enhancemem to restoring salmon runs.

2. PURPOSE AND APPLICATION OF MODEL

The EDT model, as currently configured, is a tool to be used in planning supplementation projects. Its purpose is to enable managers to consider possible outcomes of supplementation under different sets of assumptions about the natural production system and the integration of artificially propagated fish into. that system. The model was designed to help assess uncertainty and relative risks and benefits of alternative supplementation strategies.

The full- value of using the model will only be obtained within its proper context of the planning process. We recommend that the model user review the RASP planning process described in Part III of RASP (1992). A broader application of that process to ecosystem planning has been described in Lichatowich et al., *(in press).* Certain aspects of the process bear emphasis here to help clarify the intended use of the-model.

This planning process was developed to be applied to projects implemented using the principles of adaptive management (Walters 1986; Lee 1993). The adaptive approach recognizes that inforniation is almost always incomplete on which to make resource management decisions. It therefore treats management decisions as experiments with this imperative--learn *from them* (Bunnell 1989; Lee 1993). This approach necessitates that actions, in this case supplementation, utilize an iterative planning approach throughout their existence, thereby ensuring that new information is systematically considered and incorporated (RASP 1992). An important purpose of this planning is to identify and manage the critical uncertainties of the project, i.e., those uncertainties for which the choice of assumption in the supplementation plan can determine success or failure.

The Scientific Review Group (SRG 1991) identified the central uncertainty (or question) regarding supplementation as:

> ***"Under what set of conditions w ill supplementation of natural and wild production with hatchery production add to the total production of salmon, steelhead, or other targeted fishes- over the long term?"***

All of the more specific uncertainties that supplementation projects seek to resolve are related to that central question. These various uncertainties are essentially the *"set of conditions"* referred to in the- question posed by the SRG. In other words, what set of credible assumptions must a project planner make to demonstrate that the project's objectives are achievable. These assumptions will necessarily encompass the prop&d treatment, i.e., the specific supplementation strategy selected, and a'diagnosis 'about the production problem that is being addressed. Linking treatment and diagnosis in such manner requires conceptualizing how the stream/population system functions--both in its current and some healthy state. Once the assumptions associated with these steps are clearly defined, the risks associated with each can be analyzed. Alternative diagnoses and treatments must also be considered.

The use of models, like the EDT model, can serve an important role in identifying-and analyzing these uncertainties and associated risks (Walters 1986; RASP 1992; Lichatowich et al. (in *press*)). Modeling within this context is meant to be a catalyst for thinking and helps 'to ensure accountability to the planning process. Its primary value in this regard is in facilitating both planning and learning, not to predict outcome (Bunnell 1989). Walters (1986) aptly described the purpose of such modeling:

"The value of modeling in fields like biology has not been to make precise predictions, but rather to provide clear caricatures of nature against which to test and expand experience. It seems to be a very fundamental human need or requirement to construct such caricatures as a basis for learning....It should be obvious who will benefit most from it: those who engage in it directly." (emphasis added)

Hypotheses, rationale, and expectation for a project are clarified and refined through a planning process that incorporates modeling in this way. Refining expectations, or objectives, for a project using a model in this manner should not be confused with modeling for predictive' purposes. Modeling for understanding (Bunnell 1989)' is used to develop a more accountable set of objectives, ones that are linked directly to assumptions about the diagnosis and treatment. This linkage is essentially the rationale for a project. Without modeling to aid in such a process, objective setting frequently resorts to wishful thinking or broadly worded social-political goals.

The assessment of critical uncertainties and associated risks using this process also helps identify those, elements of the project that must be addressed through the monitoring and evaluation phases of implementation (RASP 1992). The extent of risk associated with these elements provides a way of identifying high priority items for monitoring.

The EDT model was designed to be highly interactive with the user. Once the basic concepts that comprise the model are grasped, exploring the effect of 'changing various parameters and inputs c'an be extremely enlightening. The model can be especially useful for examining interactions between life stages, effects of population- density, and the role of habitat quantity and quality characteristics. If the model is used in the same manner as the Systems Planning Model (NPPC 1989), i.e., by applying 'a standardized set of parameter values, its purpose will be defeated. One conclusion of RASP (1992) is that all stream/population systems are different; the unique conditions of each need to be assessed in identifying appropriate treatments. The process of diagnosis and treatment selection for a specific natural production system must also consider alternative diagnoses (or hypotheses) and treatments.

3. GENERAL DESCRIPTION OF THE MODEL

The basic structure of the model and its principal components are described below. Due to the many variables: involved and the model's complexity, we introduce the basic concepts with an overview of the model's general structure to provide some familiarity before giving more complete descriptions.

3.1 Overview

The overviewis given in two parts. The first describes the major components of the conceptual framework, while the second shows how the spreadsheet containing the model is organized.

3.1.1 Conceptual Framework

The conceptual framework for the model consists of five major components: life history and demographics, ecological factors, supplementation strategies, genetic and non-genetic survival yardsticks, and benefits/risks assessment.* Figure I shows the framework in highly conceptualized -fashion. These components define the production characteristics by life stage of the natural unsupplemented population, the specific supplementation strategy to be modeled and related factors involved in treatment, and potential outcomes of treatment.

The model simulates changes in population abundance over successive generations in response to different environmental and biological factors that affect survival and to supplementation. All calculations of production associated with a single brood year are made on a brood year time step. Although there is provision for annual variation of some survival factors, the model is deterministic.

The model divides the fish's life cycle into a number of discreet life stages associated with the predominant life history pattern of spring chinook east of the Cascade Mountains, i.e., smoltification is assumed to occur in spring of the second year of life (age I+). Abundance is tracked in the model from egg deposition through return back to the spawning grounds through each life stage, incorporating appropriate demographic inputs for fecundity and age structure.

Survival of fish in each stage is determined by various ecological factors-that-affect density-independent and, where appropriate, density-dependent mortality. These survival values can be affected when supplementation fish are introduced into the natural environment. The ecological factors are defined by stage-specific stock production functions for each life stage prior to smoltification, a predator response function during smolt migration within the subbasin, and, if selected by the user, interannual variation in passage and estuarine survival conditions. Survivals within the Columbia River, estuarine, and marine environments are assumed to be density-independent.

Supplementation strategies are modeled by simulating production responses to outplanting hatchery propagated fish as one or more of the following: eggs (or spawners), fry , fall parr, and smolts (Fig. 1). The model allows for the supplementation strategy to be shaped.

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[2] The presentation of the conceptual framework here is modified somewhat from that in RASP **(1992).**

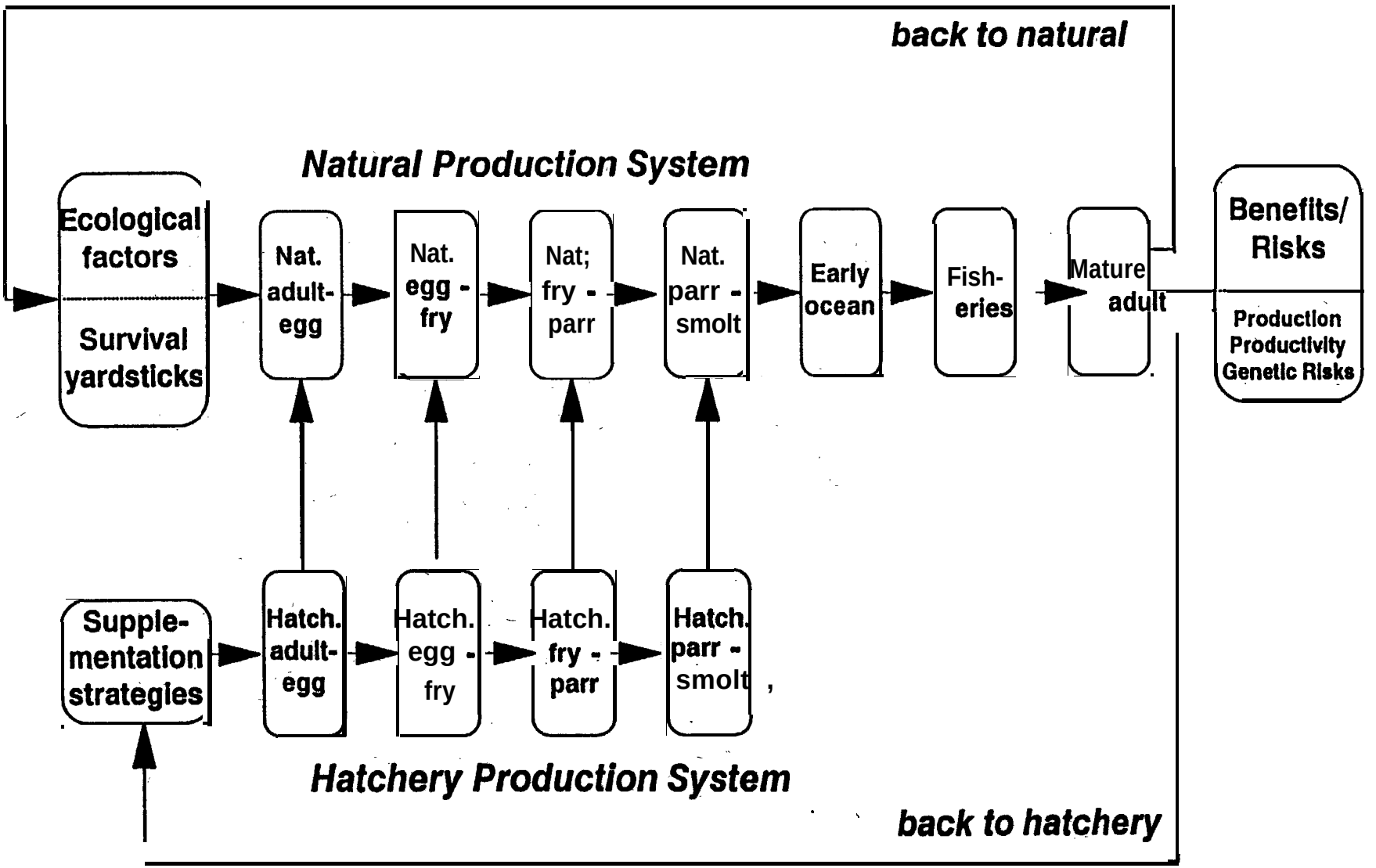

Figure 1. Simplified conceptual framework of the EDT model.

according to specific outplanting goals, broodstock policies, spawning escapement policies, and culture practices. Each of these can determine how supplementation fish affect naturally produced fish both in the short and long term.

When supplementation fish are introduced in the model, the survivals associated with the ecological factors previously described are modified by what are called survival yardsticks. These are factors that adjust the survival of fish in the natural environment in response to reduced performance of hatchery fish compared to a wild fish standard. The term "yardsticks" implies a range of possible effects of hatchery propagation on survival in the natural environment. These yardsticks can also affect the survival of the progeny of hatchery fish that reproduce in the natural environment.

The final element of the framework is the summary of risks and benefits that is produced by the model (Fig. 1). Output summaries are provided for a convenient comparison of population abundance, composition of the population by genetic type, reproductive success, 'and harvest levels.

3.1.2 Organization of Snreadsheet

The Quattro Pro spreadsheet that contains the model is organized as shown in Figure 2. It is' not necessary to understand this layout to operate the model using the menu system. Individuals wanting to understand more about the workings of the model, or to **customize** it, will need to understand the layout.

3.2 Model Components

A detailed diagram of the model's structure, showing variables affecting mortality and introductions of supplementation fish, is given in Figure 3. The model simulates.how a population responds quantitatively and qualitatively to supplementation by tracking different genetic types of fish (described below)

stepwise through each of the, life stages **shown**. Beginning with an initial run size to the subbasin, computations of survivors or their progeny are **made** at each stage. Part III of this document provides the detailed theoretical documentation of each computational step in the model.

3.2.1 Life Historv and Demoaranhics

The model assumes that all natural produced fish exhibit the same'life -history 'pattern **in** freshwater (Fig. 3). Therefore, freshwater stock-production parameters are assumed to be uniform for the entire population within each life stage, except as noted for how the

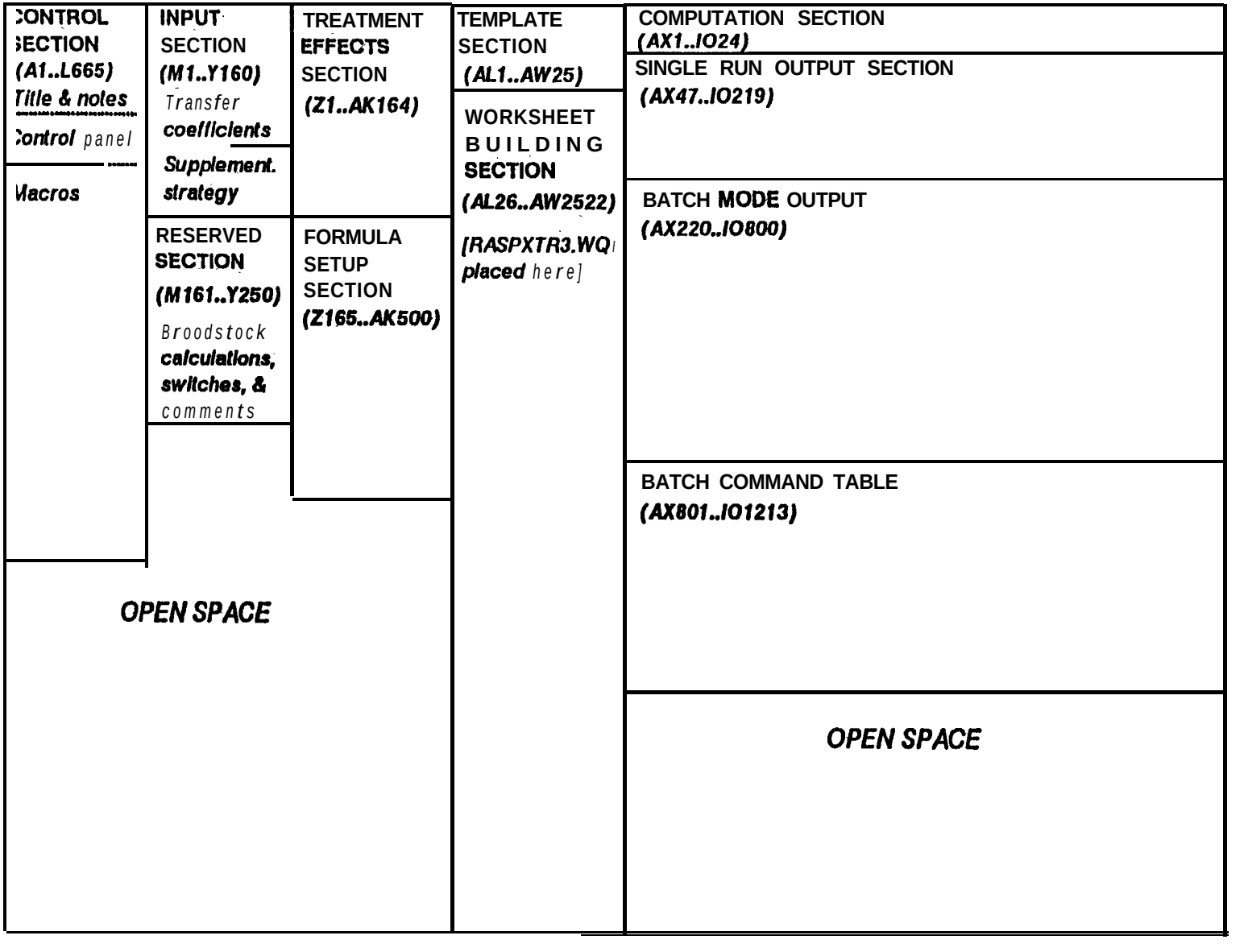

Figure 2. Layout of the model within the Quattro Pro spreadsheet. Areas not shown to scale.

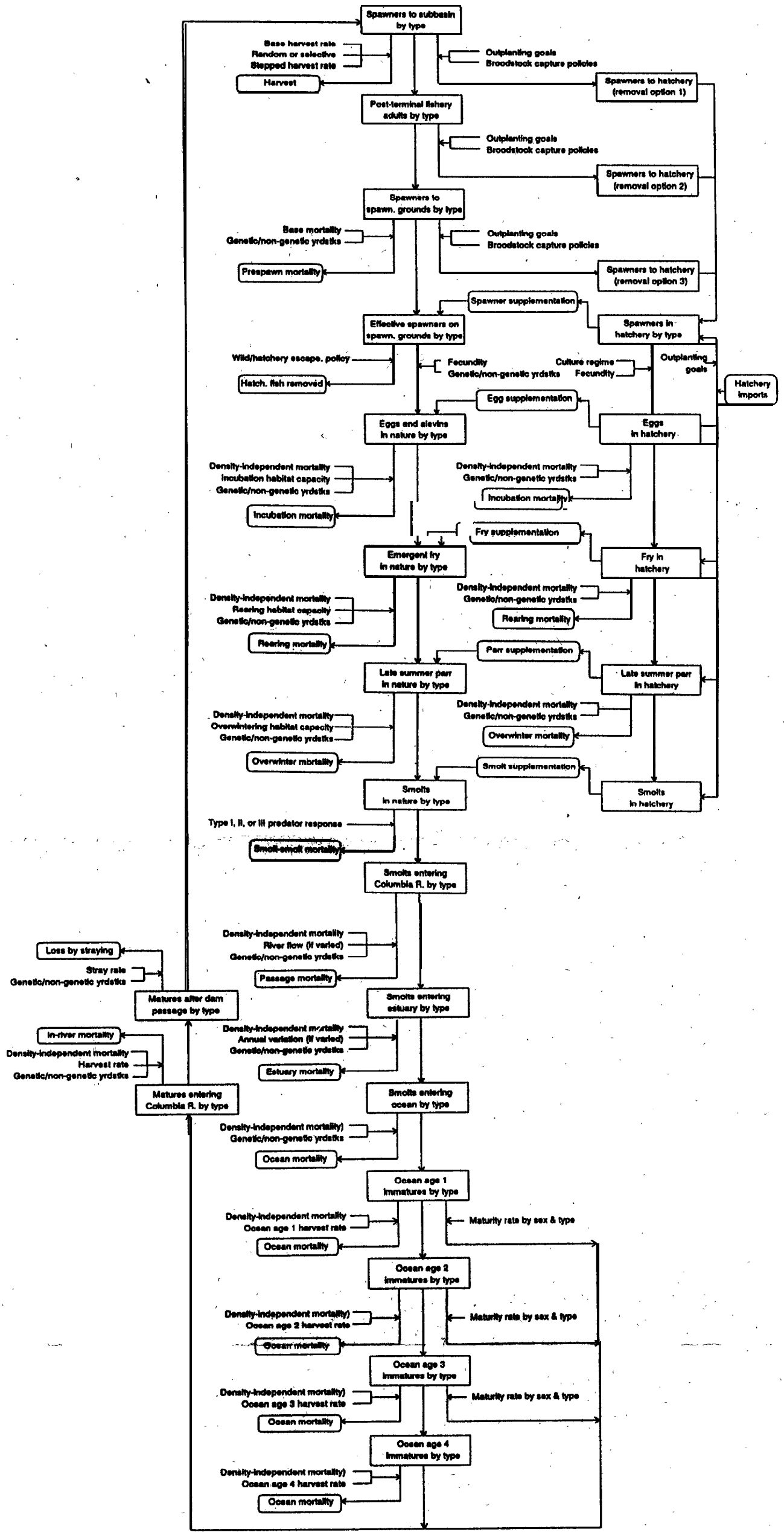

Figure 3. Detailed flow diagram of the EDT model.

yardsticks affect survival.[3] All fish, both natural and hatchery produced, are assumed to emigrate seaward as smolts at age 1+.

Basic demographic characteristics of the natural and hatchery fish populations for fecundity and maturity schedules are incorporated at the appropriate life history stage (Fig. 3). Age-specific fecundities are input for both natural and 'hatchery fish. Maturity schedules, i.e., the schedules that determine when fish mature and depart the ocean, are calculated within the model based on inputs of steady state age composition of the spawner population. These schedules are calculated for males and females separately- and remain fixed for a model. run. We recognize, however, that maturation has a genetic component 'which can be altered through fisheries (Ricker 1981) and hatchery practices (papers cited in Steward and Bjornn 1990). A mechanism for heritability of maturation rate could be added to the model if warranted, as done in Larkin and Hourston (1964).

The model assumes random mating of hatchery and wild fish in nature. The number of zygotes of each genetic type (see below) is determined simply by the proportion of the types present at time of spawning.

3.2.2 Ecological Factors

Ecological factors in the model determine how the simulated population responds to different types of environmental and biological conditions. These factors are related to habitat quantity and quality, the abundance and feeding behavior of predators, flow regimes in the Columbia River during outmigration, and interannual variability in estuarine/marine survival.

We strongly encourage individuals interested in using the model to closely review the concepts associated with these factors. We especially consider the following section on stock-production relationships to be important in operating the model consistent with its purpose and application (see Section 1.1).

3.2.2.1 Stage-Specific Stock-Production Relationshins. Understanding how stock-production relationships operate in the model is a key to formulating hypotheses about the condition of the stream/population system and the potential outcomes of supplementation. Once these simple concepts are grasped, the model can be a powerful tool in considering how the natural production system is operating. Gaining such insight may be the most important step in diagnosing the nature of the production problem and identifying an appropriate treatment.

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[3] As noted in Section 4.5 (Special Applications), the model has been modified to model several subpopulations simultaneously for one subbasin. These subpopulations can have different stage-specific stock-production characteristics. The subpopulations can be modeled to interact at certain life stages.

The model assumes that the underlying relationship between spawner stock size and resultant production in nature can be represented by simple stock-production (S-P) relationships. In real&, factors affecting production are more complex than can be reflected in these simple functions; still, they can provide valuable insights into the mechanisms that likely affect population abundance (Hilbom and Walters 1992; Lestelle et al. 1993). We have found that the disaggregation approach (described below) to using S-P functions provides an effective framework for thinking about the processes that regulate population abundance.

We assume that the underlying S-P relationship for spring chinook populations in the Columbia Basin follows the Beverton-Holt form (Fig. 4), which is consistent with the Systems Planning Model (NPPC 1989) and Bjomn (1990). It is important to understand how the shape of the relationship in Figure 4 is determined.

The Beverton-Holt relationship is described by two parameters (see Equation B-l in Appendix B). Each of these can be thought of-in ecological terms. One of the parameters defines the operation of mechanisms that ***affect density-independent*** survival, i.e., the survival component not affected by population density. Even when population density is l&h, there is still a component of survival not affected by that density. This parameter defines ***the productivity*** (Hilborn and Walters 1992) of the stream/population system, and it. characterizes total survival when the population is at very low density. In the Systems Planning Model, this parameter is the S_0 value (NPPC 1989).

The productivity parameter determines a population's resilience to many mortality pressures, such as caused by certain forms of land use practices, passage problems at dams, and fishing. The environmental characteristic that affects productivity is habitat ***quality*** (Moussalli and Hilbom 1986). Habitat quality is reflected by spawning gravel composition (amount of fine sediment), substrate stability, and the distribution and complexity of colonization, rearing, and overwintering habitat. A decline in productivity associated with habitat deterioration has likely been a major contributor to the sharp decline of many salmonid populations in recent decades. Hankin and Healey (1986), in considering the prospects for future declines of chinook populations, urged that more attention be given to diagnosing productivity for populations of concern. Biologists using the EDT model in the Columbia Basin should not simply adopt the productivity parameter (S_0) used in the Systems Planning Model.

The second parameter that defines the Beverton-Holt relationship specifies the level of the asymptote in Fig. 4. It defines carrying capacity and determines the amount of production at very large spawning escapements. The ***capacity*** parameter determines the 'action of ***density-dependent*** mechanisms working on the population. This parameter is affected to a large extent by habitat ***quantity,*** though certain quality aspects like temperature can influence this.

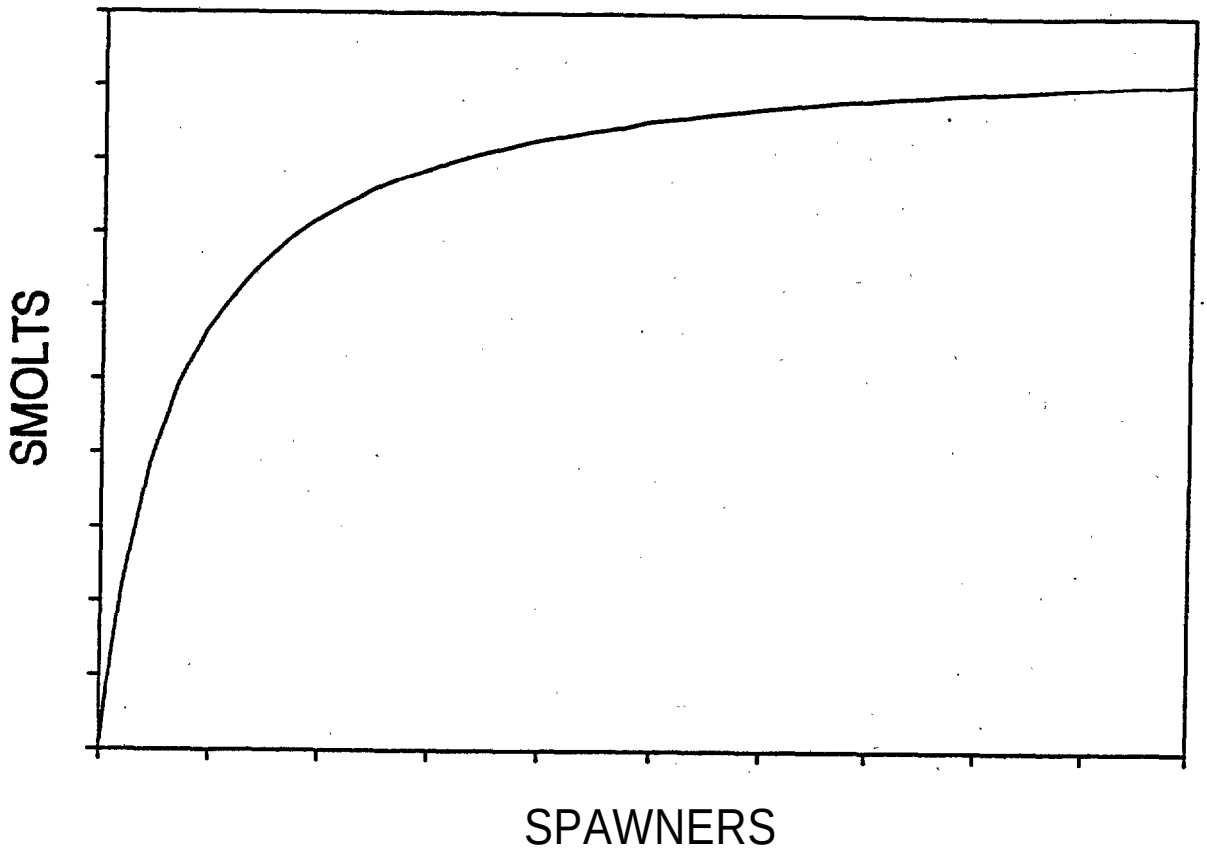


Figure 4. Beverton-Holt stock-production relationship.

The Beverton-Holt relationship can be easily disaggregated into separate life-stage specific functions (Moussalli and Hilbom 1986; Hilbom and Walters 1992). Each function takes the form of a Beverton-Holt equation, though the S-P relationship for a specific stage may appear linear if an immense quantity of habitat exists for that stage. For a given spawning escapement, the same number of recruits is computed using the aggregated S-P equation as is calculated by progressing through a series of disaggregated S-P functions for intermediate life stages. Appendix B describes in simplified fashion the terms of the disaggregated stock-production relatibnship. It is especially important to note that the productivities of each stage are multiplicative.

This disaggregation approach provides a powerful way to consider the unique features of a stream by life stage and the interactions that occur between stages in regulating population abundance. Moreover, it provides a means of deriving stage-specific capacities and productivities for modeling. We have found these concepts useful in attempting to diagnose the conditions of a stream/population system. Different assumptions about the relative amounts of incubation, summer rearing, or winter capacities can be evaluated. Since supplementation can occur at different life stages, this procedure of disaggregation is also needed to evaluate interactions between natural and supplementation fish at appropriate times in their freshwater life history.

This modeling approach requires that the model user have empirical information on habitat quantities by life stage for the subbasin of interest or make assumptions about their relative values. When stage-specific capacities are based on assumptions, the model can be used to test the relative effect of uncertainty in those assumptions on supplementation outcome. This approach also provides a convenient framework to link habitat characteristics, either quantity or quality, to the stock-production parameters. This technique can be used to consider the effects of enhancing habitat during specific seasons or to examine the effects of habitat deterioration. See Lestelle et al. (1993) for a more detailed description of how this can be done.

3.2.2.2 Prev-Predator Relationship. The model allows for different assumptions to be made about the effect of predators on the modeled population during smolt migration within the subbasin. One of three different assumptions is required to be made. The first is that predators prey on migrant smolts at a constant rate with no provision for predator satiation, regardless of smolt density (Fig. 5A). Holljng (1959) described the predator response in this case as ,a Type I functional response. Much of the modeling in the Columbia River uses this approach. The second and third possible assumptions are that. the rate of predation is dependent on the density of migrants (prey). These assume either a Type II or Type III functional response by predators (Figs. 5B and 5C), as described by Holling (1959). A severe Type II response leads to extinction of the prey population at low densities, while a severe Type III response would tend to produce multiple stability domains (Peterman 1977 and 1987). Mace (1983), Wood (1984), and Fresh and Schroder (1987) provide evidence for Type II and Type III functional responses by either birds or fish to juvenile salmon populations. Peterman (1987) argues that

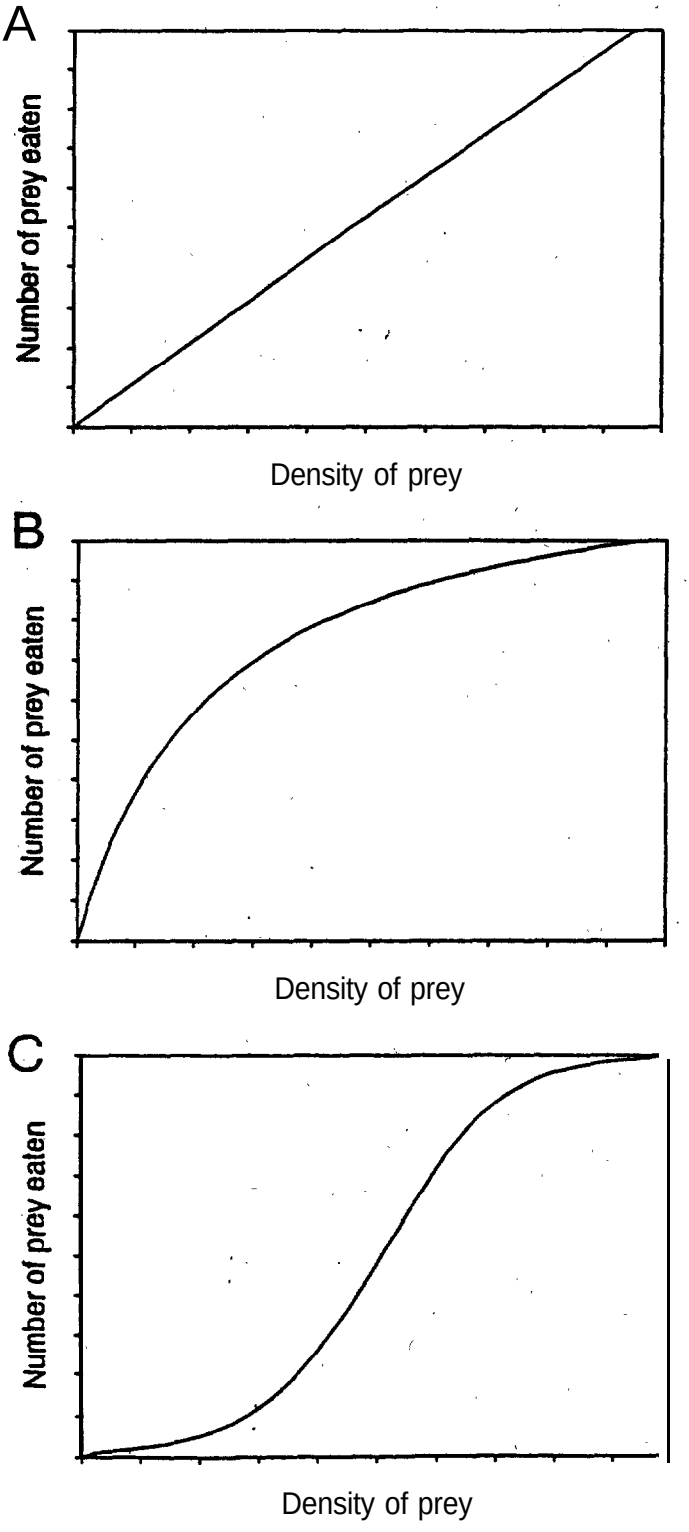


Figure 5. Functional responses of predators to increasing prey density.

the Type II or III responses are likely more prevalent in nature than Type I. The techniques used to model the two predator responses were described by Peterman (1977) for Type III and by Hilbom and Walters (1992) for Type II.

3.2.2.3 Variable Passage and Estuarine Survival Conditions. The model incorporates two' sources of environmental variation in a manner similar to the Systems Planning Model (NPPC 1989). First, survival during downstream passage through the Snake and Columbia mainstems can' be varied in the EDT model using the same survival-flow relationship employed in the Systems Planning Model. A 50-year runoff record (1929-l 978) was used to generate a set of passage survivals to below Bonneville Dam, assuming flows were regulated for-the entire period under "current operations." The model currently estimates passage survival past four or eight dams (or none, if this feature is turned off); additional data sets can be generated as 'needed. The 50-year survival record was converted to six different survival files; three that maintain the same sequence of years but vary the start year, and three that apply a random selection of survivals.

The second source of variation is meant to encompass all other influences of environmental variation on survival, but is expressed through variable survival in the estuarine life stage. The annual values are computed using a log-normal function.

3.2.3 Supplementation Strategies

The model was designed to examine a wide range of different supplementation strategies. RASP (1992) described a question&e that was distributed to help identify the types of supplementation strategies in the Columbia Basin and to characterize recipient stocks and streams for planned and ongoing supplementation projects. The questionnaire (SUPQUEST) covered eight general categories: project duration, targeted life stage, broodstock strategies, mating procedures, incubation strategies, rearing strategies, release strategies, and quality-control strategies. Information obtained through the survey was used in designing the model to cover the types of policies and strategies being employed to implement supplementation in the basin. The information was also used to develop yardsticks for incorporating the effects of hatchery propagation on survival in nature.

Supplementation strategy can be defined in the model on the basis of life stage to be supplemented, treatment duration, numeric release goals, broodstock source, a broodstock collection policy (e.g., maximum percent of natural run that can be taken as broodstock and minimum percent of broodstock to consist of natural fish), an escapement management policy to specify the maximum percent of natural spawners that can consist of hatchery fish, and a hatchery culture method (Fig. 3). Each of these can affect the potential outcome of a supplementation treatment, either in positive or negative ways.

The model allows the user to assess the effects of a wide range of hatchery fish performances on outcome. The performance of hatchery fish can affect their survival and reproductive

success, as well as that of co-existing naturally produced fish and those produced in subsequent generations. For example, the time of release can have important consequences, particularly when the life stage released precedes or coincides with the stage when habitat is most limiting to smolt production (RASP 1992; Lestelle et al. 1993).

The type of fish culture method refers to whether conventional or innovative hatchery practices are to be employed. Conventional hatchery practices refer to those that are typically used in the region. Innovative practices refer to the use of new approaches, to propagate fish to reduce genetic, behavioral, and physiological changes believed to occur to fish with conventional practices (RASP 1992). Hatchery propagated fish have been found to survive at higher rates and behave more like wild fish when such innovative practices have been applied to experimental groups (Desmond Maynard, National Marine Fisheries Service, Manchester, Washington; *personal communications).*

3.2.4 Genetic and Non-Genetic Survival Yardsticks

Hatchery propagated fish typically survive at lower rates than their wild counterparts. The effects of hatchery practices on fish genetics, physiology; and behavior are incorporated into the mode1 through factors, or yardsticks, that affect survival and reproductive success. The EDT model uses the yardsticks to estimate effects of these changes on the supplemented population, as can be inferred from literature (e.g., see Steward and Bjornn 1990), though the exact nature and extent of such effects are not currently well understood. The term "yardstick" implies a range of possible effects.

The default values in the model for the yardsticks were obtained either from consultation with experts or as a result of discussions among the members of RASP (RASP 1992). The mode1 can be used to explore the effect of uncertainty in these yardsticks. It can also help assess the, needed level of performance by supplementation fish to achieve success by the project.

3.2.4.1 Genetic Yardsticks. Genetic yardsticks are intended to represent possible' adverse effects of supplementation on genetic fitness.[4] Such changes may result 'in reduced stock productivity with significant implications to potential risks and benefits of supplementation. Genetic fitness in the model can vary for four basic types of fish that are tracked through each life stage and in successive generations (Fig. 3; Table 1). A fish is assigned to a type based on its parental history (hatchery or wild) and a genetic recovery scenario.

[4] RASP (1992) recognized that the term "fitness" has a restricted definition when used in a genetic sense; for example, Falconer (1970) stated: "The proportionate contribution of offspring to the next generation is called fitness of the individual." However, the term fitness has a wide variety of applied meanings, Use of the term "fitness" by RASP refers to the long-term, phenotypic 'performance and not the more restrictive genetic definition.'

Table 1. Description of general fish types tracked in the EDT model.

Designation	Description
T_3	Hatchery produced fish that return to spawn naturally.
T_2	Progeny whose parents were both hatchery produced fish (T_3) that spawned naturally.
T_1	Progeny with one wild and one hatchery parent.
T_0	Progeny whose parents were naturally produced.*

*T_0 takes on a different definition in Scenario I, II, and III (see Fig. 6).

Genetic recovery scenarios were developed by RASP (1992) to address the question: How rapidly does the hatchery influence on fitness diminish with successive generations of natural spawning? Due to a lack of information on this subject, RASP developed three scenarios based on different assumptions regarding the rate of recovery of fitness in the progeny of hatchery fish (Fig. 6). Scenario I assumes that progeny of fish one generation removed from the hatchery (Type T_2) attain the fitness of wild fish not yet affected by hatchery practices (Type T_0). Scenario II assumes that hatchery fish and their progeny never attain the fitness of wild fish. Scenario III is intermediate and assumes that the naturally produced progeny of a hatchery X wild cross (Type, T,) that subsequently mate with wild fish attain the fitness of wild fish (Type T_0). Wild fish not impacted by hatchery practices are always given a fitness of 1.0 (referred to as the wild fish standard in this document).

RASP (1992) received input from two geneticists in estimating fitness in the natural environment for salmon subjected to six categories- of hatchery practices (Fig. 7; Table 2). The values were provided by Dr. Craig Busack of the Washington State Department of Fisheries and reviewed by Dr. Graham Gall of the University of California' The six categories of treatment were formulated to represent three possibilities for broodstock source and the two types of culture practices described above, i.e., conventional and innovative culture. The three options for broodstock source are to use local, adjacent, or distant stock, with distance representing genetic distance, i.e., degree of genetic similaiity.

The fitness values in Table 2 are multiplicative; thus a first generation hatchery fish (T_3) produced using conventional practices whose parents-came from local broodstock is given a fitness of 0.59 (Table 3). The values given in Tables 2 and 3 were intended by Dr. Busack to

[5] Dr. Busack (personal *communicdions)* has since concluded that the fitness estimate for conventional culture of *0.7* is likely too low and has suggested that some intermediate value between 0.7 and 1.0 may be more appropriate.

Table 2. **Changes in fitness of hatchery fish exposed to different broodstock selection and culture practices. Fitness is relative to a wild standard of 1.0 and fitness factors are multiplicative.**

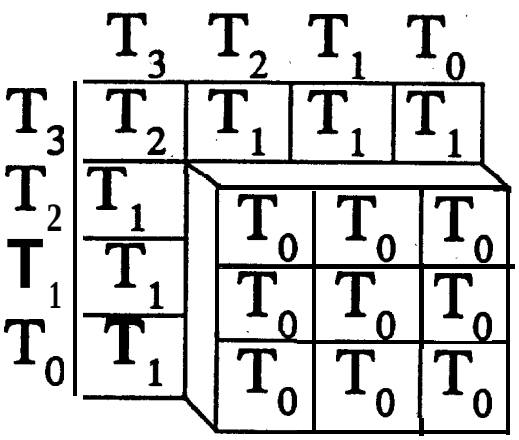
Category	Treatment or Pedigree	Fitness
Domestication effects	T_3 T_2 T_1	0.85 0.90 0.95
Broodstock obtained from:	Local stock Adjacent stock Distant stock	1.00* 0.70 0.10
Culture regime (inadvertent selection)	Innovative Conventional	1.00* 0.70**

* No loss of fitness.

** Value believed to be too low (C. Busack, Washington State Department of Fisheries *personal comm unications)*

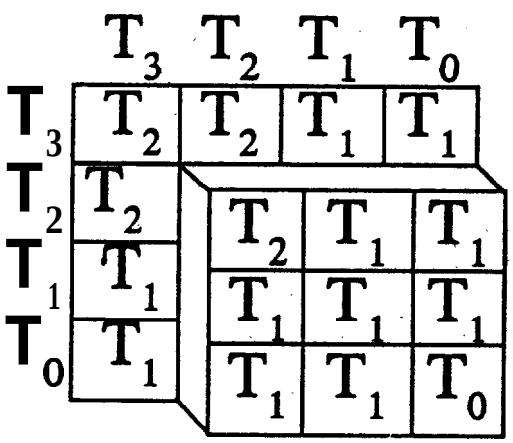
Table 3. **Fitness estimates used in the spreadsheet model for three fish types, three broodstock types, and two rearing regimes.**

Broodstock	Culture regime	TYPES		
		T_3	T_2	T_1
Local	Conventional	.59	.63	.665
	Natural	.85	.90	.95
Adjacent	Conventional	.42	.441	.466
	Natural	.59	.63	.665
Distant	Conventional	.06	.063	.066
	Natural	.085	.09	.095



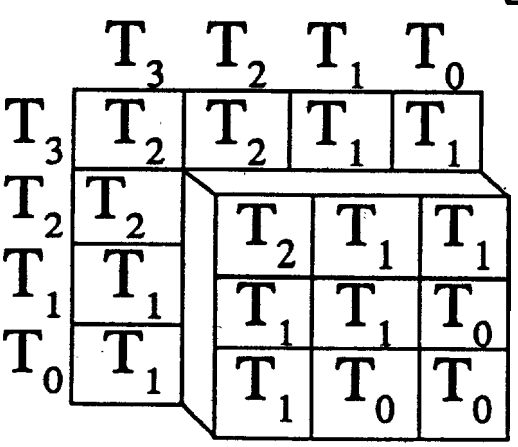
SCENARIO I

Progeny of fish one generation removed from the hatchery attain all the characteristics of the native stock.



SCENARIO II

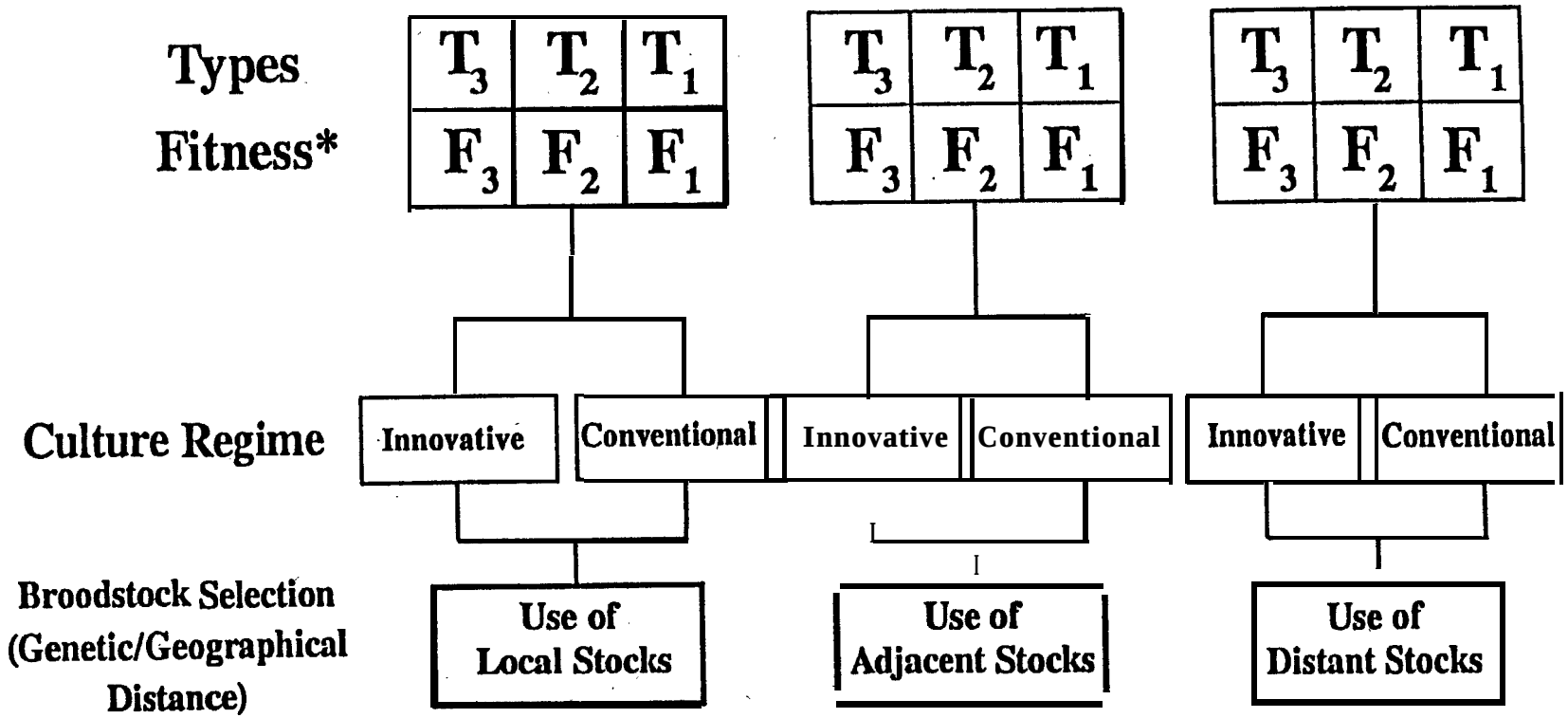
Hatchery fish never attain all the characteristics of the native fish.



SCENARIO III

Intermediate between Scenario I and II. Native fish that mate with the progeny of hatchery X native crosses (T_1) attain the characteristics of native fish (T_0).

Figure 6.' Possible breeding outcomes for the four basic fish types as modified by three recovery scenarios.



*Native fish (T_o) are always assigned a fitness coefficient of 1.

Figure 7. Categories of broodstock and culture regimes. Innovative culture refers to culture conditions that mimic conditions found in the natural environment. Conventional culture refers to standard hatchery culture techniques.

be representative of fish raised in the hatchery to the smolt stage. It was assumed in designing the EDT model that genetic changes are less for fish held in the hatchery for shorter periods than to the smolt stage. As a result, the model also tracks the abundance of several sub-types of T_3 fish, with fitness being affected by their life stage of release.

The genetic fitness yardsticks are used in the model to modify survival (or reproductive success) between life stages. Hence if a hatchery practice reduces fitness by half, the cumulative, natural survival between life stages will be reduced by half.

324.2 Non-Genetic Yardsticks. Non-genetic yardsticks represent possible adverse effects of behavioral and physiological changes caused by hatchery practices not associated-with genetic change. Behavioral modification, for example, imparted by the hatchery experience may cause part of the differential in survival between hatchery and wild fish. Lack of exposure to predators may produce behavior that makes hatchery fish more vulnerable to predation when released into the natural environment.

The model computes the values assigned to these yardsticks by simply calculating the residual effect between the total difference between wild and hatchery survival (an input value) and the amount associated with the genetic yardsticks.

3.2.5 Summary of Risks and Benefits and Related Analvsis

'The model estimates the benefits of supplementation as increased production and productivity of the combined natural and hatchery stock. Risk is measured as reduced production and productivity in the naturally spawned population and in the supplemented reach or in adjacent, nontarget reaches. Model outputs permit the evaluation of the genetic-risks described by Busack (1990).

4. MODEL IMPLEMENTATION

4.1 Model Setup and Initiation

The model is accessed from within Quattro Pro by retrieving the desired spreadsheet file containing the model. Upon retrieval, the menu system that operates the model is automatically initiated. The user can then perform all setup procedures, run the model, retrieve output, and save files entirely from within this menu system.

The user steps'through a series of.menus to enter all relevant parameter values into the spreadsheet in preparing to run the model. Each input represents an assumption that is being made about the condition of the stream/population production system, mainstem passage and natural marine survivals, harvest rates, and the characteristics and performance of supplementation fish. Some of the parameter values to be specified are smolt carrying

capacity, ratios of stage-specific juvenile capacities that define habitat limitations, fecundities, initial age composition of the spawner population; survivals between life stages, predator response characteristics in the subbasin during smolt migration, homing fidelity, and harvest rates (Fig. 3).

If modeling is to facilitate a better understanding of how the stream/population system may be functioning, it is imperative to attempt to conceptualize how the parameter values relate to one another. All sources of information should be drawn on 'in setting these values in the model: Initial values for many of these to begin the modeling process can be obtained from the subbasin specific data files used-for the Systems Planning Model (NPPC '1989). The user should examine the effect of altering these values, being willing to make assumptions on the basis of what seems intuitively correct. Beyond that,.the user may need to make assumptions about what seems intuitively correct. For example, if the S_0 value from the Systems Planning Model is used as a starting point, its disaggregation into the separate life stages would suggest values associated with relatively'high quality habitat (due to how the S_0 value was estimated). However, if it is- known that the quality of spawning environment in the subbasin of interest has been severely degraded, then it could be safely assumed that the egg-fry survival value - has been reduced accordingly. As suggested in the modeling example, the parameter values should be adjusted until the population exhibits a time series pattern that reflects what is known or assumed about the real population, i.e., increasing, stable, or declining. In a sense, parameter adjustment in this manner is a type of calibration.

The supplementation treatment to be 'modeled- for each run is specified by the user by defining numeric release goals for each life stage to be released, the duration in years for the action, a broodstock source, a broodstock policy, the culture regime, and an natural spawning escapement policy for supplementation fish (Fig. 3).

Once all setup procedures are completed, the user can initiate-the model run. Upon giving this command, the user is given final opportunity to review some of the conditions that were previously specified, which are displayed to a control screen. The user then specifies a unique run number for the model run being initiated, sets the number of years to be modeled (maximum of 150), and selects the genetic recovery scenario being assumed, prompting the computational procedure to begin.

4.2 Model Output

After all computations are completed by the model, the user is returned to the menu system for selecting, output options. If desired, the user can display a series of graphs to the screen whereby time series data and stock-production plots can be reviewed for the completed model run. Output in graphic or tabular form. can then be saved to file or printed.-

4.3 Batch Mode

The model can be operated in batch mode to perform a series of model runs without interruption. Hundreds of runs can be made consecutively in this manner. Several hundred model runs can be made overnight by using this feature.

Operating in batch mode is particularly useful for performing sensitivity analyses on ranges of values for individual parameters or various combinations of parameter values (as done in Appendix A). This enables the user to more efficiently explore the effect of uncertainty in various parameters and conditions on outcome. Such a. process of modeling and analyzing outcome/can be of great value in developing 'alternative -hypotheses about the diagnosis of the stream/population system and treatment effects. This can facilitate the identification of those conditions (or assumptions) under which specific supplementation strategies might achieve the project's objectives (see Section 1.1).

The user is required to become familiar with manipulating the spreadsheet that contains the model and output summaries to utilize this option most effectively. The tasks of doing such manipulations are not difficult, however, and are easily mastered. The benefits of using the EDT model will be enhanced significantly by those that use these techniques.

4.4 Special Applications

The EDT model can be modified from its current configuration to consider differences in production characteristics between sub-populations within a subbasin and interactions' of those sub-populations. One way that this has been done has been to remove the macro comma& and to simply create very large spreadsheets that allow for different inputs for each sub-population and interactions at certain life stages. This was done for the Yakima subbasin using three subpopulations,. each having different habitat characteristics, fecundities, and maturity rates. In that case, only one sub-population was being supplemented It was important to model the three sub-populations together because a Type III predator response is assumed to be operating in the lower Yakima subbasin during smolt migration. Therefore, mortality rate due to predation during smolt migration would be affected by the total number of smolts present.

Similar modifications to the model can be made to examine other questions related to population structure. 'Questions involving habitat connectivity and life history diversity would require such modifications.

5. MODELING EXAMPLE

We present a simple modeling example in this section to illustrate how the model can be used and the type of output that is generated. Other examples with more complexity associated ‘with them were presented in ‘RASP (1992). The simplified example given here illustrates how results can vary according to diagnosis and treatment design. Our example is for a hypothetical spring chinook population produced in a subbasin located above eight dams in the Columbia Basin. Only a very limited presentation of the results is given here for the sake of illustration; a full analysis of risks and benefits would require a much greater examination of results.

5.1 Hypothetical Diagnosis -and Treatment Selection

The relative health of spring chinook populations in the Columbia Basin varies between subbasins (Reisenbichler 1990; Petrosky and Schaller 1992; Lichatowich et al. 1993). This variation can be at least partly attributed to differences in productivities between populations (Reisenbichler 1990). Differences in productivities are likely related to the quality of habitat in each subbasin (Cramer and Neeley 1993; Lichatowich et al. 1993).

In our example, we consider three alternative diagnoses,, or states of nature, referred to as A, B, and C. These reflect uncertainty in being able to recognize the current trend (over some time period) of spawner abundance in the subbasin. The three diagnoses are associated with gradually increasing, stable, or gradually decreasing abundance. For’our example, we conclude that diagnosis C is most correct, and following the planning process outlined in Part III of RASP (1992)(see Section 1.1 of this document), a supplementation strategy is selected as being appropriate. There is, therefore, unertainty in both the diagnosis and the appropriateness of the treatment strategy.

We assume that it is strongly evident that habitat carrying capacity within the subbasin is generally not being achieved. Hence the uncertainty in the diagnosis revolves mainly around the existing estimate of productivity for all life stages combined. In this case, we assume that there is evidence that the principal difference in productivity of this population compared to another more healthy population exists within the incubation environment; survival conditions appear comparable in all other life stages. The three alternative diagnoses are described in Table 4; the only difference between each is attributed to the productivity of the first life stage, i.e., density-independent survival from egg deposition to fry emergence. Trend lines in production associated with each diagnosis differ accordingly (Figs. 8-10A and B). We purposely made the differences in egg to fry productivity slight. Diagnosis C would be associated with poorer conditions for egg incubation, as might be caused by sedimentation from road building,, logging, grazing, mining, or other natural conditions. The values in Table 4 represent plausible sets of ‘assumptions for the population.

Table 4. **Parameter values associated With three alternative diagnoses of a hypothetical spring chinook population in one subbasin of the Columbia River.**

Diagnosis:	A	B	c
Population trend	increasing	stable	decreasing
Egg - fry survival	*0.45*	*0.42*	*0.39*

Elements common to each diagnosis:	
Smolt carrying capacity	2,000,000
Fry - parr survival	0.56
Parr - smolt survival	0.56
Smolt - smolt survival	0.90 (assume Type I response)
Downstream passage survival	0.30
Estuarine survival	0.15
Ocean survival	0.5, 0.6, 0.7. 0.8 for ocean ages 1-4
Ocean harvest rate	'0.05
Columbia River harvest rate	0.0;
Homing fidelity	0.97
Terminal harvest rate	0.02
Prespawning survival	0.80
Fecundity	age-specific
Initial subbasin returns	500 males, 500 females

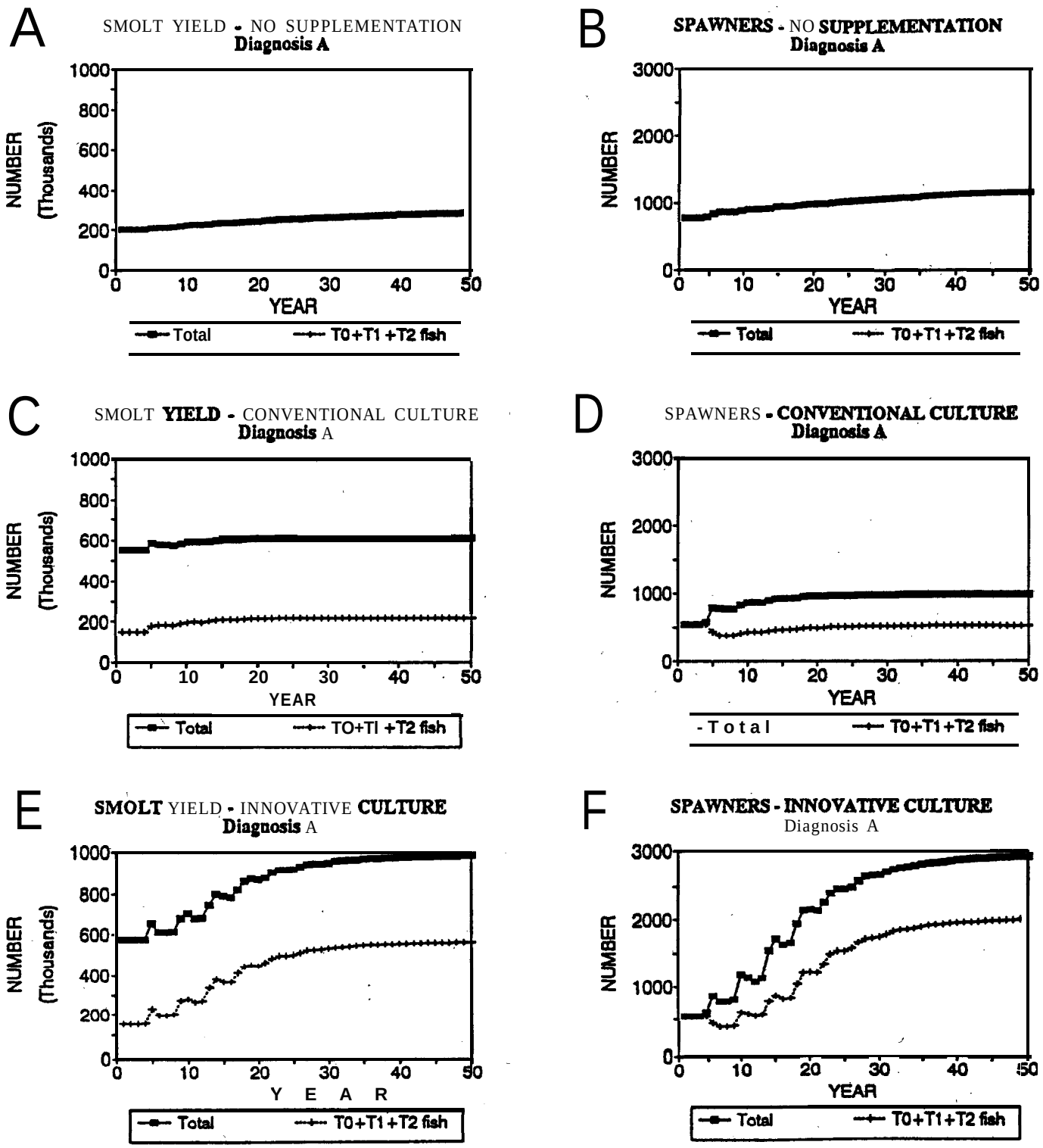


Figure 8. **Model results for diagnosis A: Smolt yield and natural spawners with no supplementation (A and B), supplementation with conventional culture (C and D), and supplementation with innovative culture (E and F).**

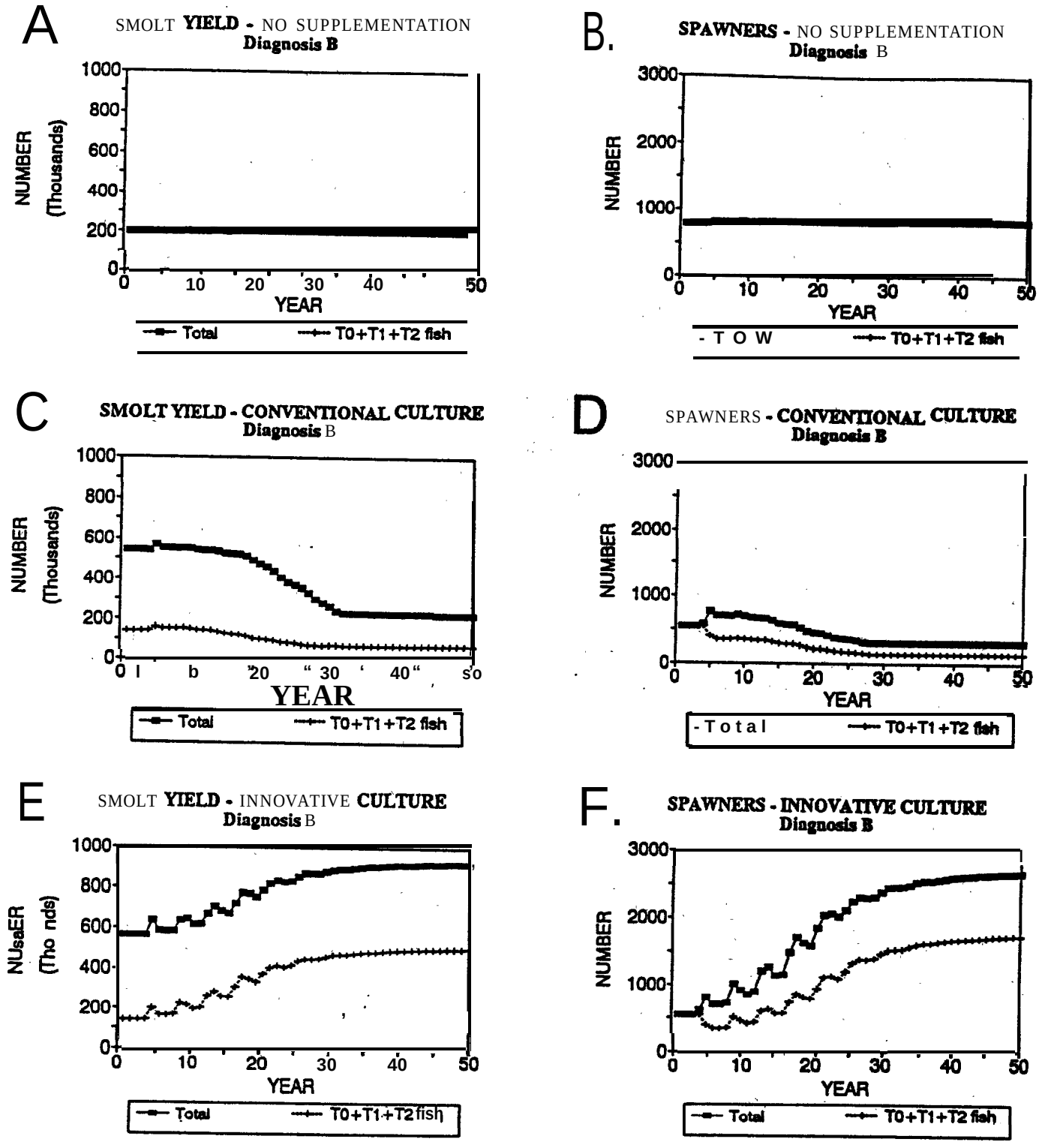


Figure 9. **Model results for diagnosis B: Smolt yield and natural spawneq with no supplementation (A and B), supplementation with conventional culture (C and D), and supplementation with innovative culture (E and F).**

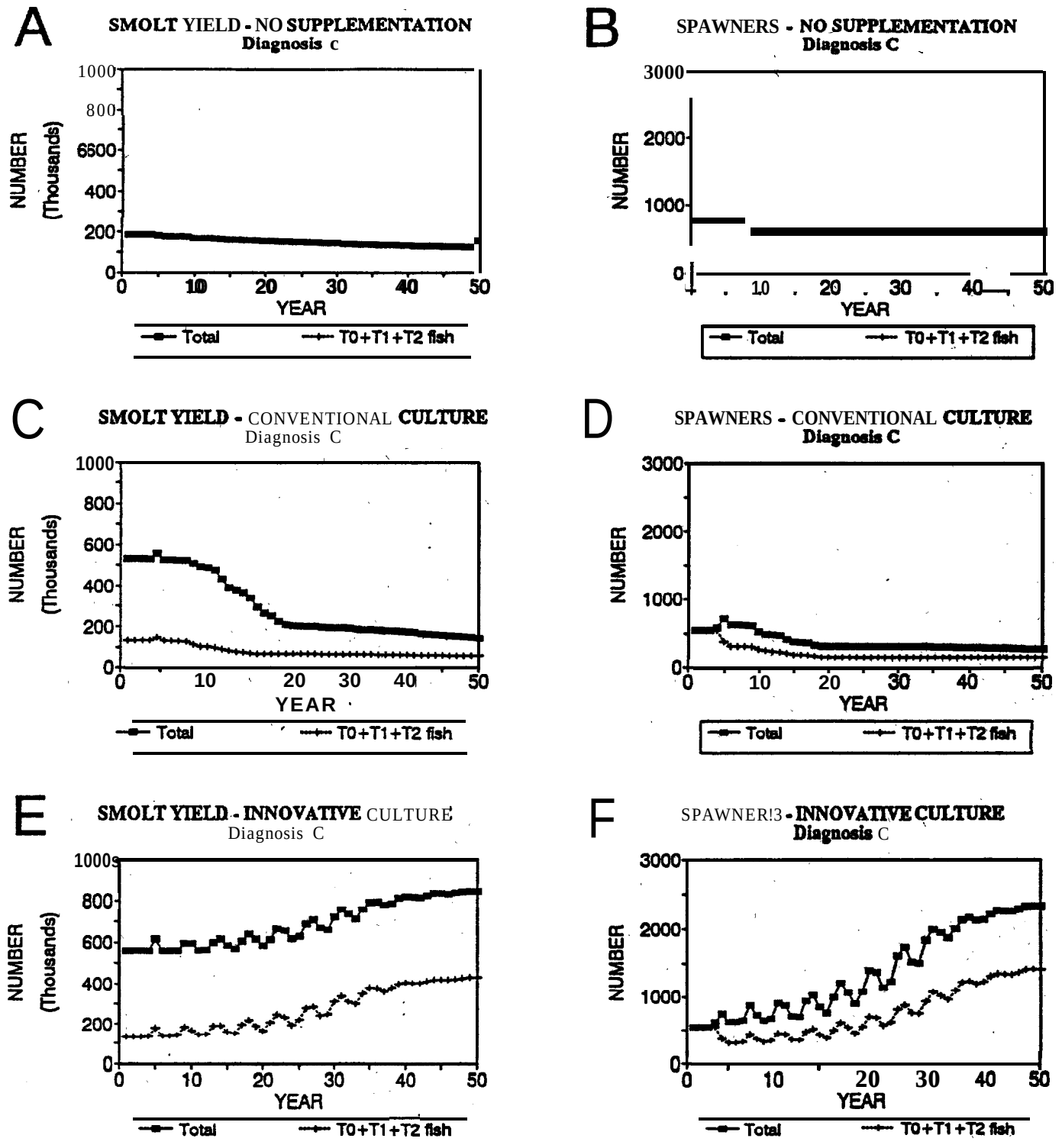


Figure 10. **Model results for diagnosis C: Smolt yield and natural spawners with no supplementation (A and B), supplementation with conventional culture (C and D), and supplementation with innovative culture (E and F).**

Two supplementation strategies were applied, differing only in whether hatchery fish were produced using conventional or innvotative culture practices (Table 5). **Supplementation** fish were outplanted' as smolts. The numeric release goal was set at 500,000 **smolts,** though this **was** often not achieved because of constraints imposed by the **broodstock** collection,policy (Table 5). Wild fish of local stock were'used exclusively for broodstock, i.e., no first generation hatchery produced fish were used.

We **assumed that** hatchery smolts produced using conventional **culture techniques** survived at '25% of the rate of wild T_0 fish. We then assumed that **innovative hatchery** practices **could** effectively double survival, compared to conventional practices, so that fish produced with innovative practices survived at 50% of the rate of wild fish, We also assumed that genetic recovery scenario 3 characterized the recovery of fitness in the naturally produced' population.

Table 5. Description of two alternative supplementation strategies applied to a hypothetical spdng chinook population.

Supplementation treatment:	
1.	**Conventional** culture practices (relative survival of hatchery fish = 0.250)
2.	**Innovative culture practices (relative survival of hatchery fish = 0.50)**

Elements common to each:	
Life stage of release	smolt
Numeric release goal	500,000
Broodstock source	local
Maximum % natural fish in broodstock	100%
Maximum % used of natural run for broodstock	50%
Maximum % used of total' run for broodstock	50%
Maximum % T_3 fish allowed in natural escapement	50%
Minimum wild males allowed in natural escapement	**100**
Minimum wild females allowed in. natural escapement	**100**
Recovery scenario assumed	**3**

5.2 Modeling Results

All model runs were made for 50 years and were made without varying downstream passage or estuarine survivals. Running the model in this manner is a way of looking at how the population could be expected to respond to the treatment under average conditions and how production trends might be affected.

The results suggest that supplementation with conventional culture would pose considerable risk to the hypothetical population with any of the three diagnoses (Figs. 8-10). Serious declines in natural smolt yield and spawning escapements could occur with this supplementation strategy, particularly with diagnoses B and C. Adverse effects would be mainly due to what is sometimes referred to as "broodstock mining." Spawners removed from the natural spawning population for broodstock purposes would produce fewer progeny returning to the natural spawning grounds than those that reproduce naturally. Only in the case of diagnosis A would the number of fish that continue to spawn naturally come close to the unsupplemented situation.' Production trends would be radically altered for the worse under diagnoses B and C with conventional culture practices in place.

Supplementation with innovative culture would produce substantial increases in production during the period of treatment for all three diagnoses. In this case, increased survivals within the hatchery environment during the egg to smolt stages would more than offset the survival differential between wild and hatchery fish during post-release stages. The effect would be an increase in productivity for the integrated wild-hatchery population compared to the wild population in the absence of supplementation.

It should be noted that the results do not show how the effects of supplementation could persist after terminating the treatment. The model can be used to examine changes in fitness and reproductive success of the natural population after stopping supplementation.

The example illustrates that results can vary markedly depending on the set of assumptions that are made about the natural production system and the treatment strategy. The model does not predict outcome. Too little is currently known about supplementation to predict its result (RASP 1992; Lee 1993).

The EDT model provides, however, a way to help identify a set of assumptions that, if valid, will minimize risks and provide the desired benefits. In the example shown,, the model would help identify. the level of performance needed by hatchery fish to achieve the project's objectives. Once these critical assumptions are identified, the project biologist must be prepared to analyze each one. How likely is each of these assumptions? What is the evidence in support of and against each one? How do risks and benefits compare between alternative sets of assumptions? Which assumptions, that if invalid, pose the greatest risk of failing to achieve the assumption? The user should refer to RASP (1992) for a discussion on addressing such uncertainties.

ECOSYSTEM DIAGNOSIS AND TREATMENT MODEL AS APPLIitD TO SUPPLEMENTATION

PART II
USER GUIDE

1. INTRODUCTION

The EDT model is operated through Quattro Pro using a system of customized menus. The user can perform all basic setup procedures, run the model, retrieve output, and save files entirely from within this menu system. The User Guide describes this menu system and the various operational options available. Operating the model is quite simple, however, and the guide will not be needed after only a relatively small amount of experience is gained in running it,

Certain model applications will require pefforming some tasks outside of the menu system. These items are discussed in Section 4.8.

2. PREPARING SOFTWARE AND FILE DISKS

The model was developed within Quattro Pro version 4.0 for DOS. The many macros that are used to operate the model will not perform exactly as intended with Quattro Pro for Windows. Modifications are required to operate the model using' the Windows version of Quattro Pro. It should be noted, however, that the model would run substantially slower under Windows. We also recommend that the model not be run within the Windows environment even though Quattro Pro for DOS is being used., Quattro Pro for DOS can be used within the Windows environment if desired, but model computations in the model will be slowed if this option is used. Therefore, if you normally use Quattro Pro for DOS under Windows, exit Windows and return to the DOS prompt before loading Quattro Pro. This will improve efficiency of modeling exercises.

The model requires at least three megabytes of RAM though even larger amounts of RAM would increase modeling efficiency. Processing'time is enhanced significantly with an 80386 and coprocessor or 80486 system.

The model is contained in the spreadsheet file EDTM30.WQl. An auxiliary file, EDTMXTR3.WQ1, is also required to run the model. The diskette that contains these files

also holds other auxiliary files that are used to introduce variation. The variation files are provided to aid in learning how the model can be used and not necessarily for analyzing actions on specific streams. Users interested in modeling variation will likely need to produce their own files more applicable to their specific situations: All of these files should be placed in the same work subdirectory. ***Important note:*** Set the default subdirectory to correspond to where these files are placed. This is done easily by using the command **/OSD** (FORWARD-, SLASH, OPTIONS, STARTUP, DIRECTORY). This can be done when you enter Quattro Pro. The model will not work properly unless the default directory is correctly set.

On-screen displays will be easiest to read if WYSIWYG is turned off (use the command **/OD,** then set the display to 80x25). Also, the default color schemes for Quattro Pro 4.0 and 5.0 are very difficult to read once WYSIWYG is switched off. Therefore, change the color scheme to the default for Quattro Pro version 3.0. Do this using the command **/OCPV (FORWARD-**SLASH, OPTIONS, COLOR **PALETTES, VERSION** 3 COLOR). This will produce a blue background, instead of black, among many other color changes. Once these changes are made, press UPDATE under OPTIONS to avoid having to repeat them when initiating the next work session.

Individuals who have not run large 'spreadsheets on their computers may need to first set the Expanded Memory option under OPTIONS to BOTH (the alternative is to set this to SPREADSHEETS). The. former option allows larger spreadsheets to be run with a given amount of RAM. Do this using the commend **/OOEB** (FORWARD-SLASH, **OPTIONS,** OTHER EXPANDED MEMORY, BOTH). ***Important note:*** After specifying this option, exit Quattro Pro, then reload it. This' action is necessary to change how the software utilizes available memory. This step is only required once (i.e., not every time Quattro Pro is loaded), unless the SPREADSHEET option is subsequently selected. Also, newcomers to Quattro Pro should be aware that this spreadsheet software operates with expanded memory and not extended memory. The **CONFIG.SYS** file may need to be altered to manage available extended memory as if it were expanded (see your DOS manual, or better yet, talk to somebody who knows how to make' the needed change).

3. INITIATING A WORK SESSION AND THE MODEL MENU SYSTEM

The model is accessed by retrieving the appropriate spreadsheet file from within the Quattro Pro'environment (this will be the file **EDTM30.WQ1,** unless the file has been updated and saved under a different name). Upon retrieval, the spreadsheet containing the model automatically activates the model's Main Menu. If for some reason this does not occur 'when opening the spreadsheet, the user can do so by pressing ALT-Q (hold the ALT button down while simultaneously pressing Q).

The model is operated entirely through menus, used in model setup and parameter specification, creation of input files (excluding variation tiles), running the model, obtaining

output, and saving files. Most of these menus will be illustrated in this manual. When operating within the model, a short description of each menu item is displayed at the bottom of the screen when the cursor is placed on it.

The Main Menu identifies the major options that can be used during a modeling session:

MAIN MENU

DRAINAGE/STOCK
TREATMENT,
VARIATION
PREDATOR EFFECTS
Go
OUTPUT
SAVE
BATCH. MODE
QUIT

The first two options, **DRAINAGE/STOCK** and **TREATMENT,** are used to define the existing characteristics of the -population/stream production system and the supplementation treatment to be applied, respectively. **VARIATION** is- used to attach input files that annually vary downstream. passage survival within the Columbia River or estuarine survival. **PREDATOR EFFECTS** is used to specify the type of predator response function during **smolt** migration within the subbasin..GO prompts the model to begin processing a specific model run. **OUTPUT** enables the user to obtain, various kinds of output. SAVE is used to save file specific sections of input or output, or the entire current 'spreadsheet file as configured. **BATCH MODE** enables the user to initiate a batch job, whereby more than one model run is made without interruption. QUIT ends the work session, leaving **the** spreadsheet open but the model and menu system deactivated. Press **ALT-Q** to reactivate the menu system.

N O T E : If during a work session, any command fails to. initiate properly, or you wish to abort a specific command path with seemingly no menu options available, press **CTRL-BREAK** (hold the **CTRL** key, **down while** simultaneously pressing BREAK). A beep will sound and an error message will be **given.** Press **ESC** to turn off the error message, leaving you within the spreadsheet with the model and menu 'system deactivated. Press **ALT-Q** to reactivate the menu system.

4. OPERATING THE MODEL

Each of the functions performed through the Main Menu are described in the sections that follow. Each Main Menu option is described in the order that it appears within the menu.

4.1 Drainage/Stock

Selection of **DRAINAGE/STOCK** enables the user to define the characteristics of the subbasin and fish stock to be modeled. When selected, another menu is given:

DRAINAGE/STOCK MENU

ON FILE
NEW
MODIFY SUBBASIN/STOCK PARAMETERS

5

The user can specify an input file, if one has already been created and saved, modify characteristics (parameters) of a subbasin/stock already specified, or can build an input parameter set for a new subbasin/stock. Once created the input parameter set is saved to file through **SAVE** in the Main Menu. If a new parameter input set is being built, the user is asked to first:

"ENTER THE NAME OF THE RIVER TO MODEL?

(a maximum of nine letters or characters are allowed, including spaces) and,

"ENTER A UNIQUE TWO-LETTER CODE FOR THE SUBBASIN:"

The user may want to use the, two letter codes for Columbia River subbasins as specified within the Systems Planning Model (SPM) (NPPC 1989).

The user is then given another menu for specifying parameter and variable values:

DRAINAGE/STOCK
PARAMETER SETUP MENU

HABITAT CAPACITIES
STAGE SURVIVAL
FECUNDITY
AGE/SEX
CATCH RATES/POLICY
INITIAL POPULATION SIZE

4. I. 1 Habitat Capacities

Selection of this item takes the user to an input screen to enter estimates of smolt carrying capacity, and two ratios that define seasonal habitat limitations, as follows:

(1) **Smolt carrying capacity -** This is the estimated smolt capacity of the subbasin just prior to smolt outmigration. This value might be obtained from existing studies within the drainage, from the SPM, or through application of literature values of smolt'density. The value can be varied to examine the effect of: uncertainty in this parameter.

(2) **Incubation capacity/smolt carrying capacity -** This is the ratio of egg or alevin capacity to the smolt carrying capacity. This input specifies the relative limitation imposed by the amount of spawning habitat on smolt carrying capacity. Any value can be input; values of 500, 10 and 0.2 indicate no spawning habitat limitation, moderate limitation and strong limitation, respectively. If no subbasin specific data. are available, then the- user must employ best judgement. The value is varied to examine the effect of uncertainty in this parameter.

(3) **Winter capacity/summer capacity -** This is the ratio of winter pi-e-smolt capacity to summer parr capacity. This input specifies the relative amount of production limitation imposed by the amount of overwintering habitat compared to summer rearing habitat. Any value can be input; values of 2.0, 1.0 and 0.2 indicate strong summer limitations; roughly balanced limitations, and strong winter limitations, respectively. If no subbasin specific data are available, then the user must employ 'best judgement. The value is 'varied to examine the effect of uncertainty in this parameter.

These parameters are used in the life stage-specific' Beverton-Holt stock-production relationships in the model. Appendix B describes their use in more detail and how the model can be utilized to explore the effect of habitat modifications.

4.1.2 Stage survival

This menu item takes the user to an input screen where life stage-specific survival values are input for wild native fish at the following stages:

1) egg to emergent fry
2) fry to late summer parr
3) parr to smolt (start of smolt migration)
4) smolt to smolt (within subbasin)
5) downstream passage (subbasin mouth to below Bonneville)
6) estuarine
7) ocean
8) upstream passage
9) stray rate to other subbasins
10) pre-spawning

Survival values for stages, prior to smolt are at low density (density independent) and therefore comprise the productivity component of freshwater survival (see Appendix B). The smolt to smolt value is varied by the model if predator effects are assumed to be density dependent (see Predator Effects). 'Downstream passage and estuarine survival are modified by the model if environmental variation is switched on (see Variation). Modifiers of survival for naturally produced hatchery x wild fish are input through the Treatment menu selection.

Survival of hatchery fish within the hatchery must also be specified, as well as modifiers to these values, for wild native fish taken into the hatchery. Modifiers are specified through an input screen labeled **PEDIGREE RELATIVE SURVIVAL ADJUSTMENT, These** modifiers can be used to adjust the in-hatchery survival of fish with wild parents 'downward compared to fish with hatchery parents. A value of 1.0 sets survivals equal to one another; a value of 0.9 would adjust the in-hatchery survival of fish with wild parents to 90% of that 'of fish with hatchery parents. In this latter case, it would be assumed'that hatchery domestication results in fish surviving better in the hatchery environment than fish with wild parents.

4.1.3 Fecundity

Selection of this item prompts an input screen where estimated fecundity by age is specified for both wild native fish and hatchery fish in the subbasin. These values are fixed in the model; naturally produced hatchery x wild native hybrids are assumed to have the same fecundity as wild native fish. All first generation hatchery fish are assigned the hatchery stock values. No mechanism is provided for inheritance of fecundity.

4.1.4 Age/Sex

Selection of this item prompts an input screen where steady state sex-specific age composition and sex ratios are specified. Age data for the sexually mature population within the subbasin are to be used. Values can be different for first generation hatchery fish than for naturally produced fish. No mechanism is provided for inheritance of age or sex. The age composition data are used by the model to calculate maturation rates for a fish at each ocean 'age.

4.1.5 Catch Rates/Policy

Selection of this item prompts an input screen where catch rates are specified for marine fisheries (all marine fisheries combined), mainstem Columbia fisheries (all fisheries combined), and 'for the terminal area in the subbasin. Catch rates represent the proportion of fish available to the fisheries that die due to the fisheries (includes all-fishery induced losses). Rates can differ by fish age.

4.1.6 Initial Population Size

This item is selected to specify initial population sizes, which are input as the number of mature fish entering the subbasin. Estimates of average numbers that currently exist for the population of interest should be used. Numbers of fish by, type (TO, T1, T2, and. T3) can be input. Provision is given for specifying the number of hatchery fish returning that originated from non-native stock.

4.2 Treatment

Selection of TREATMENT within the Main Menu produces another menu, shown below, enabling the user to define the components of the supplementation strategy to be modeled:

TREATMENT MENU

ON FILE
USE PRE-SET TREATMENT
MODIFY TREATMENT

If an input file has already been created and saved, the user can select ON FILE to load it into the model at this time. Files that have previously been saved automatically are given the prefix SU-enabling the model to recognize them and display them in a menu of available file.

Selection of USE PRE-SET TREATMENT keeps the supplementation strategy settings unchanged'and takes the user back to the previous menu.

Selection of **MODIFY TREATMENT** enables the user to change the existing settings of the supplementation strategy; the following menu is prompted:

TREATMENT COMPONENTS MENU

OUTPLANTING GOALS
DURATION
BROODSTOCK STRATEGIES
HATCHERY CULTURE METHODS

4.2.1 Outplantine Goals

Selection of this item produces an input screen to specify the annual numeric'release goals for the number of hatchery produced fish by life stage. Targets can be specified for fish to be released in the spawner, egg, emergent fry, pre-smolt (fall release), or smolt stages. A release of spawners i's assumed to consist entirely of imported stock. Fish can be released in one or more stages.

4.2.2 Duration

Selection of this item produces an input screen to specify the number of years in which supplementation might occur, provided all the required conditions are met. Durations can be different for each life stage of release. The number of years specified can -be less than the total number of years that the model is run for.

4.2.3 Broodstock Strategies

Selection of this item calls up the following menu; a sub-menu is attached to the second choice, POLICY **FOR MANAGING BROODSTOCK**:

SOURCE OF BROOD
POLICY FOR MANAGING BROODSTOCK

TIME PERIODS FOR CONSTANT OR 2-PHASED POLICY
CONSTRAINTS ON ESCAPEMENT MANAGEMENT
SEX RATIO

(1) **Source of brood** - Selection of this item produces the following input screen, shown with hypothetical input values, for specifying where the broodstock is to be collected from:

BROOD COLLECTION SCHEDULE (rows must add to 100%)						
	SOURCE					
DESTINATION	Imported	Pre-t-har	Post-t-har	Spwng grnd	Fry	P-smolt
Spawners	0%	0%	0%	0%	0%	0%
Eggs	0%	0%	0%	0%	0%	0%
Fry	50%	0%	50%	0%	0%	0%
Presmolt	0%	0%	0%	0%	0%	0%
Smolt	0%	0%	100%	0%	0%	0%

The total of each row must add exactly to 100%; there is no connection between rows. Choices for where broodstock can be taken are (1) to import stock from outside the stream or (2) to use fish returning to the stream of interest. If broodstock is taken from the stream of interest, then the user must specify where (or when) they will be captured, i.e., (1) prior to terminal harvest, (2) after terminal harvest, (3) on the spawning grounds, (4) as wild fry (fry are captured and taken into the hatchery for rearing until a subsequent life stage when they are released), or (5) as wild fall presmolts (presmolts are captured and taken into the hatchery for rearing until the smolt stage when they are released). *Note:* The capture of wild juveniles for subsequent rearing in the hatchery is not the same as captive broodstock.

If imported stock is used in any part, then the user is prompted to specify whether that stock is an adjacent or distant stock, based on assumptions about genetic distance.

(2) **Policy for Managing Broodstock** - This item defines the policy for managing the broodstock and escapement of hatchery produced fish to the natural spawning grounds. The policy is defined through the following menu items:

(a) **Time Periods for Constant or 2-Phased Policy** - This allows for specifying different broodstock policies for the period of supplementation; e.g., the user may choose to designate a different allowable proportion of the natural run to be taken as broodstock for each of two time periods. Input is made by specifying the end years of the two time periods. Set the numbers to be the same if only one constant policy is desired.

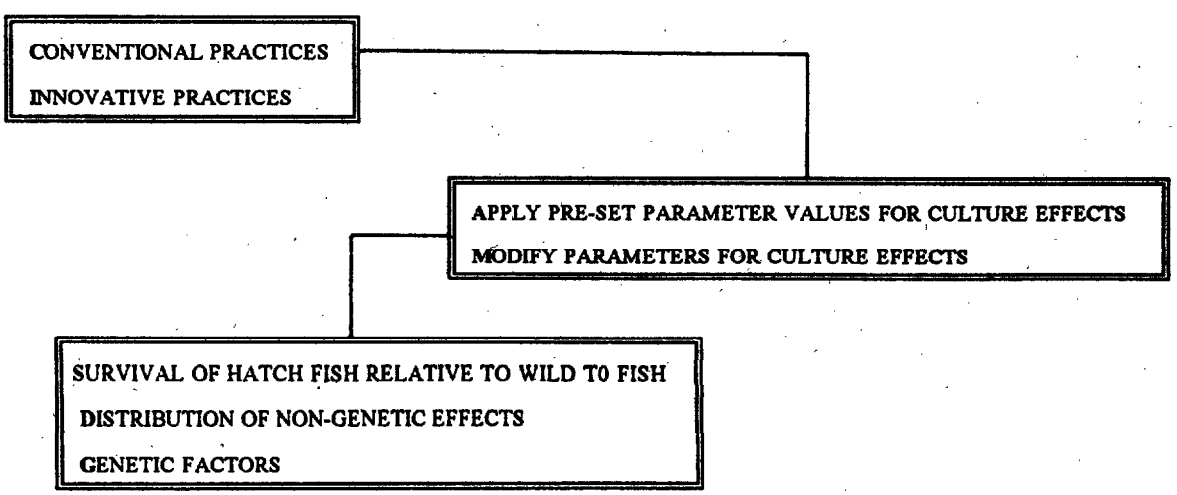
(b) **Constraints on Escapement Management -** This sets the constraints on managing broodstock and escapement 'by the time periods specified above. Five constraints can be specified: i) the minimum percent of broodstock required to be naturally produced fish [0 indicates totally random collection]; ii) the maximum percent of the natural run allowed to be taken as broodstock; iii) the maximum percent of the, total run (including hatchery fish) that can be taken as broodstock; iv) the maximum percent of naturally **spawning** fish that can consist of hatchery produced (T3) fish; v) a **minimum** requirement for the natural run to spawn naturally before broodstock can be removed (input males and females separately). **Item** iv would be controlled by operation of a weir in the lower reaches of the river in reality.

(c) Sex Ratio - This defines the sex ratio to be used for the broodstock.

4.2.4 **Hatchery** Culture Methods

Selection of this item enables the user to specify the type of fish culture methods to be employed in the model run; methods refer to either conventional or innovative. Conventional practices are those that are currently being **used**. Innovative practices would incorporate new concepts to improve survival using such techniques as exposure to habitat complexity, predator trainirig, use of live food, etc.-Begin the first modeling exercise using conventional practices. In this case, the user assumes that fish **will** be cultured with standard culture, practices at all phases of hatchery propagation.

(1) **Conventional Practices -** Selection of this item leads to the following menu options (via **MODIFY PARAMETERS . ..).**



(a) **Survival of Hatch Fish Relative to Wild T0 Fish -** This specifies the relative survival of hatchery produced (type **T3)** fish compared to wild native (type TO) fish from release through the pre-spawning phase ***using conventional culture pmctices.*** This assumes that the hatchery stock was **derived** from native broodstock. Input values are obtained from whatever sources might be available for the stock of interest or nearby stocks, or simply based **on** the -best, judgement. of individuals knowledgeable about this subject. The values are varied to examine the effect of uncertainty in this variable, Default values in the model are:

RELATIVE SURVIVAL OF T3 FISH COMPARED TO T0 FISH BY RELEASE STAGE				
EGG	FRY	PRE-SMOLT	SMOLT	ADULT
0.20	0.20	0.25	0.33	0.75

The relative survival values of fish of imported stock but cultured using conventional practices are computed by the model. The model assumes that survival is reduced for imported stock, the difference in survival' from using local stock being due to genetic factors alone. The model calculates the contribution of non-genetic factors contributing to the relative survival values given above, then incorporates the genetic factors for the imported stock to obtain corresponding relative survival values for that stock.

The model allocates the reduction in survival for hatchery fish to non-genetic factors (those due to behavioral and physiological changes) and genetic factors. The genetic factors are set within the model (see below); the non-genetic factors are simply, the residual between total reduction in survival for T3 fish and the reduction due to **genetic** effects.

(b) **Distribution** of **Non-Genetic Effects -** This specifies' the relative distribution of **how** non-genetic effects to 'survival from hatchery **propagation** are spread through the **post-release life** of hatchery fish. This provision enables the user to consider how different assumptions about the distribution of these effects might **affect** outcome. Default values are based on the assumption that most of the non-genetic effects occur soon after release; default values are listed below:

DISTRIBUTION OF NON-GENETIC TREATMENT EFFECTS BY LIFE AND RELEASE STAGE					
LIFE STAGE	EGG RELEASE	FRY RELEASE	PRE-SMOLT RELEASE	SMOLT RELEASE	ADULT RELEASE
Egg-fry	50%				
Fry-presmolt	30%	50%			
Presmolt-smolt	10%	30%	50%		
Smolt-smolt	0%	10%	30%	50%	
Juv. pass.	0%	0%	10%	30%	
Estuary	0%	0%	0%	10%	
Ocean	0%	0%	0%	0%	
Ocean harvest	0%	0%	0%	0%	
River harvest	0%	0%	0%	0%	
Adult pass.	0%	0%	0%	0%	
Prespawning	10%	10%	10%	10%	100%
Home. fidelity	0%	0%	0%	0%	0%
TOTAL	100%	100%	100%	100%	100%

Values within the columns must add to 100%; input is made as **proportions**.

Important note: Be aware that the value input for the smolt-smolt stage may create an illogical condition when a Type II or III predator response is operative (see Section 4.4 Predator Effects), if the amount of mortality assigned to this stage is too high. In such a case, the model will create new naturally' produced fish in this stage to satisfy the conditions of the Type II or III response functions. If that occurs, a message will be given to the user following completion of the model run to indicate an adjustment is necessary and the run should be repeated.

(c) Genetic **Factors -** This specifies the relative contribution of different genetic components to the overall genetic effect of culturing fish 'in the hatchery. Changes **in genetic** fitness are attributed to three categories: domestication effects, broodstock source, and culture practices (see Tables 2 and 3 in Part I). Fitness **is** relative to a wild standard of 1.0 and fitness factors are multiplicative.

The default values for each category were originally, formulated for fish to be cultured in the hatchery to the smolt stage.[6] The model assumes that genetic changes are less for fish held in the hatchery for shorter periods. Hence genetic changes associated with hatchery culture are less for fish supplemented at the pre-smolt stage than at the smolt stage, and so on. Selection of **GENETIC FACTORS** enables the user to change the default values for smolt releases only; the model then recomputes fitness values for each category for fish released at other stages by interpolation, assuming that domestication and culture effects have values of 1.0 for egg and adult releases. The user is given the following screen for making this input; default values are shown [shaded cells are values computed by the model; input is made in the unshaded cells]:

FITNESS FACTORS BY COMPONENT CATEGORY AND RELEASE STAGE						
CATEGORY	TREATMENT OR TYPE	EGG RELEASE	FRY RELEASE	PRE-SMOLT RELEASE	SMOLT RELEASE	ADULT RELEASE
Domestication	T1	1.00	0.98	0.97	0.95	1.00
	T2	1.00	0.97	0.93	0.90	1.00
	T3	1.00	0.95	0.90	0.85	1.00
Stock source	Local	1.00	1.00	1.00	1.00	1.00
	Adjacent	0.70	0.70	0.70	0.70	0.70
	Distant	0.10	0.10	0.10	0.10	0.10
Culture	Conventional	1.00	0.90	0.80	0.70	1.00
	Innovative	1.00	1.00	1.00	1.00	1.00

The model uses the values contained in the above screen to compute total genetic fitness factors associated with each fish type (T1, T2, T3) for each stage of release (see Table 3).

(2) Innovative Practices - Selection of this item enables the user to prescribe the amount of improvement in hatchery, fish survival, to be gained by using innovative culture techniques. This feature allows the user to explore the overall effect of gaining particular levels of improved survival using innovative culture. The amount of improvement assigned to genetic factors is stipulated by

6. Values provided by Dr. Craig Busack were intended to be applied to smolt released fish. Dr. Busack assumes that fish held in the hatchery for shorter periods of time will experience less-genetic change *(personal communications).* Note: The value shown for conventional, culture under smolt release of 0.70 is now considered too low by Dr. Busack; an intermediate value between 0.70 and 1.0 is likely more appropriate.

the values shown above under GENETIC **FACTORS**. The residual between total survival and the' amount assigned to genetics is allocated to non-genetic effects, as described earlier. The input screen with example improvement values is shown below:

PERCENT IMPROVEMENT IN POST-RELEASE SURVIVAL OF HATCHERY FISH WITH INNOVATIVE CULTURE				
EGG RELEASE	FRY RELEASE	PRE-SMOLT RELEASE	SMOLT RELEASE	ADULT RELEASE
100%	100%	100%	100%	100%

Values are entered as proportions; hence a value of 0.10 would represent a 10% increase in survival, a value of 1.0 would be a **100%** increase in survival, a value of 2.0 would be a 200% increase. The model **limits, however,** the maximum survival of hatchery **fish** to that of'wild TO fish.

Upon leaving this input screen, the user is given the choice **of modifying** the parameters associated with culture effects, as shown under **CONVENTIONAL PRACTICES** above.

4 3 Variation

Selection of this item within the Main Menu enables the user to choose whether to introduce environmental variation into 'the model runs. The user is given the following menu:

ENVIRONMENTAL VARIATION MENU

NO ENVIRONMENTAL VARIATION
SWITCH ON ENVIRONMENTAL VARIATION

If variation is not introduced, the user is returned to the Main Menu to continue with setup procedures. If variation' is switched on; the user is then taken to several, subsequent menus for defining how variation is to occur. Two'sources of variation can be introduced: variation in downstream passage survival within the **mainstem** Columbia River (and Snake, if pertinent), and all other types of environmental variation.

The first source of variation to **be** defined is due to variable downstream passage survival assumed to be caused by variation in flow regimes. This variation is introduced in the same manner as in the Systems Planning Model, i.e., based' on an estimated relationship **between** flow and passage survival. The EDT model utilizes a SO-year runoff record (1929-1978) for

the Columbia, assuming that flows were regulated for the entire period' under '*current operations." The user is given a menu for selecting how many mainstem dams are below the subbasin being modeled. If 0 dams are selected, the passage variatidn file submenu is skipped by the model. Passage variation is defined by the following:

NO DAMS TO PASS IN MAINSTEM MIGRATION
FOUR DAMS TO PASS IN MAINSTEM MIGRATION
EIGHT DAMS TO PASS IN MAINSTEM MIGRATION

SUBMENU OF FILES TO VARY DOWNSTREAM PASSAGE SURVIVAL

1. Passage file HIST4A (historical runoff pattern)
2. Passage file HIST4B (historical runoff pattern)
3. Passage file HIST4C (historical runoff pattern)
4. Passage file RAND4A (random runoff pattern)
5. Passage file RAND4B (random runoff pattern)
6. Passage file RAND4C (random runoff pattern)

The submenu of passage survival files is 'used to select a specific file that contains a flow pattern and associated survival rates. A pattern can be selected that either follows a historic sequencing with a randomly selected start year (HIST files) or a completely random sequencing of flows (RAND files). Three files exist for each. The user should use the same variation files in comparing multiple model runs to evaluate treatment or predator effects.

If different variation patterns are desired, they can be created outside the model and substituted for one of the files in the submenu shown above.

After defining passage survival, the user is given another submenu- to select' one 'of three possible files for defining all other sources of environmental variation. Variation is determined based on a log-normal function and is applied entirely during the, estuarine life stage. The user should use the same file in comparing treatment effects for multiple model runs. The choices are:

SUBMENU OF FILES FOR NON-PASSAGE VARIATION

1. Estuary survival file ESTURN1
2. Estuary survival file ESTURN2
3. Estuary survival file ESTURN3

If different variation patterns are desired, they can be created outside the model and substituted for one of the files in the submenu shown.

4.4 Predator Effects

Selection of this item enables the user to define the type of prey-predator interactions that occur within the subbasin during smolt migration. The smolt population istreated as the prey. The user is given the following menu:

RATE OF LOSS DUE TO PREDATORS MENU

CONSTANT RATE OF LOSS
HIGH RATE OF LOSS AT LOW'POPULATION SIZES
LOW RATE OF LOSS AT LOW POPULATION SIZES
MODIFY DENSITY-DEPENDENT PARAMETERS
VIEW FUNCTIONAL RESPONSES

4.4.1 Constant Rate of Loss

This choice is equivalent to a Type I functional response for predators without any ceiling to how many smolts can be eaten. Loss is assumed-to be independent of the density of smolts. The survival rate for the smolt-smolt life stage that was specified when defining subbasin/stock characteristics (under **STAGE SURVIVAL)** is. used in this case.

4.4.2 High Rate of Loss at Low Pooulation Sizes

This choice is equivalent to a Type II' functional response for predators, with the highest rate of loss occurring at the lowest prey densities. Predator efficiency at killing (or rate of handling, i.e., digestion, etc.) decreases as prey density increases. Strong Type II responses will push the wild salmon population toward extinction at low initial stock size.

4.4.3 Low Rate of Loss at Low Population 'Sizes

This choice is equivalent to a Type III functional response for predators, with the lowest rate of loss occurring at the lowest prey densities. Predators switch to more abundant prey at low densities of salmon smolts. Strong Type III responses may tend to create- multiple population stability domains; thus the wild population may remain low at low initial stock sizes.

4.4.4 Modify Density-Dependent Parameters

This choice enables the user to modify one or both of the parameters that determine the severity of the Type II or III functional responses. The two parameters are: (1) maximum percent of the smolt carrying capacity that can be eaten by the predator population; and (2) the percent of the carrying capacity that needs to be available for predators to eat one-half the maximum number that can be eaten. Default values for these parameters are set at 50% and 32.5% respectively. *Note: enter the values as proportions, hence 50% becomes 0.5. Severity* of the functional response8 is increased by increasing the first parameter value and decreasing the second. Think of it like this: divide the first parameter by two, then set the second parameter value higher than that number by an amount that represents the ability of prey to evade capture. The closer the second parameter is to one-half of the first, the greater the severity of effect. The second parameter value should always be set greater than one-half the first parameter. The VIEW optionallows the user to review the effect of changing parameter values.

4.4.5 View Functional Resoonses

This choice, provides a graphic display of th'e three functional responses using the values 'that have been selected by the user (or for default values if no changes have been made).

4.5 **Output**

Selection of this item enables the user to generate a variety of output, including on-screen graphics, printed graphics and tables and graphic, and tabular files. For each choice, the user must specify whether the model run was made with one or all three genetic recovery scenarios. Outputs are different for the two ways of running the model. Choices are:

OUTPUT MENU

- DISPLAY GRAPHS
- GRAPH PRINT
- SAVE GRAPHS
- PRINT TABLES

- SINGLE RECOVERY SCENARIO MODEL RUN
- MULTIPLE RECOVERY SCENARIO MODEL RUN

4.5.1 Display Graphs

For a single genetic recovery scenario model run, the choices for graphics are as follows:

MENUOFGRAPHS
(single scenario model run)

A.	Total natural spawners time series.
B.	Composition of in-nature spawning population time series.
C.	Composition of in-hatchery spawning population time series.
D.	Smolt yield time series (numbers leaving subbasin).
E	Recruits to Columbia plus ocean catch time series.
F.	S-R plot for natural spawning populations.
G.	S-R plot for total subbasin populations.
H.	R/S for in-nature spawners time series.
I.	R/S-for in-hatchery spawners time series.
J.	R/S for total spawners time series.
K	Eggs per natural female spawner.
L.	Numbers of fish released time series.

When a graph is displayed to the screen, the model first brings up a template that contains some or all of the output. The graph contains only a generic title at that point. Press **RETURN** and the model will add titles and bring in all of the remaining output data. Depending on the speed of the computer being used this may take a few seconds - wait. This two-step process to creating a graph is due to how Quattro processes the macro. The meaning

of each graph is self-explanatory, from either the descriptions attached to the menu or by the graph itself. The user can easily modify the graphs or create different ones by quitting the EDT model and working through the normal Quattro Pro routine under **/GRAPH.**

For multiple-scenario model runs the choices for graphics are as follows:

MENU OF GRAPHS
(multiple scenario model run)

A. TO + T1 + T2 natural spawners time series.
B. Total natural spawners time series.
C. TO + T1 + T2 smolt yield time series (numbers leaving subbasin).
D. Total smolt yield time series (numbers leaving subbasin).
E TO + T1 + T2 recruits to Columbia plus ocean catch time series.
F. Total recruits to Columbia plus ocean catch time series.

4.5.2 Graph Print

Selection of this item produces the menu of graph choices as shown above for the purpose of printing graphs from within the model. Graphs to be printed must first have been viewed through the **DISPLAY GRAPHS** option above **because** they are created,during that procedure. *Note: if sets **of graphics for** different model **runs are desired** with the same scaling on the **Y-**axis **(for easily** comparing **treatment effects) then the user should QUIT** the **model** and **re-**scale **manually.***

4.5.3 Save Graphs

Selection of this item produces the menu of graphs for the purpose of saving to file one or more. Any graphs to be saved must first have been 'viewed through the **DISPLAY GRAPHS** option above because they are created during that procedure. The graphic is displayed again at this step just prior to saving to file. Graphs are saved as **.PIC** files, **but this** can easily be changed to create **.PRN** files instead; **.PRN** files use' much larger amounts of memory, however.

4.5.4 Print Tables

Output tables used in creating the. graphics can be printed at this time. The user must go. through the same kind of **submenus** as shown above to specify whether .a single or multiple recovery scenario was modeled. Selection of single' recovery scenario run produces the following menu of tables to print:

MENU OF TABLES TO PRINT

A. In-nature spawners time series by fish type.

B. In-hatchery spawners time series by fish type.

C. Smolt yields by type and brood year.

D. Recruits to Columbia plus ocean catch time series.

E Stock-recruit data.

F. Fecundity and natural egg deposition.

G. Outplanting summary.

Selection of multiple recovery scenarios run produces the following menu of tables to print:

MENU OF TABLES TO PRINT

A. In-nature spawners time series by fish type.

B. Smolt yields by type and brood year.

C. Recruits to Columbia plus ocean catch time series.

The user is given an additional choice to be able to print the input and setup tables within the model also. This choice calls up the following menu:

MENU OF INPUT AND SETUP TABLES TO PRINT

A. Basic setup (information from CONTROL, PANEL),

B. Input tables to define Subbasin/Stock.

C. Input tables to define supplementation strategy.

D. Treatment effects setup tables.

E. Predator-prey interactions parameters.

4.6 Go

When the setup procedures have been completed, the user selects GO at the Main Menu., The Control Panel is displayed on the screen, enabling the user. to see some of the basic instructions that have been selected in the setup routine. The user must then respond to the' following:

'Enter an assigned nm number (3 characters: 001-999)"

Enter up to a three digit number as shown.

"What year to begin treatment?"

This question enables the treatment to begin' any year in the sequence of years being modeled.

"Run all genetic recovery scenarios? (Y or N)"

If Yes is selected, then the model will run each **scenario the** full number of years being run beginning with scenario 1, then move to scenario 2 and so on. Each- model run takes three times as long when running all scenarios together.

If Yes is selected, the model begins to run. If No is selected the next question must be answered.

"Which genetic scenario for a one scenario run? (1,2, or 3)?"

Be sure to enter a number here even if no supplementation is actually going to occur. If there is no supplementation, the choice of which scenario does not matter, ***but the model wants a number here.***

"Enter a short description of the treatment
(MAX *36* characters or ENTER for none)"

This description is placed on the second line of the graphics that are produced. The following is then asked:

"How many years should be simulated (MAX = 150)?"

The model then begins to run. The current, year that is being run is reported to the control Panel. For multiple scenario runs, the scenario that is being run is also shown.

The model will beep after it is completed running, then return to the Main Menu,

4.7 Save

Selection of this item in the Main' Menu allows the user to save to file the input sections that were setup, including the supplementation strategy, and the entire model with results if desired. The following menu is given:

SAVE FILE MENU

INPUT SECTION FOR SUBBASIN/STOCK
SUPPLEMENTATION STRATEGY SECTION
MODEL WITH INPUTS AND RESULTS

The files are automatically named using up to seven characters. Input sections, including those for treatments, are given two character prefixes as follows:

Input section for subbasin/stock	IN-
Supplem entation treatm ent Sections:	SU-

The two characters following the prefix are the two letters of the subbasin/stock system that the user input when setting up the model run. The last three characters are those of the model run number. So, the file INEX001.WQ1 would be the input section (IN) defining the subbasin/stock for Example River (EX) for model run number 001.

When the entire model is saved with results, the file name begins, 'with the two character abbreviation for the subbasin/stock, followed by the model run number.

4.8 Batch Mode

Selection of BATCH MODE from the Main Menu enables the user to make a series of model runs uninterrupted. This option is used to perform sensitivity analyses over ranges of input values, as was done in Appendix A. Before initiating a batch job, the user is required to set up the Batch Command Table, which controls how input values are changed for each run. This is done outside of the model and requires- a greater level of knowledge. about spreadsheets than needed to operate the -model on a single run basis.

To set up the Batch Command Table, quit the model. (but not the spreadsheet). Go to cell BATTABX (address AX803). The screen will appear similar to Figure 11; only truncated with fewer columns shown. *(Note:* Figure 11 displays only the first part of the Batch Command Table). Row numbers and column addresses are shown along the left. and top margins in Figure 1 I. ***Unless the size or basic structure of the table is to be changed, do not make any changes or input any values between the double horizonital lines that are shown.***

The box beginning in cell AX803 in Figure 11 is reserved for storing information used to name the output file created at the end of a series of model runs. The user is required to answer several questions when a batch job is initiated; the answers are stored in this box.

	AX	AY	AZ	BA	BB	BC	BD	BE	BF	BG	BH	BI	BJ	BK	BL
802															
803	BATCH COMMAND TABLE - reserved			Notes:	Variable names shown below in box; standard run values shown in row 812.										
804	SUMMARY OUTPUT FILE:		BR2FEB11		Do not fill in col."RUN ID"; this done automatically.										
805	BATCH CODE:		BR2		Fill in col. run no.; do not fill in the reserved box to left - this done automatically.										
806	MONTH:		FEB		Table allows for 400 model runs - this can be expanded if desired.										
807	DAY:		11		1	2	3	4	5	6	7	8	9	10	11
808	VARIABLE ROW:		808		CC	ICCC	RWSC	EPFT01	EPFT02	EPFT03	EPFT04	E.FSURVT0	F.PSSURVT0	PS.SSURVT0	S.SSURV
809				Save	Smlt	Incub.	Ratio	T0 fec	T0 fec	T0 fec	T0 fec	Egg-fry	Fry-psmt	Psmt-smt	Den. ind.
810				detail?	carry.	cap/CC	win/sum	age 1	age 2	age 3	age 4	surv	surv	surv	surv
811			No. years	0 - no	cap.		cap								
812	RUN NO.	RUN ID	to run	1 - yes	2,000,000	300	0.800	1,656	4,201	6,305	7,289	0.600	0.563	0.563	0.730
813															
814	1	001	60	0	2,000,000	300	0.800	1,656	4,201	6,305	7,289	0.600	0.563	0.563	0.730
815	2	002	60	0	500,000										
816	3	003	60	0								0.300			
817	4	004	60	0	1,000,000							0.600			
818	5	005	60	0								0.300			

Figure 11. Batch Command Table, showing example input for some model parameters.

Parameter names that 'can be altered through the batch job are shown within a long rectangle beginning in cell **BB809,** extending off the screen to the right. The table is set up within **EDTM30.WQ1** with 66 different parameters. The names shown are those given in Table 6 in Part III. Short definitions **of** the parameters are given in the two or three rows immediately below the names. The numeric values in the row beneath the **definitions (beginning** in BB812) are the values that are current within the model; the values in these cells are updated with each run.

Input values to be changed with each model run are entered beginning in row 814. Set up this table from left to right as follows:

1. **Under** column "RUN NO." (AX), enter consecutive numbers for 'the number of the run. If formulas are used to speed the process, be sure to convert them to valuesbefore **leaving** this step. So, for example, if 100 runs. are being made, numbers would progress from 1 to 100 in this 'column.

2. Leave column "RUN ID" (AY) **blank**. Erase anything that is there when setting up the table. This column is filled in automatically at the start of the batch job.

3. Under column "No. years to run" (AZ), enter the -number of years to be modeled for each run.

4. **Under** column "Save detail?" **(BA),** enter a 0 or 1 to indicate the type of output to be saved. If **a "1"** is entered, then the entire output record by year will be saved for that run for Natural Spawners (by fish type). The model can' be customized to save output for other items if desired. In all cases, the output will include the ***last*** year in the model run for all relevant response measures.

5. Numeric values for each parameter are input beginning in column BB. ***Important note:*** Enter all of the values **associated with** a ***standard run*** in the first row of the table (row 8 14). In subsequent rows enter ***only*** the. items that are to be changed from the previous run. Remember to 'reenter 'the standard run values when a parameter 'value is intended to be reset to the starting value. Figure 1 **1** illustrates an example where smolt carrying. capacity and egg-fry survival are being changed. The third run uses the same carrying capacity as in the second run. The carrying capacity is changed again in the fourth run; then is **unchanged** in the fifth run.

The model is currently configured to run up to 400 model runs per batch job. This'can be increased through minor modifications.

If the user wants to examine the effect of other parameters besides those shown, the table would need to be modified slightly. Go to far right side of the table and extend it further to the right (using the Move command). Be sure to also move the summary table shown

immediately to the right of the Batch Command Table. Set up the new portions of the table following the pattern used for the existing table.

When BATCH MODE is selected from the Main Menu, the user is prompted to respond to the following:

"Enter a three character batch M code (e.g., BR1)"

This is used in naming the output files. A second prompt is given:

"Enter the month abbreviation (e.g., FEB)"

Enter a three letter abbreviation for the current month; this is used to name the output file. A third prompt is given:

"Enter the day of the month (e.g.; 2)"

Enter the current day of the month; this is used to name the output file.

The Control Panel is then displayed to the screen where the user can monitor the progress of the batch job. If a large number of runs-is being made, initiate the job just before quitting work for the day and let it proceed overnight.

When the user attempts to initiate a batch job for the first time, be sure to interrupt the job after a short period (say, 15 minutes) to check whether the job is proceeding as planned.

Output that is obtained will need to be analyzed according to the specific needs of the user. No pre-programmed graphics can be obtained for the results.

4.9 Quit

To save the model with its current configuration for all input parameters but without the lengthy results attached, quit the model (QUIT), then press ALT-Z, which will strip out the results for saving a smaller file. Save the model through the standard Save routine,in Quattro, using whatever name is desired.

ECOSYSTEM DIAGNOSIS AND TREATMENT MODEL AS APPLIED TO; SUPPLEMENTATION

PART III
THEORETICAL DOCUMENTATION

1. INTRODUCTION

Part III presents the theoretical, documentation for the model. Formulas for all but the most trivial computations in the model are provided. The presentation is given following the same order as shown for the spreadsheet layout' (see Fig. 2).

The numerous formulas that follow will be intimidating and of little value to many individuals interested in using the model. An understanding of these algorithms is not necessary to use the, model for the purpose it was designed; they' are provided to ensure full accountability for all its components. The documentation provided here will be of use to individuals wanting to customize the model, use portions of it in other modeling tasks, or to better understand a set of computations.

2. DEFINITIONS AND NOTATION

Input narameters are defined as those values in the spreadsheet that are provided by the user and define specific attributes associated with the stock and management strategies under consideration. The code name for each input parameter is made up of two components, a generic component and a specific component. The generic component is upper Case, italicized bold alphabets taken from the parameter definition. For example,,.the input parameter,. eggs produced per female, is $\boldsymbol{EPFk_h}$ where '$\boldsymbol{EPF}$ ', the generic component, refers to eggs per female. The specific component is small case, italicized (not bold) alphabets and is used to define specific genetic stock, age, sex, or life-stage elements for which the generic name is associated. The specific Components are variables that take on a range of values to define' which genetic stock, age, sex, or life-stage (for example) is being referenced. The values of these parameters are not italicized. In the example, $\boldsymbol{EPFk_h}$, the letter $\boldsymbol{k}$ can reference either TO or T3 genetic stock, and the letter $\boldsymbol{h}$ can equal 1, 2,' 3, or 4 which delineates the number of years fish are in the ocean. Thus, $\boldsymbol{EPFT0_2}$ is the number of eggs produced per female of TO genetic stock fish that have remained in the ocean for 2 years. Table 6 presents a complete list of all input parameters.

Calculated variables are defined as those values which **are** a function of input parameters and other calculated variables. Again, the code name for each calculated variable is made up of a generic and a specific component. For calculated variables, however, the generic component is upper case, italicized, non-bold alphabets. The format for the specific component is the same as that used for input parameters. Table 7 presents a complete list of all calculated variables.

State variables are a subset of the calculated variables and are those variables associated with an interesting life stage. These variables are often tracked through the model simulation and are used to produce plots for data interpretation.

3. MODEL FORMULATION

Each calculated variable is first described in non-mathematical terms; followed by its mathematical expression. We proceed through the spreadsheet by section, as shown in **Figure** 2. The spreadsheet address of each **variable** precedes the name of the term to facilitate locating it within the spreadsheet. *Note: **these** addresses **will** be **made obsolete if the spreadsheet structure** is altered*

3.1 Input Section

N12 Summer **Capacity** (*SC*) is the carrying capacity of the **subbasin for parr** during the summer rearing period.. The estimation of this parameter is **based on** the **disaggregation** of the Beverton-Holt stock-production equation (see Appendix B), the user input of smolt carrying capacity (CC), **and** the estimates of the seasonal limitations of habitat to smolt carrying capacity. Summer capacity is defined a

$$SC = \frac{CC \cdot F.PSSURVTO \cdot (RWSC + PS.SSURVTO)}{RWSC \cdot \left(F.PSSURVTO \cdot PS.SSURVTO - \frac{1}{RICC}\right)} \quad (1)$$

where CC is the smolt carrying capacity (input); ***F.PSURV*TO** is the fry to presmolt density independent survival rate; ***RWSC*** is the ratio of winter capacity to summer capacity; ***PS.SURV*TO** is the presmolt to **smolt** density independent survival rate; and ***RICC*** is **the** ratio of egg incubation capacity to **smolt** carrying capacity.

Table 6. Input parameters, code names, and their associated location in the EDT model.

Spreadsheet location	Parameter description	Input parameter	Index range
N9	Smolt carrying capacity	*CC*	
N10	Incubation capacity/*CC*	*RICC*	
N11	Ratio of winter to summer smolt capacity	*RWSC*	
O26..R27	Eggs produced per female	$EPFk_h$	k=T0,T3; h=1..4
O29..O30	Egg-to-fry survival rate	*E.FSURVk*	k=T0,T3
O32..O33	Fry-to-presmolt survival rate	*F.PSSURVk*	k=T0,T3
O35..O36	Presmolt-to-smolt survival rate	*PS.SSURVk*	k=T0,T3
O38	Density independent smolt-smolt survival	*S.SSURV*	
O40	Juvenile passage survival rate	*JPSURV*	
O42	Estuary survival rate	*ESURV*	
O44..R44	Natural ocean survival	$OSURV_h$	h=1..4
O46..R46	Adult passage survival	$PSURV_h$	h=1..4
O48	Homing fidelity to subbasin	*HF*	
O50..R51	Prespawning survival rate	$P.SPSURVk_h$	k=T0,T3; h=1..4
O53..O54	Spawn efficiency of jacks	$JESP_k$	k=T0,T3
O59..R59	Ocean harvest rate	OHR_h	h=1..4
O60..R60	Mainstem harvest rate	MHR_h	h=1..4
O63	Terminal harvest area policy; harvest random or hatchery fish only	*HARV*	
O67	Minimum harvest rate in terminal area	*MIHR*	

Table. 6. Continued.

Spreadsheet location	Parameter description	Input parameter	Index range
068	Harvest rate in excess of the breakpoint	HREBP	
069	Harvest rate breakpoint	HRBP	
079..R82	Steady-state age distribution in subbasin	$ADks_h$	k=T0,T3; s=M,F; h=1..4
O90..P94	Initial returns to the subbasin	$IRSs_{k,ss}$	s=M,F; k=T0,T1,T2,T3; SS=l,a,d
N110..N114	. Supplementation. number (numeric release goal)	$SUPNUM_i$	i= e,f,sp,s,a
01 10..O114	Supplementation duration	$SUPDUR_i$	i=e,f,ps,s,a
N128..S132	Broodstock collection schedule (source)	$BRDCS_{i,c}$	i=e,f,ps,s,a; c=1..6
O145..P145	Brood collection policy years	BCY_t	t - 1 . 2
O146..P146	Minimum percent used of the natural broodstock	$Mi\%NBS_t$	t=1,2
O147..P147	Maximum percent used of the natural run	$Mx\%UNR_t$	t-1.2
O148..P148	Maximum percent used of the total run	$Mx\%UTR_t$	t=1,2
O149..P149	Maximum percent of T3 fish in the natural escapement	$Mx\%T3E_t$	t=1,2
O150..P150	Minimum number of natural males in escapement (constraint on broodstook)	Mi#NEM	
O151..P151	Minimum number of natural females in escapement (constraint on broodstock)	Mi#NEF	
0162	Broodstock percent female	BRDCSR	

Table 6. Continued.

Spreadsheet Location	Parameter description	Input parameter	Index Range
u29	Egg-to-fry pedigree relative survival adjustment	*E. FRSA*	
U32	Fry-to-presmolt pedigree relative survival adjustment	*F. PSRSA*	
U35	Presmolt-to-smelt pedigree relative survival adjustment	*PS. SRSA*	
AI170	. Maximum percent of CC eaten	*Mx%CC*	
AII 73	Percent of CC needed for 1/2 maximum no. eaten	*PCCB2*	
U50	Prespawning survival of TO fish in the hatchery	*P.SPSURVHTO*	
AAB13..AF20	Genetic fitness components for smolt release stage	$GFC_{o,j}$	j=T1,T2,T3,l,a,d,con,inn
AB89..AF92	Relative survival	$RELSURV_{i,CULT,ss}$	i=e,f,ps,s,a; CULT=con; SS=l
Z71..AD71	Percent improved performance of hatchery fish with innovative, culture	$PIINN_i$	i=e,f,ps,s,a
AA107..AE118	Non-genetic treatment effects (distribution)	$NGE_{i,L}$	i=e,f,ps,s,a; L=e-f,f-ps,ps-s, s-s,jp,est,o,oh,rh,ap,psp,hf
AB317..AB366	Juvenile passage variable survival rate (vector)	*VPAS*	
AC317..AC416	Variable estuary survival rate (vector)	*VEST*	
0240	Functional response	*F*	F=1..3
A03	Culture method	*CULT*	
AE3	Stock source	s s	

Table 7. Calculated variables, code names, and their associated locations within the EDT model, ,

Spreadsheet location	Variable description	Variable name	Index Range
0181	Genetic recovery scenario	*SCEN*	
N12	Summer capacity	SC	
N13	Winter capacity	*WC*	
O84..R87	Maturation rates	$MRks_h$	k = T0,T3; s = M,F; h = 1..4
O167..S170	Broodstock required	$BRDSTK_{i,c}$	i = e,f,ps,s,a; c = 1..6
AB13..AF20	Genetic fitness components by release stage	$GFC_{i,j}$	i = e,f,ps,s,a; j = T1,T2,T3,l,a,d,con,inn
AC34..AG63	Genetic fitness factors (genetic effects)	$GEk_{i,CULT,ss,E}$	k = T1,T2,T3; i = e,f,ps,s,a; CULT = con,inn; SS = l,a,d; E = t,s
AB89..AF92	Relative survival of hatchery fish (T3) to wild fish (TO)	$RELSURV_{i,CULT,ss}$	i = e,f,ps,s,a; CULT = con,inn; SS = l,a,d
AA131..AE162	Total effects	$TEj_{i,CULT,L}$	j = l,a,d; i = e,f,ps,s,a; CULT = con,inn; L = e-f,f-ps,ps-s,s-s,jp,est,o,oh,rh,ap,psp,hf
AA169..AE237 (placed in GA8..GA23)	Smolts after smolt-smolt survival, based on either a Type I, Type II, or Type III functional response	$S.SSURVF_{k,y}$	f = 1..3; k = TO,T1,T2,T3,j-i; j = l,a,d,l; i = e,f,ps,s,a; y-year
AA243..AA275 (placed in GB8..GB23)	No variation in survival after downstream passage	$NVADP_{k,y}$	k = TO,T1,T2,T3,j-i; j = l,a,d,l; i = e,f,ps,s,a; y-year
AB243..AB275 (placed in GC8..GC23)	No variation in survival after estuary	$NVAE_{k,y}$	k = TO,T1,T2,T3,j-i; j = l,a,d,l; i = e,f,ps,s,a; y = year

Table 7. Continued.

Spreadsheet location	Variable description	Variable name	Index Range
AA280..AA312 (placed in GB8..GB23)	Variation in survival after downstream passage	$VADP_{k,y}$	k=T0,T1,T2,T3,j-i; j=l,a,d,l; i =e,f,ps,s,a; y-year
AB280..AB312 (placed in GC8..GC23)	Variation in survival after estuary	$VAE_{k,y}$	k=T0,T1,T2,T3,j-i; j=l,a,d,l; i=e,f,ps,s,a; y-year
AZ8..BG23	Adults returning to subbasin	$ARSsh_{k,y}$	s=M,F; h=1..4; k=T0,T1,T2,T3,j-i; j=l,a,d,l; i=e,f,ps,s,a; y-year
AZ24..BG24	Initial ninth root genetic fitness factors	$KIFF_{e,h,y}$	K=T1, T2; h=1..4; y-year
BH8..BH23	Adults plus jacks returning to spawn	$ARSJ_{k,y}$	k=T0,T1,T2,T3,j-i; j=l,a,d,l; i=e,f,ps,s,a; y=year
BM9..BR23	Broodstock limits	$BSLr_{k,y}$	r=1..3; k=T1,T3,j-i; j=l,a,d,l; i=e,f,ps,s,a; y=year
BT8..CD23	Adults after broodstock REM 1	$AABS1sh_{k,y}$	s=M,F; h=1..4; k=TO,TI ,T2,T3,j-i; j=l,a,d,l; i=e,f,ps,s,a; y-year
CG8..CQ23	Adults after terminal harvest	$AATHsh_{k,y}$	s=M,F; h=1..4; k=T0,T1,T2,T3,j-i; j=l,a,d,l; i=e,f,ps,s,a; y-year
CR8..DB23	'Adults after broodstock REM 2	$AABS2sh_{k,y}$	s=M,F; h=1..4; k=T0,T1,T2,T3,j-i; j=l,a,d,l; i=e,f,ps,s,a; y=year
DE8..DN23	Adults after prespawning mortality	$AAPSMsh_{k,y}$	s=M,F; h=1..4; k=T0,T1,T2,T3,j-i; j=l,a,d,l; i=e,f,ps,s,a; y=year
DP8..DZ23	Adults after NBroodstock REM 3	$AABS3sh_{k,y}$	s=M,F; h=1..4; k=T0,T1,T2,T3,j-i; j=l,a,d,l; i=e,f,ps,s,a; y=year

Table 7. Continued.

Spreadsheet Location	Variable description	Variable name	Index Range
EA8..EI23	Spawners in hatchery prior to egg take	$SPHsh_{k,y}$	s=M,F; h=1..4; k=T0,T1,T2,T3,j-i; j=l,a,d,l; i=e,f,ps,s,a; y-year
EJ8..ER23	Spawners in nature prior to spawning	$SPNsh_{k,y}$	s=M,F; h=1..4; k=T0,T1,T2,T3,j-i; j=l,a,d,l; i=e,f,ps,s,a; y-year
ES8..ES23	Total number of -males in nature	$TNMN_{k,y}$	k = TO,TI ,T2,T3; y-year
EW8..EW23	. Total number of eggs in nature	$TNEN_{k,y}$	k=T0,T1,T2,T3,j-i; j=l,a,d,l; i=e,f,ps,s,a; y - y e a r
FA8..FE11	Scenario matrix	$SM_{k-k',y}$	k=T0,T1,T2,T3; k' =T0,T1,T2,T3; y-year
FI9..FK10	Weighted genetic fitness factors (weighted genetic effects)	kFF_y	k=T1,T2; y-year
	REM factors	kRF_y	k=T1,T2; y-year
FL9..FL10	9-th root genetic fitness factor (weighted factors)	$kFF_{g,y}$	k=T1,T2; y-year
FF9..FF12	Potential zygotes in hatchery before egg plant	$PZH_{k,y}$	k=T1,T3; y-year
FG11..FG14	Eggs planted	$EP_{k,y}$	k=T3,l-e,l-e; y - y e a r
FH8..FH 14	Potential zygotes in nature after egg planting	$PZNAP_{k,y}$	k =T0,T1 ,T2,T3,l-e,l-e; y-year
FN9..FN 12	Fry in hatchery before fry plant	$FH_{k,y}$	k=T1,T3; y=year
FO11..FO16	Fry planted	$FP_{k,y}$	k=T3,l-f,l-f; y-year
FP8..FP16	Fry in nature after fry planting	$FNAP_{k,y}$	k=T0,T1,T2,T3,j-i; j =l,l; i = e,f; y=year
FQ8..FQ12	Fry in hatchery after fry collection	$FHAC_{k,y}$	k=T1,T3; y=year

Table 7. Continued.

Spreadshret Location	Variable description	Variable name	Index Range
FR8..FR16	Fry in nature after fry collection	$FNAC_{k,y}$	k = T0,T1,T2,T3,j-i; j = l,l; i = e,f; y-year
FS9..FS11	Presmolts in hatchery before planting	$PSH_{k,y}$	k = T1,T3; y-year
FT1 1 ..FTIB	Presmolts planted	$PSP_{k,y}$	k = T3,l-ps,l-ps; y = year
FV8..FV18	Presmolts in nature after planting	$PSNAP_{k,y}$	k = T0,T1,T2,T3,j-i; j-1.1; i = e,f,ps; y = year
FV9..FV11	Presmolts in hatchery after collection	$PSHAC_{k,y}$	k = T1,T3; y = year
FW8..FW18	Presmolts in nature after collection	$PSNAC_{k,y}$	k = T0,T1,T2,T3,j-i; j = l,l; i = e,f,ps; y -year
FX9..FX11	Smolts in hatchery before planting	$SH_{k,y}$	k = T1,T3; y-year
FY 11..FY20	Smolts planted	$SP_{k,y}$	k = T3,l-s,l-s; y-year
FZ8..FZ20	Smolts in nature after planting	SNAP,,	k = T0,T1,T2,T3,j-i; j = l,l; i = e,f,ps,s; y-year
GAB..GA23	Smolts after smolt-smolt survival, based on either a Type I, Type II, or Type III functional response	$S.SSURVF_{k,y}$	f = 1..3; k = T0,T1,T2,T3,j-i; j = l,a,d,l; i = e,f,ps,s,a; y - y e a r
GB8..GB23	Smolts after downstream passage	$SADP_{k,y}$	k = T0,T1,T2,T3,j-i; j = l,l; i = e,f,ps,s; y - y e a r
GC8..GC23	Smolts after estuary	$SAE_{k,y}$	k = T0,T1,T2,T3,j-i; j = l,l; i = e,f ,ps,s; y -year
GD8..GE23 GI8..GU23 HJ8..HK23 HZ8..IA23	Adults in the ocean	$AOsh_{k,y}$	s = M,F; h = 1. .4; k = T0,T1,T2,T3,j-i; j = l,a,d,l; i = e,f,ps,s,a; y = year

Table 7. Continued.

Spreadsheet Location	Variable description	Variable name	Index Range
GF8..GG23 GV8..GW23 HL8..HM23 IB8..IC23	Ocean harvest	$OHsh_{k,y}$	s=M,F; h=1..4; k=T0,T1,T2,T3,j-i; j=l,a,d,l; i=e,f,ps,s,a; y=year
GH8..GH23 GX8..GY23 HN8..HO23 ID8..IE23	Adults in ocean after harvest	$AOAHsh_{k,y}$	s=M,F; h=1..4; k=T0,T1,T2,T3,j-i; j=l,a,d,l; i=e,f,ps,s,a; y-year
GI8..GK23 GZ8..HA23 HP8..HQ23 IF8..IG23	Adults in river returns	$ARRsh_{k,y}$	s=M,F; h=1..4; k=T0,T1,T2,T3,j-i; j=l,a,d,l; i=e,f,ps,s,a; y-year
GL8..GM23 HB8..HC23 HR8..HS23 IH8..II23	Adults in river harvest	$RHsh_{k,y}$	s=M,F; h=1..4; k=T0,T1,T2,T3,j-i; j=l,a,d,l; i=e,f,ps,s,a; y-year,
GN8..GO23 HD8..HE23 HT8..HU23 IJ8..IK23	Strays after adult passage	$STRYsh_{k,y}$	s=M,F; h=1..4; k=T0,T1,T2,T3,j-i; j=l,a,d,l; i=e,f,ps,s,a; y-year
GR8..GS23 HH8..HI23 HX8..HY23	Adults left in the ocean	$LIOsh_{k,y}$	s=M,F; h=1..4; k=T0,T1,T2,T3,j-i; j=l,a,d,l; i=e,f,ps,s,a; y=year

N13 Winter Capacity (WC) is the carrying capacity of the **subbasin** for presmolts during the overwintering period. The estimation of this parameter is based on the same procedure used to estimate summer capacity.. Winter capacity is defined **as**

$$WC = \frac{RWSC}{SC} \tag{2}$$

where terms are as, described above.

O84..R87 Maturation Rates ($MRks_h$ for k=T0,T3 genetic stock, s=M,F [male and female fish respectively], and h=1..4 years fish are in the ocean) are the rates at which fish depart the ocean after some number of years and start their spawning run to the **subbasin**. Maturity schedules are based on specific **subbasin** information to the extent possible. These values remain fixed for a model run, though it is recognized that maturation has a genetic component which can be altered through fisheries (**Ricker** 1981) and hatchery practices (papers cited in Steward and Bjomn 1990). The maturation rates are defined in the EDT model as

$$MRks_h = \begin{cases} 1 & \text{if } h > 3 \text{ or if } ADks_{h+1} = 0 \text{ and } h > 1 \\ 0 & \text{if } ADks_{h+1} = 0 \text{ and } h = 1 \\ \left[\dfrac{ADks_{h+1} \cdot (1 - MHR_h) \cdot PSURV_h}{ADks_h \cdot (1 - MHR_{h+1}) \cdot PSURV_{h+1} \cdot (1 - OHR_{h+1}) \cdot OSURV_{h+1} \cdot MRks_{h+1}} \right]^{-1} & \text{else} \end{cases} \tag{3}$$

where $ADks_h$, for k=T0,T3 **genetic** stock, s=M,F [male and female fish respectively], and h=1..4 years **fish** are in the ocean, is steady state age distribution (input) for by sex on the spawning grounds; MHR_h, for h=1..4 years fish are in the ocean, is the **mainstem** harvest rate (input), $PSURV_h$, for h=1..4 **years fish** are in the **ocean, is** the adult passage survival (inp.ut), OHR,,, for h=1..4 years fish are in the ocean, 'is the ocean harvest rate (input), and $OSURV_h$, for h=1..4 years fish are in the ocean, is the natural ocean survival (input).

O167..S170 Broods&k ($BRDSTK_{i,c}$ **for** i=e,f,ps,s release life-stage **[eggs, fry, presmolts,** and smolts respectively] and c=1..5 collection periods **[pre-t-harv,** post-t-harv, **spwn-grd, fry,** and presmolts respectively]) is the number of adult fish required. **for** broodstock 'to **achieve the** numeric release goals associated with each release and, collection period. 'Broodstock **can** be collected **from** the river as adults during the pre-terminal, harvest stage, at the post-terminal harvest stage, on the spawning grounds, or collected **as** fry or presmolts from the **subbasin**. Spawners that are supplemented to the natural spawning population are imported from outside stock and thus are not shown here. Broodstock required for egg supplementation is defined as

$$BRDSTK_{e,c} = \begin{cases} 0 \text{ if } YRST \geq SUPDUR_e \\ \left[\dfrac{BRDCS_{e,c} \cdot SUPNUM_e \cdot \sum_{h=1}^{4} ADTOF_h}{P.SPSURVHT0 \cdot \left(\sum_{h=1}^{4} ADTOF_h \cdot EPFTO_h \cdot P.SPSURVT3_h \right)} \right] \cdot \dfrac{1}{BRDCSR} \text{ for } c = 1..3 \\ NA \quad \text{for } c = 4,5 \end{cases} \quad (4)$$

where ***YRST*** is the current brood year for calculations; $SUPDUR_i$, for i=e,f,ps,s life-stage [eggs, fry, presmolts, and **smolts** respectively], is the duration of supplementation for each life-stage (input); $BRDCS_{i,c}$, for i=e,f,ps,s release stage and c=1..6 collection source [pre-t-harv, post-t-harv, spwn-grd, fry, 'presmolts; and imported respectively] is the broodstock collection schedule (input as percent of each source and, release stage); $SUPNUM_i$, for i=e,f,ps,s,a life-stage, is the numeric release goal to be **supplemented** for each life stage (input); $P.SPSURVT3_1$ is the prespawning survival rate for T3 genetic stock and **fish** returning from the ocean after 1 year (input); $EPFTO_h$, h=1..4 years in the **ocean,** is the number of eggs produced per TO females (input); ***P.SPURVHT0*** **is** the prespawning pedigree relative survival adjustment (input); ***BRDCSR*** is the percent female-of the broodstock (input); and NA means not **applicable** for this calculation. Broodstock for the production of fry is defined as

$$BRDSTK_{f,c} = \begin{cases} 0 \text{ if } YRST \geq SUPDUR_f \\ \left[\dfrac{BRDCS_{f,c} \cdot SUPNUM_f \cdot \sum_{h=2}^{4} ADTOF_h}{BRDSTK_{calc1}} \right] \cdot \dfrac{1}{BRDCSR} \text{ for } c = 1..3 \\ NA \quad \text{for } c = 4,5 \end{cases} \quad (5)$$

for

$$BRDSTK_{calc1} = E.FSURVT3 \cdot E.FRSA \cdot P.SPSURVHT0 \cdot \left(\sum_{h=1}^{4} ADTOF_h \cdot EPFTO_h \cdot P.SPSURVT3_h \right) \quad (6)$$

where **E.FSURVT3** is the egg-to-fry survival rate for T3 fish (input); and ***E.FRSA*** is the egg to fry pedigree relative survival adjustment (input). Broodstock **for** the production of presmolts is 'defined as

$$BRDSTK_{pa,c} = \begin{cases} 0 \text{ if } YRST \geq SUPDUR_{pa} \\ \left[\dfrac{BRDCS_{pa,c} \cdot SUPNUM_{pa} \cdot \sum_{h=1}^{4} ADTOF_h}{BRDSTK_{calc2}} \right] \cdot \dfrac{1}{BRDCSR} \quad \text{for } c = 1..3 \\ \dfrac{BRDCS_{pa,c} \cdot SUPNUM_{pa}}{F.PSSURVT3 \cdot F.PSRSA} \quad \text{for } c = 4 \\ NA \quad \text{for } c = 5 \end{cases} \tag{7}$$

for

$$BRDSTK_{calc2} = E.FSURVT3 \cdot E.FRSA \cdot F.PSSURVT3 \cdot F.PSRSA \cdot P.SPSURVHT0 \cdot \left(\sum_{h=1}^{4} ADTOF_h \cdot EPFTO_h \cdot P.SPSURVT3_h \right) \tag{8}$$

where **F.PSSURVT3** is the fry-to-presmolt survival rate (input) **for** T3 fish; and E.PSRSA is the 'fry to presmolt pedigree relative **survival** adjustment (input). Broodstock for the production of smolts is defined as

$$BRDSTK_{s} = \begin{cases} 0 \text{ if } YRST \geq SUPDUR_{s} \\ \left[\dfrac{BRDCS_{s,c} \cdot SUPNUM_{s} \cdot \sum_{h=1}^{4} ADTOF_h}{BRDSTK_{calc4} \left(\sum_{h=1}^{4} ADTOF_h \cdot EPFTO_h \cdot P.SPSURVT3_h \right)} \right] \cdot \dfrac{1}{BRDCSR} \quad \text{for } c = 1..3 \\ \dfrac{BRDCS_{s,c} \cdot SUPNUM_{s}}{F.PSSURVT3 \cdot F.PSRSA \cdot PS.SSURVT3 \cdot PS.SRSA} \quad \text{for } c = 4 \\ \dfrac{BRDCS_{s,c} \cdot SUPNUM_{s}}{PS.SSURVT \cdot .SRSA} \quad \text{for } c = 5 \end{cases} \tag{9}$$

for

$$BRDSTK_{calc4} = E.FSURVT3 \cdot E.FRSA \cdot F.PSSURVT3 \cdot F.PSSURVT3 \tag{10}$$

and

$$BRDSTK_{s} = PS.SSURVT3 \cdot PS.SRSAT3 \cdot P.SPSURVHT0 \tag{11}$$

where **PS.SSURVT3** is the presmolt-to-smelt survival rate (input) for T3 fish; and ***PS.SRS*** is the presmolt to **smolt** relative survival adjustment (input).

3.2 Treatment Effects Section

AB13..AF20 Genetic Fitness **Components** by release stage (**$GFC_{i,j}$** for ***i*=e,f,ps,s,a** [for egg, **and *j*=T1,T2,T3,l,a,d,con,inn**

T1, T2, and T3 fish; for stock source effects for local, adjacent, and distant **broodstock** sources; and for hatchery culture effects using conventional and innovative culture methods respectively]) are estimates of components of fitness in the natural environment for **salmon** subjected to six categories of hatchery practices consisting of a stock source (i.e., local, adjacent, and distant) and culture method **(i.e.,** conventional and innovative). The product of these components form genetic fitness factors that modify survival rates between life history stages. For example, if a hatchery practice reduces fitness by half, the cumulative, natural survival across all life-history stages will be reduced by half, Wild fish are always assigned a fitness of 1. Genetic fitness components for each genetic stock and culture method for fry are defined **as**

$$GFC_{i,j} = GFC_{e,j} - \frac{GFC_{e,j} - GFC_{e,j}}{3} \quad \text{for } j = \text{T1, T2, T3, con, and inn} \tag{12}$$

where the genetic fitness components **$GFC_{e,j}$** are defined as 1 except as noted in Equation 13

$$GFC_{i,j} = GFC_{e,j} \quad \text{for } i = e, f, \text{ and } ps \tag{13}$$

and for j = 1, a, and d [local, adjacent, **and** distant broodstock sources] stock source effects.

Genetic fitness components for each genetic stock and culture method for presmolts are defined as

$$GFC_{ps,j} = GFC_{i,j} - \frac{GFC_{e,j} - GFC_{e,j}}{3} \quad \text{for } j = \text{T1, T2, T3, con, and inn} \tag{14}$$

for stock source effects as noted in Equation 13. Genetic fitness components for adults are defined as

$$GFC_{a,j} = GFC_{e,j} \quad \text{for all } j \tag{15}$$

AC34..AG63 Genetic Fitness Factors (Genetic **Effects**) (*$GEk_{i,CULT,SS,E}$* for ***k*=T1,T2,T3** [for genetic stock **T1,** T2, and T3 fish], i=e,f,ps,s,a [for egg, fry, presmolt, smolt, and adult respectively] and ***CULT*=con,inn** [for conventional and innovative culture methods respectively] (input), ***SS*=l,a,d** [for local, adjacent, and distant stock sources] (input), and **E=t,s** [for total and **stage** effects]) are factors that 'adjust survival of fish **downward** compared to TO fish due to the effects of genetic alteration associated with supplementation. These factors are the product of the three fitness components (domestication; stock **source** and culture method). They are defined as

$$GEk_{i,CULT,SS,E} = \begin{cases} GFC_{i,CULT} \cdot GFC_{i,SS} \cdot GFC_{i,k} & \text{for } E = t \\ (GEk_{i,CULT,SS,E})^{\frac{1}{3}} & \text{for } E = s \end{cases} \tag{16}$$

and are used to modify survival between life history stages.

AB89..AF92 Relative Survival of hatchery fish (T3) to wild fish (TO) (***$RELSURV_{i,CULT,SS}$*** for ***i*=e,f,ps,s,a** [for egg, fry, presmolt, smolt, and adult respectively]; ***CULT*=con,inn** [for conventional and innovative culture methods] (input); and ***SS*=l,a,d** [for local, adjacent, and distant stock sources respectively (input)] is a function of genetic and non-genetic (behavioral and physiological changes not caused by genetic changes) alterations caused by hatchery propagation. The relative survival for imported hatchery fish, either of adjacent or distant stock (genetic distance), **using** conventional culture **methods** is based on the user **input of** relative survival for local stock using conventional culture as defined by

$$RELSURV_{i,con,SS} = \left[\frac{RELSURV_{i,con,l}}{GFC_{i,l}} \right] \cdot GFC_{i,SS} \quad \text{for } SS = a,d \tag{17}$$

where ***$RELSURV_{i,con,l}$*** is user input. The relative survival for innovative culture methods with local stock is defined as.

$$RELSURV_{i,inn,l} = \begin{cases} 1 & \text{if } RELSURV_{i,con,l}\,(1 + PIINN_i) > 1 \\ & \text{else} \\ & RELSURV_{i,con,l} \cdot (1 + PIINN_i) \end{cases} \tag{18}$$

where ***$PIINN_i$*** for ***i*=e,f,ps,s,a** **is** the percent improved performance of hatchery fish with innovative culture (input), and the relative survival for innovative culture methods with adjacent and distant stock is

$$RELSURV_{i,inn,ss} = \begin{cases} 1 & \text{if } \left(\frac{RELSURV_{i,inn,j}}{GFC_{i,j}}\right) \cdot GFC_{i,ss} > 1 \text{ for } ss = a,d \\ \left(\frac{RELSURV_{i,inn,j}}{GFC_{i,j}}\right) \cdot GFC_{i,ss} & \text{else} \end{cases} \quad (19)$$

A A 1 3 **1..AE162** Total Effects ($TEj_{i,CULT,L}$ for j=**l,a,d** [for local, adjacent, or distant stock source], i=**e,f,ps,s,a** [for egg, fry, presmolt, smolt, and adult respectively], $CULT$=**con,inn** [for conventional and innovative culture methods], and L=**e-f,f-ps,ps-s,s-s,jp,est,o,oh,rh,ap,psp,hf** [for life survival stages egg-fry, fry-presmolt, presmolt-smolt, smolt-smolt before passage, juvenile passage, estuary, **ocean, ocean harvest, river harvest, adult passage, prespawn, and** homing fidelity respectively]) is the relative survival of hatchery fish **(T3)** to wild fish (TO) by life stage and is a function of the genetic and non-genetic effects **affecting** survival at each life stage. It is defined as

$$TEj_{i,CULT,L} = \begin{cases} GET3_{i,CULT,j,e} \cdot \left(\frac{RELSURV_{i,CULT,j}}{GET3_{i,CULT,j,t}}\right)^{NGE_{i,L}} & \text{for } L \neq oh,rh,hf \\ \left(\frac{RELSURV_{i,CULT,j}}{GET3_{i,CULT,j,t}}\right)^{NGE_{i,L}} & \text{for } L = oh,rh,hf \end{cases} \quad (20)$$

where. $NGE_{i,L}$, for i=**e,f,ps,s,a** and L=**e-f,f-ps,ps-s,s-s,jp,est,o,oh,rh,ap,psp,** hf is **the proportion** of the total non-genetic treatment effectsthat occurs during life stage L (input).

3.3 Formula Setup Section

AA169..AE237 (equations placed at **GA8..GA23** for calculations) **Smolts** After Smolt-Smolt Survival based on either a Type I, Type II, or Type III predator-prey functional response ($S.SSURVF_{k,y}$ for F=**1..3** [type I, II, or III functional **response](input),** k=**T0,T1,T2,T3**,j-i for j=**l,a,d**,I [local, adjacent, distant, or imported - a place holder for adjacent or distant - stock sources] and i=**e,f,ps,s,a** [egg, fry, presmolts, **smolts,** and adults respectively], y = year) is the number of smolts surviving the effects of predators during the smolt migration within the subbasin.

The Type I functional response (Holling 1959) assumes that predators prey on migrant smolts at a constant rate with no provision for predator satiation, regardless of smolt density (Fig. **5A)**. The other two functional responses assume that the rate of predation is dependent on the **density of migrants (prey). The Type II response results in the highest rate of predation at low** prey density (Fig. **5B)**. The Type **III** response results in a low predation rate at low prey density and highest rates at intermediate densities (Fig. **5C)**. The techniques used to model the

two predator responses were described by **Peterman** (1977) for Type III and by Hilbom and Walters (1992) for Type II.

Smolts after smolt-smolt survival based on a Type I predator-prey functional response is defined as

$$S.SSURV1_{k,y} = \begin{cases} SNAP_{T0,y} \cdot S.SSURV \text{ for } k = T0 \\ SNAP_{k,y} \cdot S.SSURV \cdot kFF_{9,y} \text{ for } k = T1, T2 \\ \sum_{j=l,d} \sum_{i=e,f,ps,s,a} S.SSURV1_{j-i,y} \text{ for } k = T3 \end{cases} \quad (21)$$

where ***SNAP,*** for ***k*=T0,T1,T2,T3,*j-i*** for ***j*=l,a,d,*I*** [local, adjacent, distant, or imported - a place holder for adjacent or distant - stock sources] and ***i*=e,f,ps,s,a** [egg, fry, presmolts, smolts, and adults respectively], and y = year is the number of smolts surviving in nature after planting; ***S.SSURV*** is the density independent smolt-smolt survival (input); and $kFF_{9,y}$ for ***k*=T1,T2** genetic strains and y = year total genetic fitness factor (weighted by spawning **T3** types) taken to the ninth root. For hatchery fish from each release stage, the smolt-smolt survival with a Type I response function is

$$S.SSURV1_{j-i,y} = \begin{cases} SNAP_{j-i,y} \cdot S.SSURV \cdot TEj_{i,CULT,s-a} \\ NA \quad \text{for } i = a \end{cases} \quad (22)$$

for ***j*=l,a,d,*I*** where if ***j=I,*** then j=a if ***SS*=a** else j-d; for ***i*=e,f,ps,s,a** [egg, **fry,** presmolts, smolts, and adults respectively]; and ***CULT*=con** or inn culture method (input).

Smolts after smolt-smolt survival using a Type II and **III** predator-prey functional response for wild fish (TO) becomes

$$S.SSURVF_{T0,y} = \max\left[\frac{S.SSURVF_{subcale} \cdot SNAP_{T0,y}}{SNAP_{T0,y} + \left(\sum_{j=T1,T2} kFF_{9,y} \cdot SNAP_{j,y}\right) + \left(\sum_{j=l,d} \sum_{i=e,f,ps,s,a} TEj_{i,CULT,s,a} \cdot SNAP_{j-i,y}\right) + \varepsilon}, 0 \right] \quad (23)$$

where

$$S.SSURVF_{subcalc} = \begin{cases} \max\left[\sum_{k=T0,T1,T2,T3} SNAP_{k,y} - \dfrac{Mx\%CC \cdot CC \cdot \sum_{k=T0,T1,T2,T3} SNAP_{k,y}}{PCCB2 \cdot CC + \sum_{k=T0,T1,T2,T3} SNAP_{k,y}}, 0 \right] & \text{for } F = 2 \\ \sum_{k=T0,T1,T2,T3} SNAP_{k,y} - \dfrac{Mx\%CC \cdot CC \cdot \left(\sum_{k=T0,T1,T2,T3} SNAP_{k,y}\right)^2}{(PCCB2 \cdot CC)^2 + \left(\sum_{k=T0,T1,T2,T3} SNAP_{k,y}\right)^2} & \text{for } F = 3 \end{cases} \quad (24)$$

for F=2,3 [type II or III functional response] (input); j=l,a,d,I [local; adjacent, distant, or imported - a place holder for adjacent or distant - stock sources] and i=e,f,ps,s,a [egg, fry, presmolts, smolts, and adults respectively]; $CULT$=con or inn culture method (input);. $Mx\%CC$ is an estimate of the maximum percent of the smolt carrying capacity (CC) that can be eaten by the predator population (input); $PCCB2$ is percent of CC that must be present for one-half of $Mx\%CC$ to be consumed (input); and $\varepsilon = 1x10^{-50}$. For progeny of naturally spawning hatchery fish (T1 and T2), this quantity is defined as;

$$S.SSURVF_{k,y} = \frac{kFF_{0,y} \cdot S.SSURVF_{T0,y} \cdot SNAP_{k,y}}{SNAP_{T0,y} + \varepsilon} \quad (25)$$

for F=2,3 [type II or III functional response](input), and k=T1,T2. For hatchery fish (T3), number of smolts after smolt-smolt survival is defined as

$$S.SSURVF_{T3,y} = \sum_{j=l,d} \sum_{i=e,f,ps,s,a} S.SSURVF_{j-i,y} \quad (26)$$

for F=2,3 [type II or III functional response]; j=l,a,d,I [local, adjacent, 'distant, or' imported - a place holder for adjacent or distant - stock sources], and i=e,f,ps,s,a [egg, fry, presmolts, smolts, and adults respectively]; and

$$S.SSURVF_{j-i,y} = \begin{cases} \dfrac{TEj_{i,CULT,e-s} \cdot S.SSURVF_{T0,y} \cdot SNAP_{j-i,y}}{SNAP_{T0,y} + \varepsilon} \\ NA \quad \text{for } i = a \end{cases} \quad (27)$$

for F=2,3 [type II or III functional response]; j=l,a,d,I where if j=I then j=a if SS=a, else j=d; and $CULT$=con or inn culture method (input).

AA243..AA275 (equations placed at **GB8..GB23** for calculations) No Variation in Survival After -Downstream Passage (*$NVADP_{k,y}$* for ***k*=T0,T1,T2,T3,*j-i*** for j=l,a,d,Z [local, adjacent, distant, or imported - a place holder for adjacent or distant - stock sources], and i=e,f,ps,s,a [egg, fry, presmolts, smolts, and adults respectively], and y = year) is one of several options the user has to incorporate environmental variation. If no yearly variation is desired in survival from downstream migration through the- Snake **and** Columbia mainstems, then the number' of wild smolts surviving to the estuary is

$$NVADP_{k,y} = \begin{cases} S.SSURVF_{T0,y} \cdot JPSURV & \text{for } k = TO \\ S.SSURVF_{k,y} \cdot JPSURV \cdot kFF_{e,y} & \text{for } k = T1, T2 \end{cases} \quad (28)$$

for ***JPSURV*** the **juvenile** passage survival rate (input) and ***F*=1,2,3** predator-prey functional response (input). The number of hatchery smofts surviving to the estuary is

$$NVADP_{T3,y} = \sum_{j=l,} \sum_{i=e,f,ps,s,a} SADP_{j-i,y} \quad (29)$$

for $SADP_{k,y}$ the number of smolts surviving after downstream passage ***k*=T0,T1,T2,T3,*j-i*** for ***j*=l,a,d,*I*** [local, adjacent, distant, or imported - a place holder for adjacent or distant - stock sources], and ***i*=e,f,ps,s,a** [egg, fry, presmolts, **smolts,** and adults respectively], and y = year and

$$NVADP_{j-i,y} = \begin{cases} S.SSURVF_{j-i,y} \cdot JPSURV \cdot TEj_{i,CULT,y} \\ NA \quad \text{for } i = a \end{cases} \quad (30)$$

for ***CULT*=con** or inn culture method (input) and ***F*=1,2,3** predator-prey functional response (input).

AB243..AB275 (equations placed at **GB8..GB23** for calculations) No Variation in Survival After **Estuary** (*$NVAE_{k,y}$* for ***k*=T0,T1,T2,T3,*j-i*** for ***j*=l,a,d,*I*** [local, adjacent, distant, or imported - a place holder for adjacent or distant - stock sources], and i=e,f,ps,s,a [egg, fry, presmolts, smolts, and adults respectively], and y = year) is the number of smolts surviving to the ocean assuming no yearly variation in estuary survival. It is defined for wild fish as

$$NVAE_{k,y} = \begin{cases} SADP_{T0,y} \cdot ESURV & \text{for } k = T0 \\ SADP_{k,y} \cdot ESURV \cdot kFF_{0,y} & \text{for } k = T1,T2 \end{cases} \quad (31)$$

for ***ESURV*** the estuary survival rate (input), and for hatchery fish as

$$NVAE_{T3,y} = \sum_{j=1,l} \cdot \sum_{e,f,ps,s,a} SAE_{j-i,y} \quad (32)$$

for $SAE_{k,y}$, k=T0,T1,T2,T3,j-i for j=l,a,d,I [local, adjacent, distant, or. imported - a place holder for adjacent or distant - stock **sources],** and i=e,f,ps,s,a **[egg, fry, presmolts, smolts,** and adults respectively], and y = year, the number of **smolts** surviving **after** estuary and

$$NVAE_{j-i,y} = \begin{cases} SADP_{j-i,y} \cdot ESURV \cdot TEj_{i,CUL\ T,con} & \\ NA & \text{for } i = a \end{cases} \quad (33)$$

for ***CULT***=**con** or inn culture method (input).

AA280..AA312 (equations placed at **GB8..GB23** for calculations) <u>Variation in Survival After Downstream Passage (</u> $VADP_{k,y}$ for k=T0,T1,T2,T3,j-i -for j=l,a,d,I [local, adjacent, distant, or imported - a place holder for adjacent or distant - stock sources], and i=e,f,ps,s,a [egg, fry, presmolts, smolts, and adults respectively], **and** y = year) incorporates yearly variation in **mainstem** migration survival to -below Bonneville Dam. The variation is obtained through an input file and was generated from a **50-year** runoff 'record (1929-1978). The user has an option to supply one of four input files or one of his/her **own.** If variable **mainstem** migration survival is assumed, the number of wild smolts surviving to **the** estuary is

$$VADP_{k,y} = \begin{cases} S.SSURVF_{T0,y} \cdot VFAS & \text{for } k = T0 \\ S.SSURVF_{k,y} \cdot WAS \cdot kFF_{0,y} & \text{for } k = T1,T2 \end{cases} \quad (34)$$

for ***VPAS*** the juvenile passage variable survival rate (input file) **and F=1,2,3** predator-prey functional response (input). The number of hatchery smolts surviving to the estuary is

$$VADP_{T3,y} = \sum_{j=l,l} \sum_{i=e,f,ps,s,a} SADP_{j-i,y} \quad (35)$$

for $SADP_{k,y}$, k=T0,T1,T2,T3,j-i for j=l,a,d,I [local, adjacent, distant, or imported - a place holder for adjacent or distant - stock sources],, and i=e,f,ps,s,a [egg, fry, presmolts, smoits, and adults respectively], and y = year, the number of smolts surviving after downstream passage and

$$VADP_{j-i,y} = \begin{cases} S.SSURVF_{j-i,y} \cdot VPAS \cdot TEj_{i,CULT,ip} \\ NA \quad for\ i = a \end{cases} \quad (36)$$

for $CULT$=con or inn culture method (input) and F=1,2,3 predator-prey functional response (input).

AB280..AB312 (equations placed at GC8..GC23 for calculations) Variation in Survival After Estuary ($VAE_{k,y}$ for k=T0,T1,T2,T3,j-i for j=l,a,d,I [local, -adjacent, distant, or imported - a place holder for adjacent or distant - stock sources],' and i=e,f,ps,s,a [egg, fry, presmolts, smolts, and adults respectively], and y = year) is meant to encompass all other influences of environmental variation on survival. This variation in survival is based on a log-normal function, and for wild fish is defined as

$$VAE_{k,y} = \begin{cases} SADP_{T0,y} \cdot VEST \quad for\ k = T0 \\ SADP_{k,y} \cdot VEST \cdot kFF_{0,y} \quad for\ k = T1,T2 \end{cases} \quad (37)$$

for $VEST$ the variable estuary survival rate (input file). For hatchery fish, the variation in survival is defined as

$$VAE_{T3,y} = \sum_{k=T0,T1,T2,T3} SAE_{k,y} \quad (38)$$

for $SAE_{k,y}$, k=T0,T1,T2,T3,j-i for j=l,a,d,I [local, adjacent, distant, or imported - a place holder for adjacent or distant - stock sources], and i=e,f,ps,s,a [egg, fry, presmolts, smolts, and adults respectively], and y = year, the number of smolts surviving after estuary and

$$VAE_{j-i,y} = \begin{cases} SADP_{j-i,y} \cdot VEST \cdot TEj_{i,CULT,con} \\ NA \quad for\ i = a \end{cases} \tag{39}$$

for ***CULT***=**con** or inn culture method (input).

3.4 Computation Section

AZ8..BG23 Adults Returning to Subbasin (*$ARSsh_{k,y}$* for ***s***=**M,F** [male or female]; ***h***=**1..4** years fish are in the ocean; ***k***=**T0,T1 ,T2,T3,*j-i*** for ***j***=**l,a,d,*I*** stock sources **[*I*=a** or d stock sources (input)], and ***i***=**e,f,ps,s,a** [egg, fry, presmolts, and adults respectively]; and **y=year)** is initially seeded by user defined numbers of returning adults. The initial seeds affect the model results for the first seven years (or time-steps), thus placing a minimum of at least 10 years before model results are applicable for any type of qualitative (or quantitative) analysis. The number of adults returning to the **subbasin** is a function of the **broodyear** for each returning age class defined as ***y-3-h+1*** **where** ***y*** is the current year (or time-step). Thus, the number of adults returning to the **subbasin** for the TO genetic stock is defined as

$$ARSsh_{T0,y} = \begin{cases} IRSs_{T0,ss} \cdot ADTOs_h \ for\ y - 3 - h \cdot 1 \le 0 \\ \text{else} \\ \left[ARRsh_{T0,y-3-h+1} - RHsh_{T0,y-3-h+1} - \dfrac{STRYsh_{T0,y-3-h+1}}{PSURV_h} \right] \cdot PSURV_h \end{cases} \tag{40}$$

for ***s***=**M,F**; ***h***=**1..4** years fish are in **the** ocean; ***$IRSs_{k,SS}$***, for ***s***=**M,F**, ***k***=**T0,T1,T2,T3,** and SS=l,a,d stock sources (input), the initial returns to the **subbasin** (input); ***$ARRsh_{k,y}$*** is the number of **adult** in-river returns to the Columbia River (defined later) ; ***$RHsh_{k,y}$*** is the adult **in-**river harvest; and ***$STRYsh_{k,y}$*** is the number of strays to other subbasins **after** adult passage. For the other genetic types of natural production **(T1** and **T2),** the number of returning adults is

$$ARSsh_{k,y} = \begin{cases} IRSs_{k,ss} \cdot ADTOs_h \ for\ y-3-h+l \le 0 \\ e\ \&\ e \\ \left[ARRsh_{k,y-3-h+1} - RHsh_{k,y-3-h+1} - \dfrac{STRYsh_{k,y-3-h+1}}{PSURV_h \cdot kFF_{9,y-3-h+1}} \right] \cdot PSURV_h \cdot kFF_{9,y-3-h+1} \end{cases} \tag{41}$$

for ***k***=**T1,T2**; ***s***=**M,F**; ***h***=**1..4** years' fish are in the ocean; and ***$kFF_{9,y}$*** the ninth root genetic fitness factor. The number of adult hatchery **fish** returning to the **subbasin** is defined **as**

$$ARSsh_{T3,y} = \sum_{j=1,1} \sum_{i=e,f,ps,s,a} ARSsh_{j-i,y} \tag{42}$$

for s=M,F; h=1..4 years fish are in the ocean; and

$$ARSsh_{j-i,y} = \begin{cases} NA \text{ for } y-3-h+1 \le 0 \text{ and } i = e,f,ps,a \\ IRSs_{T3,j} \cdot ADT3s_h \text{ for } y-3-h+1 \le 0 \text{ end } i = s \\ \text{else} \\ ARRsh_{j-i,y-3-h+1} - RHsh_{j-i,y-3-h+1} - \dfrac{STRYsh_{j-i,y-3-h+1}}{PSURV_h \cdot TEj_{i,CULT,sp}} \cdot PSURV_h \cdot TEj_{i,CULT,sp} \end{cases} \tag{43}$$

for s=M,F; h=1..4 years fish are in the ocean; j=l,a,d,I; and i=e,f,ps,s,a.

AZ24..BG24 Initial Ninth Root Genetic Fitness Factors ($kIFF_{9,h,y}$ for k=T1,T2 and y-year) are the initial ninth root genetic fitness factors applied to the seed adult returns to the subbasin. Ninth root genetic fitness factors are simply the ninth root of the genetic fitness factors ($GEk_{i,CULT,SS,E}$) because the reduction in genetic fitness of T1 and T2 fish is spread equally across nine life stages (thus the life-stage specific genetic factors are all 'equal and are multiplicative). *The initial* ninth root factors are applicable only during years when seed (user input) returns occur. After that the $kFF_{9,h}$ factors (defmed later in (Equation 91) are applicable. The ninth root fitness factors are used at this point-in the sprsadsheet to modify the grespawning survival rate of wild progeny produced with either one or both parents from hatchery stock. These genetic factors are defined as

$$kIFF_{9,h,y} = \begin{cases} \dfrac{\sum_{\substack{j=1,1 \\ s=M,F}} ARSsh_{j-s,y} \cdot GEk_{s,con,j,t}}{\sum_{\substack{j=1,1 \\ s=M,F}} ARSsh_{j-s,y}} \text{ for } y-3-h+1 \le 0 \\ \text{else} \\ kFF_{9,y} \end{cases} \tag{44}$$

where $kFF_{9,y}$ is the applicable ninth-root fitness factor after the initial seed years.

BH8..BH23 Adult Plus Jacks Returning to Subbasin ($ARSJ_{k,y}$, for k=T0,T1,T2,T3 j-i and y-year) is the number of all aged adults plus jacks returning to the subbasin and is defined for wild fish as

$$ARSJ_{k,y} = (ARSM1_{k,y} + ARSF1_{k,y}) \cdot JESP_{T0} + \sum_{\substack{h=2 \\ s=M,F}}^{4} ARSsh_{k,y} \quad (45)$$

for k=T0,T1,T2 and $JESP_k$, for k=T0,T3, the spawn efficiency of jacks (input). For hatchery fish, this is defined as

$$ARSJ_{T3,y} = \sum_{j=I,I} \sum_{i=e,f,ps,s,a} ARSJ_{j-i,y} \quad (46)$$

and

$$ARSJ_{j-i,y} = (ARSM1_{j-i,y} + ARSF1_{j-i,y}) \cdot JESP_{T0} \cdot JESP_{T3} + \sum_{\substack{h=2 \\ s=M,F}}^{4} ARSsh_{j-i,y} \quad (47)$$

for j=l,a,d,I and i=e,f,ps,s,a.

BM9..BR23 Broodstock Removal Limits[7] ($BSLr_{k,y}$ for r=1..3 REM [three time periods for collecting broodstock within the subbasin: 1) preterminal harvest, 2) post-terminal harvest, and 3) on the spawning grounds]; k=T0,T3 [here TO represents the num of all natural fish; i.e., TO, T1, and T2 fish], j-i for j=l,a,d,I [local, adjacent, distant, or imported - a place-holder for adjacent or distant - stock sources], and i=e,f,ps,s,a; and y=year) are the limits placed on the removal of wild and hatchery stock for the production of broodstock at three possible removal times (pre- and post-terminal harvest and on the spawning grounds). The broodstock limits are defined such that wild stock are taken first and are supplemented with hatchery stock only if broodstock requirements cannot be met with wild stock alone, and as provided by the broodstock policy that is defined. User defined limits to the percent of the total and natural run that can be removed affect the number of hatchery fish that are used for broodstock production. The'broodstock limits for wild fish are defined as

$$BSLr_{T1,y} = BSLr_{..y} - BSLr_{T3,y} \quad (48)$$

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7 **The following section reflects how computations were performed in EDTM2.0; equations described here have not been updated for modifications in EDTM3.0. Contact Larry Lestelle at Mobrand Biometrics if a detailed description for EDTM 3.0 is needed.**

where

$$BSLr_{i,y} = \frac{\sum_{i=T0,T1,T2} BRDSTK_{i,r}}{\sum_{i=o,1,pa,a} \sum_{s=1}^{5} BRDSTK_{i,s}} \cdot \tag{49}$$

$$\min \left[\sum_{i=o,1,pa,a} \sum_{s=1}^{5} BRDSTK_{i,s} \;,\; BSL_{scale1} \cdot \sum_{k=T0,T1,T2,T3} ARSJ_{k,y} \;,\; BSL_{scale2} \cdot \sum_{k=T0,T1,T2} ARSJ_{k,y} \right]$$

for

$$BSL_{scale1} = \begin{cases} Mx\%UTR_1 & \text{if year} < BCY_1 + 1 \\ Mx\%UTR_2 & \text{if year} < BCY_2 + 1 \\ & \text{else} \\ & 0 \end{cases} \tag{50}$$

where $Mx\%UTR_t$, for t=1,2, is the maximum percent used of the total run for two time periods (input); BCY_t, for t=1,2 time periods, the years each of two policies are conducted (input); and

$$BSL_{scale2} = \begin{cases} Mx\%UNR_1 & \text{if year} < BCY_1 + 1 \\ Mx\%UNR_2 & \text{if year} < BCY_2 + 1 \\ & \text{else} \\ & 0 \end{cases} \tag{51}$$

where $Mx\%UNR_t$, for t=1,2, is the maximum percent used of the natural run for two time periods. For hatchery fish, the broodstock limits are then

$$BSLr_{T3,y} = \begin{cases} BSLr_{..y} \cdot \min\left[\dfrac{ARSJ_{T3,y}}{ARSJ_{..y} + \varepsilon}, 1 - Mi\%NBS_1\right] & \text{if year} < BCY_1 + 1 \\ BSLr_{..y} \cdot \min\left[\dfrac{ARSJ_{T3,y}}{ARSJ_{..y} + \varepsilon}, 1 - Mi\%NBS_2\right] & \text{if year} < BCY_2 + 1 \\ 0 & \text{else} \end{cases} \quad (52)$$

where $Mi\%NBS_t$, for t=1,2 time periods, is the minimum natural **broodstock** used for two time periods (input) and

$$ARSJ_{..y} = \sum_{k = T0,T1,T2,T3} ARSJ_{k,y} \quad (53)$$

BT8..CO23 Adults After Broodstock REM 1 *(see* Footnote *7)* ($AABS1sh_{k,y}$ for s=M,F [male or female]; h=1..4 years fish are in the ocean; k=T0,T1,T2,T3,j-i for j=l,a,d,I [local, adjacent, distant, or imported - a place holder for adjacent or distant - stock sources], and i=e,f,ps,s,a [egg, fry, presmolts, and adults respectively]; and **y=year)** is the number of adults remaining in the **subbasin** after the first broodstock collection phase. For wild fish returning after only one year in the ocean, this is defined as

$$AABS1s1_{k,y} = \begin{cases} \max\left[0, ARSs1_{k,y} \cdot JESP_{T0} \cdot \left(1 - \dfrac{SRAT \cdot BSL1_{..y}}{\sum_{h=1}^{4} ARSsh_{..y} + \varepsilon}\right)\right] & \text{if } Mi\%NBS_1 = 0 \\ \max\left[0, ARSs1_{k,y} \cdot JESP_{T0} \cdot \left(1 - \dfrac{SRAT \cdot BSL1_{T1,y}}{\left[\sum_{h=1}^{4} ARSsh_{..y}\right] - ARSs1_{T3,y} \cdot JESP_{T0} \cdot JESP_{T3} - \left[\sum_{h=2}^{4} ARSsh_{T3,y}\right] + \varepsilon}\right)\right] & \text{else} \end{cases} \quad (54)$$

for k=TO,Tl ,**T2;** the sex ratio SRA T = 1 - $BRDCSR$ for s=M else SRA T = $BRDCSR$, $BSLh_{k,y}$ the broodstock limits for REM r=1..3 and pedigree k,

$$A\&h,, = \sum_{k = T0,T1,T2,T3} ARSsh_{k,y} , \quad (55)$$

for s=M,F; h=1..4 years fish are in the ocean; and $Mi\%NBS_1$ the minimum percent of natural broodstock used for time period 1. For all other wild fish,

$$AABS1sh_{k,y} = \begin{cases} \max\left[0,\ ARSsh_{k,y} \cdot \left(1 - \dfrac{SRAT \cdot BSL1_{..,y}}{\sum_{i=1}^{4} ARSsi_{..,y} + \varepsilon}\right)\right] & \text{if } MI\%NBS_1 = 0 \\ & \text{else} \\ \max\left[0,\ ARSsh_{k,y} \cdot \left(1 - \dfrac{SRAT \cdot BSL1_{T1,y}}{\left(\sum_{i=1}^{4} ARSsi_{..,y}\right) - ARSs1_{T3,y} \cdot JESP_{T0} \cdot JESP_{T3} - \sum ARSsi_{T3,y} \cdot \varepsilon}\right)\right] \end{cases} \quad (56)$$

for s=M,F; h=2..4; and k=T0,T1,T2. For hatchery fish, the number of adults remaining after the first broodstock collection phase is

$$AABS1s1_{T3,y} = \begin{cases} \max\left[0,\ ARSs1_{T3,y} \cdot JESP_{T0} \cdot JESP_{T3} \cdot \left(1 - \dfrac{SRAT \cdot BSL1_{..,y}}{\sum_{h=1}^{4} ARSsh_{..,y} + \varepsilon}\right)\right] & \text{if } MI\%NBS_1 = 0 \\ & \text{else} \\ \max\left[0,\ ARSs1_{T3,y} \cdot JESP_{T0} \cdot JESP_{T3} \cdot \left(1 - \dfrac{SRAT \cdot BSL1_{T3,y}}{ARSs1_{T3,y} \cdot JESP_{T0} \cdot JESP_{T3} + \left(\sum_{h=2}^{4} ARSsh_{T3,y}\right) + \varepsilon}\right)\right] \end{cases} \quad (57)$$

and

$$AABS1sh_{T3,y} = \begin{cases} \max\left[0,\ ARSsh_{T3,y} \cdot \left(1 - \dfrac{SRAT \cdot BSL1_{..,y}}{\sum_{i=1}^{4} ARSsi_{..,y} + \varepsilon}\right)\right] & \text{if } MI\%NBS_1 = 0 \\ & \text{else} \\ \max\left[0,\ ARSsh_{T3,y} \cdot \left(1 - \dfrac{SRAT \cdot BSL1_{T3,y}}{ARSs1_{T3,y} \cdot JESP_{T0} \cdot JESP_{T3} + \left(\sum_{i=2}^{4} ARSsi_{T3,y}\right) + \varepsilon}\right)\right] \end{cases} \quad (58)$$

for s=M,F; h=2..4; and

$$AABS1sh_{j-i,y} = \frac{ARSJ_{j-i,y} \cdot AABS1sh_{T3,y}}{\sum_{k=T0,T1,T2,T3} ARSJ_{k,y} \cdot \varepsilon} \tag{59}$$

for s=M,F; h=1..4 *years* fish are in the ocean; j=l,a,d,I; i=e,f,ps,s,a.

CG8..CQ23 Adults After Terminal Harvest ($AATHsh_{k,y}$ for s=M,F; h=1..4 **years fish** are in the ocean; k=T0,T1,T2,T3,j-i; and **y=year)** is the number of adults of all age classes remaining after the terminal harvest For natural **fish,** this is defined as

$$AATHsh_{k,y} = \begin{cases} AABS1sh_{k,y} \cdot \left[1 - \max\left[MiHR,\ HREBP \cdot \frac{\left(\sum_{i=T0,T1,T2} AABS1..{}_{i,y}\right) - HRBP}{\sum_{i=T0,T1,T2} AABS1..{}_{i,y}} \right] \right] & \text{if } HARV = 0 \\ \text{else} & \\ AABS1sh_{k,y} & \end{cases} \tag{60}$$

for k=T0,T1,T2; h=1..4 years fish are in the ocean; s=M,F; ***MiHR*** the minimum harvest rate (input); ***HREBP*** the harvest rate in excess of the breakpoint (input); ***HRBP*** **the harvest** rate breakpoint (input); ***HARV*** equal to 0 (random) or 1 (hatchery fish harvested only); **and**

$$AABS1..{}_{k,y} = \sum_{\substack{h=1 \\ s=M,F}}^{4} AABS1sh_{k,y} \tag{61}$$

For hatchery fish, the number of adults remaining after the terminal harvest is defined as

$$AATHsh_{T3,y} = \begin{cases} AABS1sh_{T3,y} \cdot \left[1 - \max\left[MiHR,\ HREBP \cdot \frac{G = E_{T1,T2} \left(AABS1..{}_{k,y}\right) - HRBP}{\sum_{k=T0,T1,T2} AABS1..{}_{k,y}} \right] \right] & \text{if } HARV = 0 \\ \text{else} & \\ AABS1sh_{T3,y} \cdot \left[1 - \max\left[MiHR,\ HREBP \cdot \frac{AABS1..{}_{T3,y} - HRBP}{AABS1..{}_{T3,y}} \right] \right] & \end{cases} \tag{62}$$

, for h=1..4 years **fish** are in the **ocean**; s=M,F; and

$$AATHsh_{j-i,y} = \frac{ARSJ_{j-i,y} \cdot AATHsh_{T3,y}}{\sum_{k = T0,T1,T2,T3} ARSJ_{k,y}} \tag{63}$$

for h=1..4 years fish are in, the ocean; s=M,F; j=l,a,d,I; and i=e,f,ps,s,a.

CR8..DB23 Adults After Broodstock REM 2 (see Footnote 7) ($AABS2sh_{k,y}$ for s=M,F; h=1..4 years fish are in the ocean; k=T0,T1,T2,T3,j-i; and y=year) is the number of adults of all age classes remaining after the second broodstock- collection phase (post-terminal harvest). For wild fish, this is defined as

$$AABS2sh_{k,y} = \begin{cases} AATHsh_{k,y} \cdot \left[1 - \dfrac{SRAT \cdot BSL2_{k,y}}{\sum_{i = T0,T1,T2,T3} AATHs_{i,y} + \varepsilon} \right] & \text{if } MI\%NBS_1 = 0 \\ \text{else} & \\ AATHsh_{k,y} \cdot \left[1 - \dfrac{SRAT \cdot BSL2_{T1,y}}{\left(\sum_{i = T0,T1,T2} AATHs_{i,y} \right) + \varepsilon} \right] & \end{cases} \tag{64}$$

for s=M,F; h=1..4 years fish are in the ocean; k=T0,T1,T2; $BSL2_{k,y}$ the broodstock limits for REM 2; and

$$AATHs_{k,y} = \sum_{h = 1}^{4} AATHsh_{k,y} \tag{65}$$

For hatchery fish, the number of adults remaining after the second broodstock collection phase is defined as

$$AABS2sh_{T3,y} = \begin{cases} \max\left[0 , AATHsh_{T3,y} \cdot \left[1 - \dfrac{SRAT \cdot BSL2_{k,y}}{\sum_{i = T0,T1,T2,T3} AATHs_{i,y} + \varepsilon} \right] \right] & \text{if } MI\%NBS_1 = 0 \\ \text{else} & \\ \max\left[0 , AATHsh_{T3,y} \cdot \left[1 - \dfrac{SRAT \cdot BSL2_{T3,y}}{AATHs_{T3,y} + \varepsilon} \right] \right] & \end{cases} \tag{66}$$

for s=M,F; h=1..4 years fish are in the ocean; and

$$AABS2sh_{j-i,y} = \frac{ARSJ_{j-i,y} \cdot AABS2sh_{T3,y}}{\sum_{k \neq T0,T1,T2,T3} ARSJ_{k,y} + \varepsilon} \quad (67)$$

for s=M,F; h=1..4 years fish are in the ocean; j=l,a,d,I; and i=e,f,ps,s,a.

DE8. .DN23 Adults After Prespawning Mortality ($AAPSMsh_{k,y}$ for s=M,F; h=1..4 *years* fish are in the ocean; k=T0,T1,T2,T3,j-i; and y=year) is the number of adults remaining after correction for a prespawning mortality rate' and genetic and environmental factors. For wild fish, this is defined as

$$AAPSMsh_{T0,y} = AABS2sh_{T0,y} \cdot P.SPSURVT0_h \quad (68)$$

for s=M,F; h=1..4 *years* fish are in the ocean; and

$$AAPSMsh_{k,y} = AABS2sh_{k,y} \cdot P.SPSURVT0_h \cdot kIFF_{9,h,y} \quad (69)$$

for k=T1,T2; s=M,F; h=1..4 years fish are in the ocean; and $kIFF_{9,h,y}$ initial ninth root genetic fitness factors for k=T1,T2 genetic stock; h=1..4 *years* fish are in the ocean; and y=year. For hatchery fish, the number of fish remaining after a correction for prespawning mortality is defined as

$$AAPSMsh_{T3,y} = \sum_{j=l,I} \sum_{i=e,f,ps,s,a} AAPSMsh_{j-i,y} \quad (70)$$

for s=M,F; h=1..4 years fish are in the ocean; and

$$AAPSMsh_{j-i,y} = AABS2sh_{j-i,y} \cdot P.SPSURVT0_h \cdot TEj_{i,CULT,pop} \quad (71)$$

for s=M,F; h=1..4 years fish are in the ocean; j=l,a,d,I; i=e,f,ps,s,a; and $CULT$=con or inn culture method (input).

DP8..DZ23 Adults After Broodstock REM 3 (see Footnote *7)* ($AABS3sh_{k,y}$ for s=M,F; h=1..4 years fish are in the ocean; k=T0,T1 ,T2,T3,j-i; and y=year) is the number of adults of all age classes remaining after the third broodstock collection phase (on the spawning grounds). For wild fish,' this. is defined as

$$AABS3sh_{k,y} = \begin{cases} AAPSMsh_{k,y} \cdot \left(1 - \dfrac{SRAT \cdot BSL3_{.,y}}{\sum_{i=T0,T1,T2,T3} AAPSMs_{\cdot i,y} + \varepsilon}\right) & \text{if } MI\%NBS_1 = 0 \\ \text{else} & \\ AAPSMsh_{k,y} \cdot \left(1 - \dfrac{SRAT \cdot BSL3_{T1,y}}{\left(\sum_{i=T0,T1,T2} AAPSMs_{\cdot i,y}\right) + \varepsilon}\right) & \end{cases} \quad (72)$$

for s=M,F; h=1..4 years fish are in the ocean; k=T0,T1,T2; $BSL3_{.,y}$ the broodstock limits for REM 3; and

$$AAPSMs_{\cdot k,y} = \sum_{h=1}^{4} AAPSMsh_{k,y} \quad (73)$$

For hatchery fish, this quantity is defined as

$$AABS3sh_{T3,y} = \begin{cases} \max\left[0, AAPSMsh_{T3,y} \cdot \left(1 - \dfrac{SRAT \cdot BSL3_{.,y}}{\sum_{i=T0,T1,T2,T3} AAPSMs_{\cdot i,y} + \varepsilon}\right)\right] & \text{if } MI\%NBS_1 = 0 \\ \text{else} & \\ \max\left[0, AAPSMsh_{T3,y} \cdot \left(1 - \dfrac{SRAT \cdot BSL3_{T3,y}}{AAPSM_{T3,y} + \varepsilon}\right)\right] & \end{cases} \quad (74)$$

for s=M,F; h=1..4 years fish are in the ocean; and

$$AABS3sh_{j-i,y} = \frac{AAPSMsh_{j-i,y} \cdot AABS3sh_{T3,y}}{\sum_{k=T0,T1,T2,T3} AAPSMsh_{k,y} + \varepsilon} \quad (75)$$

for s=M,F; h=1..4 years fish are in the ocean; j=l,a,d,I; and i=e,f,ps,s,a.

EA8..EI23 Spawners in Hatchery Prior to Egg Take ($SPHsh_{k,y}$ for s=M,F; h=1..4 years fish are in the ocean; k=T0,T1,T2,T3,j-i; and y=year) is the number of adults of all age classes in the hatchery to be used for egg production. For wild 'fish returning from the ocean after only one year and collected as broodstock, this is defined as

$$SPHs1_{k,y} = \left[ARSs1_{k,y} \cdot JESP_{T0} \cdot JESP_{T3} - \sum_{i=1}^{3} AABSrs1_{k,y} \right] \cdot AATHs1_{k,y} + AAPSMs1_{k,y} \Big] \cdot P.SPSURVT3_1 \cdot P.SPSURVHT0 \quad (76)$$

for s=M,F; k=T0,T1,T2; and ***P.SPSURVHT0*** the prespawning survival of TO fish in the hatchery (input). For all other age classes, this is defined as

$$SPHsh_{k,y} = \left[ARSsh_{k,y} - \left[\sum_{i=1}^{3} AABSrsh_{k,y} \right] + AATHsh_{k,y} + AAPSMsh_{k,y} \right] \cdot P.SPSURVT3_h \cdot P.SPSURVHT0 \quad (77)$$

for s=M,F; k=T0,T1,T2; and h=2..4 years fish are in the ocean. For hatchery fish that **either** returned to the hatchery normally or strayed and where collected as **broodstock, this** quantity is defined as

$$SPHs1_{T3,y} = \left[ARSs1_{T3,y} \cdot JESP_{T0} \cdot JESP_{T3} \left[- \sum_{i=1}^{3} AABSrs1_{T3,y} \right] + AATHs1_{T3,y} + AAPSMs1_{T3,y} \right] \cdot P.SPSURVT3_1 \quad (78)$$

for s=M,F; and

$$SPHsh_{T3,y} = \left[ARSsh_{T3,y} - \left[\sum_{i=1}^{3} AABSish_{T3,y} \right] + AATHsh_{T3,y} + AAPSMsh_{T3,y} \right] \cdot P.SPSURVT3_h \quad (79)$$

for s=M,F; and h=2..4.

EJ8..ER23 Soawneis in Nature Prior to **Spawning** ($SPNsh_{k,y}$ for s=M,F; h=1..4 years **fish** are in **the ocean**; k=T0,T1,T2,T3,j-i; and y=year) is the-number of wild **adults and any** hatchery strays retuniing to the spawning grounds. This quantity **is defined** as

$$SPNsh_{k,y} = AABS3sh_{k,y} \quad (80)$$

for s=M,F; h=1..4 *years* fish are in the ocean; k=T0,T1,T2,j-i; and

$$SPNsh_{T3,y} = \sum_{j=1,l} \sum_{i=0,1,pa,p,e} SPNsh_{j-i,y} \tag{81}$$

for s=M,F; and h=1..4 years fish are in the ocean.

ES8..ES23 Total Number of Males in Nature ($TNMN_{k,y}$ for k=T0,T1,T2,T3 and y=year) is the total number of males on the spawning ground prior to spawning. For wild fish, this is, defined as

$$TNMN_{k,y} = \sum_{h=1}^{4} SPNMh_{k,y} \tag{82}$$

for k=T0,T1,T2. For stray hatchery fish, the total number of males on the spawning ground is adjusted for a maximum percent 'of strays allowed in the natural escapement. Thus, this quantity is defined as

$$TNMN_{T3,y} = \begin{cases} \sum_{h=1}^{4} SPNMh_{T3,y} & \text{if } Mx\%T3E_1 = 1 \\ & \text{else} \\ \min\left[\sum_{h=1}^{4} SPNMh_{T3,y} , \dfrac{Mx\%T3E_1 \cdot \sum_{k=T0,T1,T2} TNMN_{k,y}}{(1 - Mx\%T3E_1)} \right] \end{cases} \tag{83}$$

where $Mx\%T3E_t$, for t=1,2, is the maximum percent of T3 fish allowed in the natural escapement for two time periods (input).

EW8..EW23 Total Number of Eggs in Nature ($TNEN_{k,y}$ for k=T0,T1,T2,T3,j-i and y=year) is the total number of eggs produced on the spawning grounds. For wild fish, this is defined as

$$TNEN_{k,y} = \sum_{h=1}^{4} EPFk_h \cdot SPNFh_{k,y} \tag{84}$$

for k=T0,T1,T2. For stray hatchery fish, this quantity is defined as

$$TNEN_{T3,y} = \begin{cases} \sum_{h=1}^{4} EPFT3_h \text{ if } Mx\%T3E_1 = 1 \\ \text{else} \\ \min\left[\sum_{h=1}^{4} EPFT3_h \cdot SPNFh_{T3,y},\ \dfrac{Mx\%T3E_1 \cdot \sum_{k=T0,T1,T2} TNEN_{k,y}}{(1 - Mx\%T3E_1)}\right] \end{cases} \quad (85)$$

and

$$THEN_{j-i,y} = \frac{SPN..._{j-i,y}}{\sum_{k=T0,T1,T2,T3} SPN..._{k,y} + \varepsilon} \quad (86)$$

where

$$SPN..._{k,y} = \sum_{h=M,F}^{4} SPNsh_{k,y} \quad (87)$$

FA8..FE11 Scenario Matrix **($SM_{k-k',y}$** for **k=T0,T1,T2,T3; k'=T0,T1,T2,T3;** and **y=year)** is a matrix that determines the number of zygotes **produced from** wild and stray hatchery **fish** on the'spawning 'grounds. The EDT model assumes random mating of hatchery **and** wild'-spawners in nature, thus the number of zygotes of **each genetic** stock is determined by the proportion of each type spawning (i.e.,

$$SM_{k-k',y} = \frac{TNEN_{k,y} \cdot TNMN_{k',y}}{\sum_{j=T0,T1,T2,T3} TNMN_{j,y} + \varepsilon} \quad (88)$$

for each k-k' pair.

FI9..FK10 Weighted **Genetic** Fitness Factors (see Footnote **7) (kFF_y** for **k=T1,T2** and **y=year) are** brood year specific genetic fitness factors **assigned to** the genetic, types produced that year based on the relative **contribution** of the **various** sub-types of hatchery fish present in **the** spawning population. These factors **are** defined as

$$kFF_y = \sum_{j=1,2} \sum_{i=e,f,pa,a,s} TNEN_{j-i,y} \cdot GEk_{i,CULT,j,t} \tag{89}$$

for ***CULT*=con** or inn culture method (input) and ***I*=a** or d stock sources (input).

REM Factors (see Footenote 7) **(kRF_y** for ***k*=T1,T2** and **y=year)** regulate (or set) the **ninth** root genetic fitness factors when Recovery Scenario 2 or 3 is operative and supplementation has ceased and thus there are no hatchery fish present on which to calculate 'the ninth root factors. **Use of** the REM factors assumes that fitness of **T1** and **T2** fish stops changing after T3 fish are no longer present (so no improvement of fitness from that point on occurs). **They** are defined as

$$kRF_y = \begin{cases} 0 \quad \text{if year} < 3 \\ kRF_y \text{ if } SCEN > 1 \text{ and } kFF_y < kRF_y \text{ and } kFF_y = \varepsilon \\ \text{else} \\ kFF_y \end{cases} \tag{90}$$

where ***SCEN*** is the assumed genetic recovery scenario (input).

FL9..FL10 Ninth Root Genetic Fitness Factor (see Footnote 7) **($kFF_{9,y}$** for ***k*=T1,T2** and **y=year)** is calculated as the ninth root of the weighted genetic fitness factors and is used to distribute the genetic effects on survival across nine life stages. The factor is defined as

$$kFF_{9,y} = \begin{cases} (kRF_y)^{\frac{1}{9}} \text{ if } SCEN > 1 \text{ and } kFF_y = \varepsilon \text{ and } kRF_y > \varepsilon \\ \text{else} \\ (kFF_y)^{\frac{1}{9}} \end{cases} \tag{91}$$

FF9..FF12 Potential **Zygotes** in **Hatchery** Before. Egg **Plant** **($PZH_{k,y}$** for ***k*=T1,T3** and **y=year)** for progeny with one wild parent is defined as

$$PZH_{T1,y} = \sum_{h=1}^{4} \left(\sum_{k=T0,T1,T2} SPHFh_{k,y} \right) \cdot EPFTO_h \tag{92}$$

and for progeny from hatchery stock as

$$PZH_{T3,y} = \sum_{h=1}^{4} SPHFh_{T3,y} \cdot EPFT3_h \tag{93}$$

FG11..FG14 Eggs Planted ($EP_{k,y}$ for k=T3,1-e,I-e and y=year) is the number of eggs produced in the hatchery that are planted in natural spawning are&. This quantity is defined as

$$EP_{T3,y} = \begin{cases} 0 \text{ If yeer} > SUPDUR_e \text{ or if } SUPNUM_e = 0 \\ \text{e\&e} \\ \min\left[SUPNUM_e,\ BRDCS_{e,\delta} \cdot SUPNUM_e + \max\left[0,\ EP_{subcalc}\right]\right] \end{cases} \tag{94}$$

where

$$EP_{subcalc} = PZH_{T1,y} + PZH_{T3,y} - \frac{(1 - BRDCS_{i,\delta}) \cdot SUPNUM_i \cdot \left[\sum_{e=1}^{5} BRDSTK_{i,e} .GT. 0\right]}{E.FSURVT3}$$

$$- \frac{(1 - BRDCS_{ps,\delta}) \cdot SUPNUM_{ps} \cdot \left[\sum_{e=1}^{5} BRDSTK_{ps,e} .GT. 0\right]}{E.FSURVT3 \cdot PSSURVT3} \tag{95}$$

$$\frac{(1 - BRDCS_{s,\delta}) \cdot SUPNUM_s \cdot \left[\sum_{e=1}^{5} BRDSTK_{s,e} .GT. 0\right]}{E.FSURVT3 \cdot F.PSSURVT3 \cdot PS.SSURVT3}$$

for (X .GT. Y) equal to 1 wheq true and 0 otherwise and $BRDCS_{i,\delta}$ is the broodstock collection schedule for imported stock i=e,f,ps,s,a (input);

$$EP_{1-e,y} = EP_{T3,y} - EP_{I-e,y} \tag{96}$$

and

$$EP_{I-e,y} = \begin{cases} 0 \text{ if year} > SUPDUR_e \text{ or if } SUPNUM_e = 0 \\ \text{else} \\ BRDCS_{e,\delta} \cdot SUPNUM_e \end{cases} \tag{97}$$

FH8..FH14 Potential Zygotes in Nature After Egg Planting ($PZNAP_{k,y}$ for k=T0,T1,T2,T3,l-e,I-e and y=year) is the number of zygotes produced naturally and from egg supplementation. For natural fish, this is defined as

$$PZNAP_{T0,y} = \begin{cases} \sum_{k=T0,T1,T2} \sum_{k'=T0,T1,T2} SM_{k-k',y} & \text{if } SCEN = 1 \\ SM_{T0-T0,y} & \text{if } SCEN = 2 \\ & \text{else} \\ SM_{T0-T0,y} + SM_{T1-T0,y} \cdot SM_{T0-T1,y} & \end{cases} \tag{98}$$

and

$$PZNAP_{T1,y} = SM_{T3-T0,y} \cdot SM_{T3-T1,y} + SM_{T1-T3,y} \cdot SM_{T1-T1,y} + PZNAP_{subcalc} \tag{99}$$

where

$$PZNAP_{subcalc} = \begin{cases} SM_{T3-T2,y} + SM_{T2-T3,y} & \text{if } SCEN = 1 \\ \left(\sum_{k=T1,T2} \sum_{k'=T0,T1} SM_{k-k',y} \right) + SM_{T0-T1,y} + SM_{T0-T2,y} + SM_{T1-T2,y} & \text{if } SCEN = 2 \\ & \text{else} \\ SM_{T2-T0,y} + SM_{T2-T1,y} + SM_{T1-T1,y} + SM_{T1-T2,y} \cdot SM_{T0-T2,y} & \end{cases} \tag{100}$$

and

$$PZNAP_{T2,y} = \begin{cases} SM_{T3-T3,y} & \text{if } SCEN = 1 \\ \text{'eke} & \\ SM_{T3-T3,y} + SM_{T2-T2,y} + SM_{T3-T2,y} \cdot SM_{T2-T3,y} & \end{cases} \tag{101}$$

For hatchery produced zygotes (T3 type), this quantity is defined 'as

$$PZNAP_{k,y} = EP_{k,y} \tag{102}$$

for k=T3,l-e,I-e.

FN9..FN12 Fry in Hatchery Before Fry Plant ($FH_{k,y}$ for k=T1,T3 and y=year) is the number of fry produced in the hatchery from broodstock that were collected. The number of fry produced from either one or both parents of wild stock is defined as

$$FH_{T1,y} = \left[PZH_{T1,y} - \left[\frac{PZH_{T1,y}}{PZH_{T1,y} + PZH_{T3,y}} + \varepsilon \right] \cdot (EP_{T3,y} - FH_{subcode}) \right] \cdot E.FSURVT3 \cdot E.FRSA \qquad (103)$$

where $E.FRSA$ is the egg to fry pedigree relative survival adjustment (input) and

$$FH_{subcode} = \begin{cases} 0 \text{ if } year > SUPDUR_{s} \text{ or if } SUPNUM_{s} = 0. \\ \text{eke} \\ BRDCS_{s,6} \cdot SUPNUM_{s} \end{cases} \qquad (104)$$

The number of fry produced from hatchery' stock is defined as

$$FH_{T3,y} = \left[PZH_{T3,y} - \left[\frac{PZH_{T3,y}}{PZH_{T1,y} + PZH_{T3,y}} + \varepsilon \right] \cdot (EP_{T3,y} - FH_{subcode}) \right] \cdot E.FSURVT3 \qquad (105)$$

FO11..FO16 Fry Planted ($FP_{k,y}$ for k=T3,l-f,I-f and y=year) is the number of fry produced from broodstock and planted in the target streams. All hatchery produced fry are considered T3 genetic stock. This quantity is defined as

$$FP_{T3,y} = \begin{cases} 0 \text{ if } year > SUPDUR_{t} \text{ or if } SUPNUM_{t} = \\ \text{eke} \\ \min \left[SUPNUM_{t} , BRDCS_{t,6} \cdot SUPNUM_{t} + \max \left[0 , FP_{subcode} \right] \right] \end{cases} \qquad (106)$$

where

$$FP_{subcalc} = \sum_{k=T1,T3} FH_{k,y} \cdot \min\left[Mx\%UNR_1 \cdot \sum_{k=T0,T1,T2} FNAP_{k,y} + \sum_{i=e,l,pe,a} BRDSTK_{i,A} \right]$$

$$\frac{(1 - BRDCS_{e,6}) \cdot SUPNUM_e \cdot \left[\sum_{a=1}^{5} BRDSTK_{e,a} .GT. 0 \right]}{PS.SSURVT3 \cdot F.PSSURVT3} \tag{107}$$

$$\frac{(1 - BRDCS_{pe,6}) \cdot SUPNUM_{pe} \cdot \left[\sum_{a=1}^{5} BRDSTK_{pe,a} .GT. 0 \right]}{F.PSSURVT3}$$

and $Mx\%UNR_1$ is the maximum percent used of the natural run for time period 1 (input). Hatchery produced fry from local and imported broodstock is defined as

$$FP_{l-f,y} = FP_{T3,y} - FP_{l-e,y} \tag{108}$$

and

$$FP_{l-f,y} = \begin{cases} 0 \text{ if } year > SUPDUR_1 \text{ or if } SUPNUM_1 = 0 \\ \text{else} \\ BRDCS_{f,6} \cdot SUPNUM_1 \end{cases} \tag{109}$$

FP8..FP16 Fry in Nature After Fry Planting ($FNAP_{k,y}$ for k=T0,T1,T2,T3,l-e, *I*-e,l-f,*I*-f and y=year) is the number of emergent fry in the streams from all sources. For wild fry (excluding T3 fish), this quantity is defined as

$$FNAP_{T0,y} = \left[\frac{PZNAP_{T0,y}}{\sum_{k=T1,T2,T3} PZNAP_{k,y} + \varepsilon} \right] \cdot \frac{E.FSURVT0 \cdot \sum_{k=T0,T1,T2,T3} PZNAP_{k,y}}{\left[1 + \frac{E.FSURVT0 \cdot \sum_{k=T0,T1,T2,T3} PZNAP_{k,y}}{RICC \cdot CC} \right]} \tag{110}$$

for $RICC$ the ratio of the incubation capacity to the, smoit carrying capacity (input) and CC the smolt carrying capacity (input) and

$$FNAP_{k,y} = \left[\frac{PZNAP_{k,y} \cdot kFF_{9,y}}{\sum_{i=T0,T1,T2,T3} PZNAP_{i,y} + \varepsilon} \right] \cdot \frac{E.FSURVT0 \cdot \sum_{i=T1,T2,T3} PZNAP_{i,y}}{1 + \frac{E.FSURVT0 \cdot \sum_{i=T0,T1,T2,T3} PZNAP_{i,y}}{RICC}} \quad (111)$$

for k=T1,T2. For hatchery produced fry, this quantity is defined as

$$FNAP_{T3,y} = FNAP_{1-e,y} + FNAP_{1-e,y} + FP_{T3,y} + \varepsilon \quad (112)$$

where

$$FNAP_{j-e,y} = \left[\frac{PZNAP_{j-e,y} \cdot TEj_{e,CULT,e-f}}{\sum_{k=T0,T1,T2,T3} PZNAP_{k,y} + \varepsilon} \right] \cdot \frac{E.FSURVT0 \cdot \sum_{k=T0,T1,T2,T3} PZNAP_{k,y}}{\left[1 + \frac{E.FSURVT0 \cdot \sum_{k=T0,T1,T2,T3} PZNAP_{k,y}}{RICC \cdot CC + \varepsilon} \right]} \quad (113)$$

for j=1,I; I=a or d stock sources (input); and $CULT$=con or inn culture method (input) and

$$FNAP_{k,y} = FP_{k,y} \quad (114)$$

for k=1-f,I-f.

FQ9..FQ12 Fry in Hatchery After Fry Collection ($FHAC_{k,y}$ for k=T1,T3 and y=year) is the number of fry in the hatchery from hatchery reared eggs and from local and imported stock. For progeny of one wild and one hatchery fish, this quantity is defined as

$$FHAC_{T1,y} = FH_{T1,y} - \left[\frac{FH_{T1,y}}{\sum_{k=T1,T3} FH_{k,y} + \varepsilon} \right] \cdot (FP_{T3,y} - FHAC_{calc1}) + FHAC_{calc2} \quad (115)$$

where

$$FHAC_{calc1} = \begin{cases} 0 \text{ if } year > SUPDUR_t \text{ or if } SUPNUM_t = 0 \\ \text{else} \\ BRDCS_{t,6} \cdot SUPNUM_t \end{cases} \quad (116)$$

and

$$FHAC_{calc2} = \begin{cases} 0 \text{ if } year > \max\left[SUPDUR_{pa}, SUPDUR_a \right] \\ \text{else} \\ \min\left[Mx\%UNR_t \cdot \sum_{k=T0,T1,T2} FNAP_{k,y}, \sum_{i=e,l,pa,a} BRDSTK_{i,A} \right] \end{cases} \quad 11171$$

For progeny of hatchery stock, this quantity is defined as

$$FHAC_{T3,y} = FH_{T3,y} - \left[\frac{FH_{T3,y}}{\sum_{k=T1,T3} FH_{k,y} + \varepsilon} \cdot (FP_{T3,y} - FHAC_{calc1}) \right] \quad (118)$$

FR8..FR16 Fry in Nature After Fry Collection ($FNAC_{k,y}$ for k=T0,T1,T2,T3,l-e, I-e,l-f,I-f and y=year) is the number of fry remaining in nature after the removal of fry for later supplementation. For wild stock, this quantity is defined as

$$FNAC_{k,y} = FNAP_{k,y} - \left[\frac{FHAC_{calc2} \; FNAP_{k,y}}{\sum_{j=T0,T1,T2} FNAP_{j,y} + \varepsilon} \right] \quad (119)$$

for k=T0,T1,T2. For hatchery produced stock, this quantity is defined as

$$FNAC_{k,y} = FNAP_{k,y} \quad (120)$$

for k=T3,l-e,I-e,l-f,I-f.

FS9..FS11 Presmolts in Hatchery Before Planting ($PSH_{k,y}$ for k=T1,T3 and y=year) is the number of presmolts produced in the hatchery from local and imported stock. For progeny from one wild and one hatchery fish, this quantity is defined as

$$PSH_{T1,y} = FHAC_{T1,y} \cdot F.PSSURVT3 \cdot F.PSRSA \tag{121}$$

for ***F.PSRSA*** the fry to presmolt pedigree relative survival adjustment (input). For progeny of hatchery stock, this quantity is defined as

$$PSH_{T3,y} = FHAC_{T3,y} \cdot F.PSSURVT3 \tag{122}$$

FT11..FT18 Presmolts Planted **($PSP_{k,y}$** for **k=T3,l-ps,I-ps** and **y=year)** is the number of presmolts produced in a hatchery and released in a target stream. For hatchery produced stock, this quantity is defined as

$$PSP_{T3,y} = \begin{cases} 0 \text{ ii } year > SUPDUR_{ps} \text{ or if } SUPNUM_{ps} = 0 \\ \text{e\&e} \\ \min\left[SUPNUM_{ps} , BRDCS_{ps,6} \cdot SUPNUM_{ps} + \max\left[0 , PSP_{subcalc} \right] \right] \end{cases} \tag{123}$$

where

$$PSP_{subcalc} = \sum_{k=T1,T3} PSH_{k,y} + \min\left[Mx\%UNR_1 \cdot \sum_{k=T0,T1,T2} PSH_{k,y} , \sum_{i=l,l,ps,A} BRDSTK_{i,5} \right] \frac{(1 - BRDCS_{s,6}) \cdot SUPNUM_s \cdot \left[\sum_{a=1}^{5} BRDSTK_{s,a} .GT. 0 \right]}{PS.SSURVT3} \tag{124}$$

For local and imported stock, this quantity is defined as

$$PSP_{l-ps,y} = PSP_{T3,y} - PSP_{l-ps,y} \tag{125}$$

and

$$PSP_{1-ps,y} = \begin{cases} 0 \text{ if year} > SUPDUR_{ps} \text{ or if } SUPNUM_{ps} = 0 \\ \text{else} \\ BRDCS_{ps,6} \cdot SUPNUM_{ps} \end{cases} \tag{126}$$

FV8..FV18 Presmolts in Nature After Planting (*$PSNAP_{k,y}$* for ***k*=T0,T1,T2,T3,l-e, *I*-e,l-f,*I*-f,l-ps,*I*-ps** 'and **y=year)** is the number of **presmolts** in **nature from all** sources after supplementation. For **wild** stock, this quantity is defined as

$$PSNAP_{T0,y} = \frac{FNAC_{T0,y} \cdot F.PSSURVT0}{PSNAP_{subcale}} \tag{127}$$

where

$$PSNAP_{subcale} = \frac{FNAC_{T0,y} \cdot F.PSSURVT0}{SC} + \frac{\sum_{k=T} FNAC_{k,y} \cdot F.PSSURVT0 \cdot kFF_{0,y}}{} + \frac{\left(\sum_{j=1,I} \sum_{i=e,f} FNAC_{j-i,y} \cdot F.PSSURVT0 \cdot TEj_{i,CULT,1-ps}\right)}{SC} \tag{128}$$

for ***CULT*=con** or inn culture method (input). For **presmolts** hatched in the wild with either one or two stray hatchery parents, this **quantity is** defined as

$$PSNAP_{k,y} = \frac{FNAC_{k,y} \cdot F.PSSURVT0 \cdot kFF_{0,y}}{PSNAP_{subcale}} \tag{129}$$

for ***k*=T1,T2**. For hatchery stock, the number of presmolts in nature after supplementation is

$$PSNAP_{T3,y} = \sum_{j=1,I} \sum_{i=e,f,ps} PSNAP_{j-i,y} + \varepsilon \quad , \tag{130}$$

where

$$PSNAP_{j-i,y} = \frac{FNAC_{j-i,y} \cdot F.PSSURVT0 \cdot TEj_{i,CULT,1-ps}}{PSNAP_{subcale}} \tag{131}$$

for ***j*=l,*I*** and ***i*=e,f**; and

$$PSNAP_{k,y} = PSP_{k,y} \tag{132}$$

for k=l-ps,I-ps and $CULT$=con or inn culture method (input).

FV9..FV11 Presmolts in Hatchery After Collection ($PSHAC_{,,}$ for k=T1,T3 and y=year) is the number of presmolts reared in the hatcher and collected for later supplementation. For progeny of one wild and one hatchery fish, this quantity is defined as

$$PSHAC_{T1,y} = PSH_{T1,y} - \left[\frac{PSH_{T1,y}}{\sum_{k=T1,T3} PSH_{k,y} + \varepsilon}\right] \cdot (PSP_{T3,y} - PSHAC_{,,} + PSHAC_{calc2}) \tag{133}$$

where

$$PSHAC_{,,} = \begin{cases} 0 \text{ if year} > SUPDUR_{ps} \text{ or if } SUPNUM_{ps} = 0 \\ \text{else} \\ BRDCS_{ps,6} \cdot SUPNUM_{ps} \end{cases} \tag{134}$$

and

$$PSHAC_{,,,} = \begin{cases} 0 \text{ if yeer} > \max[SUPDUR_{ps}, SUPDUR_{s}] \\ \text{else} \\ \min\left[Mx\%UNR_{1} \cdot \sum_{k=T0,T1,T2} PSNAP_{k,y}, \sum_{i=e,f,ps,s} BRDSTK_{i,5}\right] \end{cases} \tag{135}$$

For progeny of hatchery stock, this quantity is defined as

$$PSHAC_{T3,y} = PSH_{T3,y} - \left[\frac{PSH_{T3,y}}{\sum_{k=T1,T3} PSH_{k,y} + e}\right] \cdot (PSP_{T3,y} - PSHAC_{calc1}) \tag{136}$$

FW8..FW18 Presmolts in Nature After Collection ($PSNAC_{k,y}$ for k=T0,T1,T2,T3, l-e,I-e,l-f,I-f,l-ps,I-ps and y=year) is the number of presmolts remaining in nature after presmolt collection for later supplementation. 'For wild stock, this quantity is defined as

$$PSNAC_{k,y} = PSNAP_{k,y} - PSNAC_{subcale} \tag{137}$$

for k=T0,T1,T2 and where

$$PSP_{subcale} = \min\left[Mx\%UNR_1 \cdot \sum_{k=T0,T1,T2} PSNAP_{k,y} \cdot \sum_{i=e,l,pe,s} BRDSTK_{i,pe}\right] \frac{PSNAP_{k,y} \cdot \left(year .LE. \max\left[SUPDUR_{pe}, SUPDUR_e\right]\right)}{\sum_{l=T0,T1} PSNAP_{k,y}} \tag{138}$$

For hatchery reared stock, this quantity is defined as

$$PSNAC_{k,y} = PSNAP_{k,y} \tag{139}$$

for k=T3,l-e,I-e,l-f,I-f,l-ps,I-ps.

FX9..FX11 Smolts in Hatchery Before Planting ($SH_{k,y}$ for k=T1,T3 and y=year) is the number of smolts reared in the hatchery. For progeny of one wild and one hatchery fish; this quantity is defined as

$$SH_{T1,y} = PSHAC_{T1,y} \cdot PS.SSURVT3 \cdot PS.SRSA \tag{140}$$

for $PS.SRSA$ the presmolt to smolt pedigree relative survival adjustment (input). Por progeny of hatchery stock, the number of smolts reared in the hatchery is defined as

$$SH_{T3,y} = PSHAC_{T3,y} \cdot PS.SSURVT3 \tag{141}$$

FY 11..FY20 Smolts Planted ($SP_{k,y}$ for k=T3,l-s,I-s and y=year) is the-number of, smolts released in the subbasin and is defined as

$$SP_{T3,y} = \begin{cases} 0 \text{ if } year > SUPDUR_e \text{ or if } SUPNUM_e = 0 \\ \text{else} \\ \sum_{k=T1,T3} SH_{k,y} + BRDCS_{e,s} \cdot SUPNUM_e \end{cases} \tag{142}$$

For local and imported stock, this quantity is defined as

$$SP_{1-e,y} = SP_{T3,y} - SP_{1-e,y}$$

and

$$SP_{1-e,y} = \begin{cases} 0 \text{ if } year > SUPDUR_e \text{ or if } SUPNUM_e = 0 \\ \text{else} \\ BRDCS_{e,s} \cdot SUPNUM_e \end{cases} \quad (144)$$

FZ8..FZ20 Smolts in Nature After Planting (*SNAP*, for *k*=T0,T1,T2,T3,*j-i*; *j*=1,*I*; *i*=e,f,ps,s; and *y*=year) is the number of smolts in the subbasin from all sources. For wild fish, this quantity is defined as

$$SNAP_{T0,y} = \frac{PSNAC_{T0,y} \cdot PS.SSURVT0}{SNAP_{subcale}} \quad (145)$$

where

$$SNAP_{subcale} = \frac{PSNAC_{T0,y} \cdot PS.SSURVT0}{WC} + \sum_{k=T} \frac{PSNAC_{k,y} \cdot PS.SSURVT0 \cdot kFF_{e,y}}{WC} + \frac{\left(\sum_{j=1,I} \sum_{i=1,N} PSNAC_{j-i,y} \cdot PS.SSURVT0 \cdot TEj_{i,CULT,ps-s} \right)}{} \quad (146)$$

for *CULT*=con or inn culture method (input). For the progeny of either one or both parents of stray hatchery stock, this quantity is defined as

$$SNAP_{k,y} = \frac{PSNAC_{k,y} \cdot PS.SSURVT0 \cdot kFF_{e,y}}{SNAP_{subcale}} \quad (147)$$

for *k*=T1,T2. For hatchery reared stock, this quantity is defined as

$$SNAP_{T3,y} = \sum_{j=1,I} \sum_{i=e,f,ps,s} SNAP_{j-i,y} + \varepsilon \tag{148}$$

and

$$SNAP_{j-i,y} = \frac{PSNAC_{j-i,y} \cdot PS.SSURVT0 \cdot TEj_{i,CULT,ps-s}}{SNAP_{subcole}} \tag{149}$$

for j=1,I; i=e,f,ps; and $CULT$=con or inn culture method (input); and

$$SNAP_{k,y} = SP_{k,y} \tag{150}$$

for k=1-s,I-s.

GB8..GB23 Smolts After Downstream Passage ($SADP_{k,y}$ for k=T0,T1,T2,T3,j-i; j=1,I; i=e,f,ps,s; and y=year) are the number of smolts remaining to below Bonneville Dam. For wild and hatchery stock, this quantity is defined as

$$SADP_{k,y} = \begin{cases} NVADP_{k,y} & \text{for } V = 1 \\ VADP_{k,y} & \text{else} \end{cases} \tag{151}$$

for V=1,2 variation toggle for downstream passage survival (input).

GC8..GC23 Smolts After Estuary ($SAE_{k,y}$ for k=T0,T1,T2,T3,j-i; j=1,I; i=e,f,ps,s; and y=year) is the number of smolts that survive to the ocean. For wild and hatchery stock, this quantity is defined as

$$SAE_{k,y} = \begin{cases} NVAE_{k,y} & \text{for } E = 1 \\ VAE_{k,y} & \text{else} \end{cases} \tag{152}$$

for E=1,2 variation toggle for estuary survival (input).

GD8..GE23; GT8..GO23; HJ8..HJ23; HZ8..IA23 Adults in the Ocean ($AOsh_{k,y}$ for s=M,F; h=1..4 years fish are in the ocean; k=T0,T1,T2,T3,j-i; j=1,I; i=e,f,ps,s; and y=year) is the number of adults of all age classes in the ocean. For wild stock, this quantity is defined as

$$AOs1_{T0,y} = SAE_{T0,y} \cdot 0.5 \cdot OSURV_1 \tag{153}$$

and

$$AOsh_{T0,y} = LIOs(h-1)_{T0,y} \cdot OSURV_h \tag{154}$$

for h=2..4 *years* fish are in the ocean and $LIOsh_{k,y}$ *equal the* calculated number of adults left in the ocean for s=M,F; h=1..4 years fish are in the ocean; k=T0,T1,T2,T3,j-i; j=1,I; i=e,f,ps,s; and y=year. For progeny of one or two hatchery strays, this quantity is defined as

$$AOs1_{k,y} = SAE_{k,y} \cdot 0.5 \cdot OSURV_1 \cdot kFF_{9,y} \tag{155}$$

for k=T1,T2 and

$$AOsH_{k,y} = LIOs(h-1)_{k,y} \cdot OSURV_h \cdot kFF_{9,y} \tag{156}$$

for k=T1,T2 and h=2..4 years fish are in the ocean. For hatchery released-stock, this quantity is defined as

$$AOsh_{T3,y} = \sum_{j=1,I} \sum_{i=e,f,ps,s} AOsh_{j-i,y} + \varepsilon \tag{157}$$

for h=1..4 *years* fish are in the ocean;

$$AOs1_{j-i,y} = SAE_{j-i,y} \cdot 0.5 \cdot OSURV_1 \cdot TEj_{i,CULT,e} \tag{158}$$

for j=1,I; i=e,f,ps,s; and $CULT$=con or inn culture method (input); and

$$A\,Osh_{j-i,y} - LIOs(h-1)_{j-i,y} \cdot OSURV_h \cdot TEj_{i,CULT,o} \quad (159)$$

for h=2..4 *years* fish are in the ocean; j=l,I; i=e,f,ps,s; and $CULT$=con or inn culture method (input).

GF8..GG23; GV8..GW23; HL8..HM23; IB8..IC23 Ocean Harvest ($OHsh_{k,y}$ for s=M,F; h=1..4 years fish are in the ocean; k=T0,T1,T2,T3,j-i; j=l,I; i=e,f,ps,s; and y=year) is the number of adult fish harvested from the ocean fishery. For wild stock, the ocean harvest is defined as

$$OHsh_{k,y} - AOsh_{k,y} \cdot OHR_h \quad (160)$$

for h=1..4 years fish are in the ocean and k=T0,T1,T2. For hatchery stock, the ocean harvest is defined as

$$OHsh_{T3,y} = \sum_{j=1,I} \sum_{i=e,f,ps,s} OHsh_{j-i,y} \cdot \varepsilon \quad (161)$$

h=1..4 years fish are in the ocean and

$$OHsh_{j-i,y} - AOsh_{j-i,y} \cdot OHR_h \cdot TEj_{i,CULT,ch} \quad (162)$$

for h=1..4 years fish are in the ocean; j=l,I; i=e,f,ps,s; and $CULT$=con or inn culture method (input).

FC8..FD40; FS8..FT40; GI8..GJ40; GY8..GZ40 Adults in Ocean After Harvest ($AOAHsh_{k,y}$ for s=M,F; h=1..4 *years* fish are in the ocean; k=T0,T1,T2,T3,j-i; j=l,I; i=e,f,ps,s,a; and y=year) is the, number of adult fish remaining in the ocean after the ocean harvest. This quantity is defined- as

$$AOAHsh_{k,y} - AOsh_{k,y} - OHsh_{k,y} \quad (163)$$

for s=M,F; h=1..4 years fish are in the ocean; k=T0,T1,T2,T3,j-i; j=l,I; and i=e,f,ps,s,a.

FE8..FF40; FU8..FV40; GK8..GL40; HA8..HB40 Adult In-River Returns ($ARRsh_{k,y}$ for s=M,F; h=1..4 years fish are in the ocean; k=T0,T1,T2,T3,j-i; j=l,I; i=e,f,ps,s,a; and y=year) is the number of adult fish that return to the Columbia River after spending one to four years in the ocean. For wild stock, this quantity is defined as

$$ARRsh_{k,y} = AOAHsh_{k,y} \cdot MRT0s_h \tag{164}$$

for k=T0,T1,T2 and h=1..4 *years* fish are in the ocean. For hatchery stock, this quantity is defined as

$$ARRsh_{k,y} = AOAHsh_{k,y} \cdot MRT3s_h \tag{165}$$

for k=T3,j-i; j=l,I; i=e,f,ps,s,a; and h=1..4 years fish are in the ocean.

FG8..FH40; FW8..FX40; GM8..GN40; HC8..HD40 Adults In-River Harvest ($RHsh_{k,y}$ for s=M,F; h=1..4 years fish are in the ocean; k=T0,T1,T2,T3,j-i; j=l,I; i=e,f,ps,s,a; and y=year) is the number of adult fish taken during the pre- and-post-terminal harvest. For wild stock, this quantity is defined as

$$RHsh_{k,y} = ARRsh_{k,y} \cdot MHR_h \tag{166}$$

for k=T0,T1,T2 and h=1..4 years fish are in the ocean. For hatchery stock, this quantity is defined as

$$RHsh_{T3,y} = \sum_{j=l,I} \sum_{i=e,f,ps,s,a} RHsh_{j-i,y} \tag{167}$$

for h=1..4 years fish are in the ocean and

$$RHsh_{j-i,y} = ARRsh_{j-i,y} \cdot MHR_h \cdot TEj_{i,CULT,h} \tag{168}$$

for j=l,I; i=e,f,ps,s,a; h=1..4 years fish are in the ocean; and $CULT$=con or inn the culture method (input).

GN8..GO23; HD8..HE23; HT8..HV23; IJ8..IK23 Straw After Adult Passage (*$STRYsh_{k,y}$* for *s*=M,F; *h*=1..4 years fish are in the ocean; *k*=T0,T1,T2,T3,*j-i*; *j*=1,*I*; *i*=e,f,ps,s,a; and *y*=year) is the number of adult fish in the natural escapement. For wild stock, 'this quantity is defined as

$$STRYsh_{T0,y} = (ARRsh_{T0,y} - RHsh_{T0,y}) \cdot (1 - HF) \cdot PSURV_h \tag{169}$$

where *HF* is an estimate of homing fidelity to the **subbasin** (input) and for *h*=1..4 years fish are in the ocean, and

$$STRYsh_{k,y} = (ARRsh_{k,y} - RHsh_{k,y}) \cdot (1 - HF) \cdot PSURV_h \cdot kFF_{0,y} \tag{170}$$

for *k*=T1,T2 and *h*=1..4 years fish are in the ocean. For hatchery stock, this quantity is defined as

$$STRYsh_{T3,y} = \sum_{j=1,I} \sum_{i=e,f,ps,s,a} STRYsh_{j-i,y} \tag{171}$$

for *h*=1..4 years fish are in the ocean where

$$STRYsh_{j-i,y} = (ARRsh_{j-i,y} - RHsh_{j-i,y}) \cdot (1 - HF \cdot TEj_{i,CULT,h}) \cdot PSURV_h \cdot TEj_{i,CULT,ap} \tag{172}$$

for *j*=1,*I*; i=e,f,ps,s,a; *h*=1..4 years fish are in the ocean; and *CULT*=con or inn the culture method (input).

GR8..GS23; HH8..HI23; HX8..HY23; IN8..IO23 Adults Left in the Ocean (*$LIOsh_{k,y}$* for *s*=M,F; *h*=1..4 years fish are in the ocean; *k*=T0,T1,T2,T3,*j-i*; *j*=1,*I*; *i*=e,f,ps,s,a; and y-year) is the number of adult fish of all age classes remaining in the ocean. This quantity is **defined as**

$$LIOsh_{k,y} = \max (0 , AOAHsh_{k,y} - ARRsh_{k,y}) \tag{173}$$

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ECOSYSTEM DIAGNOSIS AND TREATMENT MODEL AS APPLIED TO SUPPLEMENTATION

APPENDIX A
SENSITIVITY ANALYSIS

1. INTRODUCTION

A general sensitivity analysis was conducted in order to 1) assess the ranges of biologically relevant, values for input parameters, 2) evaluate the relative effects of a specific set of. input parameters on the model output, and 3) examine the. reliability of the model (i-e., whether the model behaves as expected) under a variety of specific conditions. Values for input parameters were deemed biologically relevant if they provided logical results (based on literature and expert opinion) and did not drive, wild stocks to extinction. The: latter requirement reflects the association between uncertainty in parameter values and the magnitude of the effect that- a given parameter has on the model results. Even though there are no deliberate restrictions on the values for input parameters (other than specific sets adding to lOO%), we recognize the magnitude of uncertainty and provide suggestions to reduce the influence that any one parameter may have on the model simulations. Tests of model reliability, on the other hand, require that stocks go to extinction under specific conditions or produce logical results as a check on the formulation of the model:

The analysis is not meant to be an exhaustive sensitivity analysis. The interactions between input parameters were not, explored. Instead, this analysis is intended to provide insight on the relative influence. of individual input parameters under a specific set of conditions, Thus, if the relative strength of a parameter is much greater than the certainty associated about the appropriate parameter value, a range of values can be used in simulation runs. This analysis can also be used to determine what parameters require further investigation. If the relative, influence of a parameter is much greater than the certainty associated with the knowledge about a parameter value, further research is warranted. Research on specific parameter values (albeit difficult) result in a greater reliability of model comparisons and understanding of the system under investigation. Finally, this analysis can be viewed as an example, to user defined model comparisons.

2. METHODS

Fifty year simulations of **EDTM** 3.0 using the density-independent predator-prey response function (Type I response) were conducted varying one input parameter at a time (except for the age distribution parameters which must add to 100%). All other parameters were set to the value associated with a standard run except the parameter values for supplementation, culture method, and stock source. Each simulation run with supplementation was made using either fry or smolt outplants; conventional or innovative culture methods; and a stock source of either local (100% collected' during pre-terminal harvest) or imported (adjacent) stock. Genetic recovery scenario 3 was assumed in each case.

The input parameter values for the standard run and the sensitivity runs are listed in Table A-1. The parameter values for the standard run are listed in the first row below the double line, and the parameter values used in the sensitivity runs are given below the standard run values. The input parameter values for the standard run, though representing a hypothetical subbasin, are based on values associated with certain actual subbasins. The standard run has supplementation turned off; thus, all input parameters associated with a hatchery generated stock do not affect the model results. All input parameters not varied in the sensitivity 'analysis and their values are listed in Table A-2: These parameters were generally presumed to have less of an influence on the model results, or to have'effects comparable with other parameters - or. to be redundant. In order to expedite the sensitivity analysis, we did not vary these parameter values. Interannual variation in passage survival and estuary survival was not evaluated.

Seven sets-of simulation runs were conducted (Table A-3) totaling 2,490 runs. All parameters were varied as shown in Table A-l except for the numeric release goal, culture method and stock source. Plots of the resulting numbers of natural spawners, showing both the number of wild fish and total fish, were made for each input parameter. "Wild fish" refers to those having naturally spawning parents. Total natural spawners includes hatchery fish that spawn naturally in the subbasin. A visual assessment of the plots was used to determine which parameter values resulted in extinction of wild stock. The slope of each line between the largest and smallest parameter value and their resulting number of natural spawners in the subbasin was used as a gross measure of the relative effect of each parameter on the model results. The absolute value of the slopes generated within each simulation set were ranked and then compared across sets for consistency. Slopes less than 5 were considered biologically insignificant. The percent change of each simulation run from the standard run was also calculated for comparison.

3. RESULTS

-The standard run (no supplementation) produced 7,694 natural spawners (Table A-4)‘. For this set of simulations, all functional responses between input parameter values and the number of natural spawners produced were either monotonically increasing or decreasing, except for **Mx%NBS**. Thus, for input parameters yielding a positive slope, parameter values greater than the value used in the standard run produced more natural spawners than that produced in the standard run. The reverse relationship was observed for parameters yielding a negative slope. In one simulation sesries (set 3), the parameter Mx%NBS displayed a curvilinear response.

The evaluation of the gross effect of input parameters can become complicated when the’ functional response of each parameter is structurally different. However, since most functional responses were monotonic; the slope calculation between the highest and lowest input parameter value proved to be a successful way to rank effects. Out of the sixty input . parameters varied for the simulation runs, only eight parameters displayed-a significant curvature in their response (Fig. A-l). Ignoring the curvature for these parameters produces one slope which is roughly equivalent to-averaging over the individual segmental slopes in the response curve.

Table A-5 lists all the input parameters which displayed a negative response in the number-of natural spawners with natural parents and total natural spawners after 50 year simulations. Except for those parameters associated with the age distribution of adults on the spawning grounds, the negative responses of the input parameters are easily understood. As expected, increasing the minimum harvest rate while allowing a random harvest or increasing the number of fish allowed for broodstock decreases the number of natural spawners.

, Negative slopes observed in runs associated with the steady state age distribution (on the spawning ground) input parameters is, consistent with the observation that the longer, fish remain in the ocean less wild and hatchery stocks return to the subbasin (Table A-5). The age distribution parameters were varied two at a time since all four age classes must sum to 1’00% (see Table A-l). For each, genetic stock and sex, the slopes produced from varying age classes 1 and 2, 2‘ and 3, and 1 and 3, were associated with age class 1, age class 2, and age class 3, respectively. This pairing was purely for presentation and slope generation. Age class 4 **was** held constant in all runs. Note that within each set, the designation ‘for association was arbitrary, and in fact must be attributed to both varied parameters. Thus, elucidation of the negative slopes becomes more complicated.

The age distribution parameters are used to calculate the maturation schedule **($MRks_h$),** which is then held constant through the $0 year simulation (Fig. A-2). The maturation schedule defines the proportion of fish in each age class returning to spawn. Figure. A-2A shows that as we increase the initial proportion on. the spawning grounds of age class 1 and decrease the proportion of age class 2 (Table A-l), the maturation rates for the two age classes increase and decrease respectively. The maturation rate for age class 3 is unaffected. Similarly, when

we increase the proportion in the ocean of age class 2 and decrease the proportion of age class 3, the maturation rates for age classes 2 and 3 increase and decrease respectively (Fig. A-2B). The maturation rate for age class 1 is unaffected. However, when we increase the initial proportion-of age class 1 on the spawning grounds and decrease the proportion of age class 3, the maturity rates of both age classes 1 'and 2 increase, while the maturity rate of age class 3 decreases (Fig. A-2C). Therefore, when the maturation rate is increased in the younger stocks (and conversely decreased in' the older stocks) we observe an increase in the number of wild (or total) spawners. Thus, our original supposition was correct..

Table A-6 presents the range of input parameters that resulted in less than 100 spawners of' wild stock for each simulation set. Input parameter values less than or **equal** to those values listed are considered inappropriate for management consideration since wild stocks were driven to a population size of less than 100. The opposite extreme of setting the value of an input parameter too high and producing an extreme number of spawners is more difficult to address. It is' easier to recognize an extreme number of fish than to recognize the upper boundaries ,of the input parameter. However, when the uncertainty associated with an input parameter value is high, a range of values can be evaluated.

Tables A-7 and A-8 list the calculated slopes and the ranked relative effect of each parameter on the number of natural spawners. Tables A-9 and A-10 list the calculated slopes and the ranked relative effect of each parameter on the number of total spawners. Both tables of ranked effects (Tables A-8 and A-10) ignore parameters which produced a slope whose absolute value was less than 5. Tables A-8 and A-10 must be evaluated with care, since no interactions between parameters were evaluated and only density-independent smolt to smolt mortality (Type I predator response) was assumed.

For all seven sensitivity sets, the input parameters for estuary/early-marine survival (***ESURV***) and juvenile passage survival (***JPSURV***) had the greatest effect and produced a maximum of approximately 73,000 and 18,000 total spawners respectively. EDTM 3.0 is not aimed at modeling the allocation of mortality beyond the subbasin and relies on density-independent mortality, in the form of multipliers, for passage (both juvenile and adult), estuary, and ocean survival derived from models that evaluate mortality in these life-stages more explicitly. The parameter effect of estuary survival is nearly five times greater than the effect of juvenile passage, but this is due to the assumed low estuary/early marine survival (15%). Since empirical data is lacking outside of the subbasin to define exactly where mortality occurs, assigning mortality in the model to the passage, estuary, and ocean life-stages becomes. difficult. Greater mortality can be attributed to either passage or ocean stages, and thus, estuary mortality and the parameter's effect on the model results can be decreased. In any case, the level of uncertainty associated with estuary survival and the magnitude of effect this parameter has on the model results suggests that this is an area which warrants more research.

All other input parameters (Table A-l), produced a maximum number of total spawners of less than 12,000, with most less than 10,000 except for the parameters $RELSURV_{s,con,l}$ and

PIINN, in the innovative culture simulation set; in that case, both produced approximately 14,000 total spawners. Observations regarding patterns among the ranked effects of the input parameters must be couched in terms of the limits of the parameters and conditions evaluated. Thus, all observations can be considered hypotheses for further investigation. For example, the effect of adult passage survival (***PSURV***$_h$) was greatest for. age class 2 for both measures of natural spawners (Tables A-8 and A-10). It was also noted that the rank order of adult passage for each age class is the same as the rank order of the input age distribution on the spawning grounds (***ADks***$_h$). One could'then hypothesize that the relative effect of the adult passage survival parameters is directly related to the proportion of each age class returning.

In general, the relative effect of each life-stage, survival parameter (***E.FSURV***T0, ***F.SPSURV***T0, ***PS.SSURV***T0, and ***S.SSURV***) increased from egg-to-fry survival to smolt-smolt survival (Tables A-7 - A-10). This is likely due to the, cumulative decrease in #ens&-dependent effects affecting each life-stage by going from eggs to smolts. Because we assumed density-independent mortality in the smolt-smolt stage, small changes to this stage survival had a much greater influence then similar changes to egg-to-fry survival.

The rank positions associated with the age distribution parameters (***ADks***$_h$) were more consistent for the total natural spawners response than for wild fish natural spawners (Tables A-7 - A-10). In general, within each ago class, the relative effect of the TO male age distribution was greater than the effect of the TO female age distribution. For T3 fish, the pattern was the same except that the age class 2 female age distribution relative effect was always greater than the age class 2 male age distribution. The relative effects of the TO age distribution parameters by age and sex were all greater than the relative effects of the T3 age distribution parameters.

A lack of consistency. was observed among, the parameters affecting broodstock removals for hatchery stock production (***Mi%NBS***, ***Mx%UNR***, ***Mx%UTR*** and ***Mx%T3E***). For runs supplementing 3 and 5 million local fry, the relative effects. of ***Mx%UNR*** and ***Mx%UTR*** were much greater than those for ***Mi%NBS*** and ***Mx%T3E*** (Tables A-7 - A-10). However, for runs supplementing local smolts and 1 million local fry, the relative effect of ***Mi%NBS*** *was* orders' of magnitude greater. than ***Mx%UNR*** and ***Mx%UTR***. This inconsistency is likely related to the apparent greater, survival to spawning age of supplemented local smolts compared to supplemented local fry (Table A-4).

The relative effect of the smolt genetic fitness components for T1 to T3 genetic stock (***GFC***$_{s,j}$) generally decreased from Tl to T3. For the simulation runs with the numeric release goals of 1 million local fry and 5 million imported fry, however, the' relative effect of the factor for T2 genetic stock was the lowest. These are also the runs that produced the smallest'number of T2 spawners.

The slopes produced by the input parameters ***RELSURV***$_{s,con,l}$ and ***PIINN***$_s$, *the* relative survival of smolts using conventional culture methods and 'the percent improvement of smolt survival

using innovative' culture methods respectively, must be evaluated together. The standard parameter value for $RELSURV_{s,con,l}$ was set at 0.09, which is a pessimistic scenario based on past observations in one subbasin (Table A-l). The standard value for $PIINN_s$, on the other hand, was set at 0.50. Thus, with innovative culture methods using the standard values, we achieve nearly twice the number of total spawners. The parameter value for $PIINN_s$ ranged from .1 to 10 (Table A-l), however, which allowed a 99% smolt relative survival of hatchery stock compared to wild stock.

4. CONCLUSIONS

Following Bunnell (1989), the EDT model is a tool designed to promote understanding of biological processes. This designation does not preclude it from use as a decision tool when the relative risk of specific actions or goals are being assessed. However, because the EDT model is not intended for predictive purposes, the results of this sensitivity analysis must be viewed in the appropriate context. Simulations for the purpose of evaluating the relative effects of a specific set of input parameters and to determine the range of values considered biologically relevant were conducted assuming only a density-irrdependent predator-prey response function. Patterns observed between the relative effects of related input parameters must be regarded as hypotheses and considered only for their consistency with observed behavior of the population of interest. Consistency between model results and observed behavior patterns provides the necessary check on model reliability.

Complex models require selection and simplification of data unrepresentative of nature, and often when no data exist, the best guess is used for a specific functional responsk. On the other hand, a mathematical summary of a textbook does not tell us much more than we already know (Hedgpeth 1977). Models built for understanding require of themselves constant change as new understanding evolves. Thus, models in this category are constantly being examined for behavior that is not expected and often not intended To date, we have not detected unintended behavior.

Under the assumptions that these simulations were run, these results suggest that supplementation of local fry provided less benefit than releases of local stock smelts. Second, innovative culture methods provided a substantial benefit. However, since the relative survival between hatchery and wild stock was set so low; a full range of benefit can not be determined from -these runs. Note that the effect of a density dependent predator-prey response function will change these results. One cannot address whether or not supplementation is beneficial from this analysis.

Finally, it is important to stress once again the difference between models meant for prediction and those built for understanding. Policy makers far too often accept model results as realities instead of hypotheses. It is up to the user to insist that results from this model be viewed as relative responses of one action over another. A specific number of spawners plus

or minus some amount can not be guaranteed with any probability. The EDT model can be used as a decision tool for the specific purpose of developing supplementation programs with the goal of increasing the odds that the genetic integrity of wild stock is maintained.

Table A-l. Input parameter values for the simulation runs on EDT model.

CC Smlt carry. cap.	RICCC Incub. cap/CC	RWSC Ratio win/sum cap	EPFTO 1 TO fec age 1	EPFT02 TO fec age 2	EPFTO 3 TO fec age 3	EPFT04 TO fec age 4	E.FSURV TO Egg-fry W N	F.PSSURV TO Fry-punt surv	PS.SSUR VTO Punt-rmt U N	S.SSUR V Den. ind. surv	JPSUR V Juv pas surv	ESURV Estur surv	PSURV1 Adlt pas surv age1	PSURV2 Adtt par W N age1	PSURV3 Adlt pas surv age1	PSURV4 Adlt pas surv age1
2.000.000	300	0.8	1,658	4.201	8,305	7.289	0.80	0.66	0.58	0.73	0.50	0.16	0.80	0.80	0.80	0.80
500	10	0.1	1.000	2,000	3,000	4,000	0.10	0.10	0.10	0.10	0.10	0.10	0.10	0.10	0.10	0.10
1,000	50	0.4	1.656	3,000	4,000	5,000	0.20	0.20	0.20	0.20	0.20	0.20	0.20	0.20	0.20	0.20
10,000	100	0.8	2,000	4,000	5,000	6,000	0.30	0.30	0.30	0.30	0.30	0.30	0.30	0.30	0.30	0.30
50,000	150	1.0	3,000	4,201	8.306	7.289	0.40	0.40	0.40	0.40	0.40	0.40	0.40	0.40	0.40	0.40
100,000	200	1.2	4.000	5,000	7,000	8,000	0.50	0.50	0.50	0.60	0.60	0.50	0.50	0.50	0.60	0.60
500,000	250	1.4		6,000	8.000	9,000	0.80	0.80	0.60	0.80	0.80	0.60	0.80	0.60	0.60	0.80
1,000,000	300	1.8					0.70	0.70	0.70	0.70	0.70	0.70	0.70	0 70	0.70	0.70
1,500,000	350	2.0					0.80	0.80	0.80.	0.80	0.80	0.80	0.80	0.80	0.80	0.80
2,000,000	400						0.90	0.90	0.90	0.90	0.90	0.90	0.90	0.90	0.80	0.90

Table A- 1. Continued.

HARV Rnd or select harv	MiHR Term harv rate	ADTOM 1 Age dir TO mal age 1	ADTOM 2 Age dis TO mal age 2	ADTOM 3 Age dir TO mal age 3	ADTOM 4 Age dir TO mal age 4	ADTOF1 Age dir TO fem age 1	ADTOF2 Age dir TO fem age 2	ADTOF 3 Age dit TO fem age 3	ADTOF 4 Age dir TO fem age 4	ADT3M1 Age-dir T3 mal age 1	ADT3M 2 Age dit T3 mal age 2	ADT3M3 Age dir T3 mal age 3	ADT3M 4 Age dir T3 mal age 4	ADT3F1 Age dir T3 km age 1	ADT3F2 Age dim T3 fem age 2	ADT3F 3 Age dis T3 fem age 3	ADT3F 4 Age dis T3 fem age 4
0	0.00		0.727	0.205	0.008		0.894	0.293		0.080	0.727	0.205	0.008	0.011	0.894	0.293	0.002
0	0.10	0.01	0.79	0.2	0.01	0	0.8	0.2	0	0.01	0.79	0.2		0	0.8		0
1	0.20	0.06	0.74	0.2	0.01	0.01	0.79	0.2	0	0.06	0.74	0.2	0.01	0.01	0.79	0.2	0
	0.30	0.1	0.89	0.2	0.01		0.76	0.2		0.1	0.89		0.01	0.06		0.2	0
		0.15	0.88		0.01	0.1		0.2	0	0.16	0.88		0.01	0.1		0.2	0
		0.2	0.81		0.01	0.15	0.65		0	0.2		0.2	0.01		0.86	0.2	0
	0.80		0.68	0.2		0.2	0.8		0	0.26		0.2	0.01		0.8	0.2	0
	0.70		0.61	0.2		0.26	0.66	0.2		0.3	0.61		0.01	0.26	0.55	0.2	
	0.80	0.01	0.65		0.01	0		0.3	0		0.86	0.33		0	0.7	0.3	0
		0.05		0.29	0.01		0.7	0.29		0.06	0.86		0.01	0.01		0.29	0
			0.86	0.24		0.05	0.7		0	0.1		0.24	0.01		0.7	0.26	
		0.16	0.86		0.01	0.1		0.2	0		0.86	0.19		0.1	0.7		0
		0.2		0.14		0.16	0.7	0.15	0		0.86	0.14		0.16	0.7		0
		0.26		0.09	0.01		0.7	0.1		0.26	0.65	0.09	0.01		0.7	0.1	
		0.3'	0.86		0.01	0.26		0.06	0		0.86	0.04		0.26	0.7		0
		0.08		0.38	0.01		0.2		0	0.08	0.55	0.38	0.01	0.01	0.2	0.79	0
		0.08	0.8	0.33	0.01	0.01	0.3	0.69	0		0.8	0.33		0.01	0.3		0
		0.08		0.28	0.01			0.69		0.06	0.86	0.29	0.01	0.01	0.4	0.69	0
		0.08	0.7	zO.23	0.01	0.01	0.6	0.49	0	0.06	0.7	0.23		0.01	0.5	0.49	0
		0.08	0.76	0.19	0.01	0.01	0.8	0.39	0	0.08	0.76	0.19	0.01	0.01	0.8		0
		0.08		0.13		0.01	0.7		0	0.08		0.13	0.01		0.7	0.29	
							0.19					-0.01	0.8		0		

Table A-l. Continued.

IRSMTO Init ret to sub TO mal	IRSFTO Init ret to sub TO fem	IRSMT3I Init ret to sub T3 I mal	IRSFT3I Init ret to sub T3 I fem	SUPNUMf Supp # fry	SUPNUMs Supp # smlt	Mi%NBS Min % nat brdstk	Mx%UNR Max % used of nat run	Mx%UTR Max % used of tot run	Mx%T3E Max % T3 fish in nrt e
1,500	1,200	0	0'	0	0	1.00	0.60	0.60	0.60
100	100	100	100	0	0	0.1	0.1	0.1	0.1
600	500	500	6 0 0	1000000	1000000	0.2	0.2	0.2	0.2
1000	1000	1000	1000	2000000		0.3	0.3	0.3	0.3
1500	1500	1500	1500	S000000		0.4	0.4	0.4	0.4
2000	2000	2000	2000			0.6	0.6	0.6	0.5
2500	2500	2500	2500			0.8	0.8	0.8	0.8
3000	3000	3ooo	3000			0.7	'b.7	0.7	0.7
						0.8	0.8	0.8	0.8
						0.9	0.9	0.9	0.9
						1	1	1	1

Table A-l. Continued

FFT1 Fii fact domest T0	FFT2 Fii fact domest T1	FFT3 Fit fact domest T2	FFI Fii fact stk sor local	FFa Fit fact stk sor adj	FFd Fit fact stk sor dist	FFc Fit fact culture oonvont	FFi Fit fact. culture innovat	RELSURVf Rel• urv fry ml (convent)	RELSURVs Rel SUN sm ml (convent)	CULT Cult tech 1 = conv 2 = Inno	PINNs % improv perf in sm ml	Mx%CCE Max % of cc eaten	PccB2 % of cc to achieve 1/2 Mx#E
0.95	0.90	0.86	1.00	0.70	0.10	0.80	1.00	0.20	0.09	1	0.60	0.60	0.39
0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	1	0.1	0.1	0.1
0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	2	0.2	0.2	0.2
0.3	0.3	0.3	0.3	0.3	0.3	0.3	0.3	0.3	0.3		0.3	0.3	0.3
0.4	0.4	0.4	0.4	0.4	0.4	0.4	0.4	0.4	0.4		0.4	0.4	0.4
0.5	0.6	0.6	0.6	0.6	0.5	0.6	0.6	0.6	0.6		0.5	0.6	0.5
0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8		0.8	0.8	0.8
0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7		0.7	0.7	0.7
0.8	0.8	0.9	0.8	0.8	0.8	0.8	0.9	0.8	0.8		0.8	0.8	0.8
0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9		0.9	0.9	0.9
1	1	1	1	1	1	1	1	1	1		1	1	1
											2		
											3		
											4		
											5		
											8		
											7		
											9		
											9		
											10		

Table A-Z. **Input parameter values for those parameters not varied during the simulation analysis.**

Parameter	1/ALL	YEARS IN THE OCEAN 2	3	4
$OSURV_h$	50%	60%	70%	80%
$P.SPSURVT0_h$	80%	80%	80%	80%
$P.SPSURVT3_h$	80%	80%	80%	80%
$JESP_k$	100%			
OHR_h	2%	3%	4%	4%
MHR_h	7%	7%	7%	7%
HREBP		(Not Activated)		
HRBP		(Not Activated)		
$SUPDUR_i$		60		
BCY_i			60	
BRDCSR		50%		
MiMNE			100	
MiFNE			100	
E.FRSA		1.0		
F.PSRSA		1.0		
PS.SRS		1.0		
P.SPSURVHT0		1.0		
F	1			
ss	2			
SCEN	3			

$NGE_{i,L}$	EGG	FRY	P-SMLT	SMLT	ADLT
Egg-fry	50%				
Fry-psmlt	30%	50%			
Psmlt-smlt	10%	'30%	50%		
Smlt-smlt	0%	10%	30%	5%	
Juv pass	0%	0%	10%	45%	
Estuary	0%	0%	0%	40%	
Ocean	0%	0%	0%	0 %	
Ocean hr	0%	0%	0%	0%	
River hr	0%	0%	0%	0%	
Adlt pass	0%	0 %	0%	0%	
Prespawn	10%	10%	1 0 %	10%	100%
Horn fidel	0%	0%	0%	0%	
TOTAL	100%	100%	100%	100%	100%

Table A-3. Simulation sets run using the range of parameter values presented in Table A-l.

Set	Code	Supplementation		Culture Method		Stock Source	
		Fry	Smolts	CON	INN	L	I
1	W0	0	0	-	-	-	-
2	W1	1,000,000	0	x		x	
3	W3	3,000,000	0	x		x	
4	W5	5,000,000	0	x		x	
5	W5I	5,000,000	0	x			x
6	W1SC	0	1,000,000	x		x	
7	W1SI	0	1,000,000		x	x	

Table A-4. The' minimum and maximum number of wild and total spawners produced after 50 year simulations for the standard run and all runs using the range of input parameters values listed in Table A-l

	WILD STOCK			TOTAL STOCK		
SET	STANDARD'	Minimum	Maximum	STANDARD	Minimum	Maximum
wo	7,694	0	68,902	7,694	0	68,902
Wl	6,732	0	68,102	6,885	0	68,269
w3	4,093	0	66,495	4,634	0	66,999
W5	1,799	0	64,874	2,668	0	65,720
W5I	6,167	0	67,081	,680	0	67,673
W1SC	6,837	0	67,307	7,386	0	70,602
W1SI	7,251	0	68,241	8,075	0	73,184

'The standard run has all input parameter values set to the standard value except those values associated with the supplementation goals, culture method, and stock source.

Table A-5. Input parameters which produced negative slopes for wild stocks.

Parameter	SET w o	W1	w 3	W5	W5I	W1SC	W1SI
RICC		x	x	x			
RWSC		x	x	x	x	x	
MiHR RANDOM				x	x	x	x
MiHR SELECT						x	
ADT0M3	x	x	x	x	x	x	x
ADTOF 1			x	x			
ADTOF3	x	x	x	x	x	x	x
ADT3M1		x	x	x	x	x	x
ADT3M2		x	x	x	x	x	x
ADT3F1		x	x	x	x	x	x
Mi%NBS		x	x			x	x
MX%UNR		x	x	x		x	x
Mx%UTR		x	x	x		x	x
Mx%T3E					x	x	x
RELSURVf		x					

Table A-6. Input parameter values for which wild stocks went below 100.

Set	Parameter							
1,2,3,4,5,6,7	CC	500	1,000	10,000				
5	CC	50,000	100,000					
1,2,3,4,5,6,7	E.FSURVTO	0.1						
6	E.FSURVTO	0.2						
1,2,3,4,5,6,7	F.PSSURVT	0.1						
1,2,3,4,5,6,7	PS.SSURVT	0.1						
1,2,3,4,5,6,7	s.ssuRv	0.1	0.2					
1,2,3,4,5,6,7	JPSURV	0.1						
1,2,3,4,5,6,7	PSURV2	0 .	1					
2,3,4,5,6,7	MiHR RANDOM	0.8	0.9					
2,3,4,5,6	MiHR RANDOM	0.7						
6	PSURV3	0.1						
Set‘	**Parameter Values producing greater than 10,000 wild stock**							
1,5,6,7	CC	3,000,000						
1,7	S.SURV	0.9						
1,2,3,4,5,6,7	JPSURV	0.8	.09					
12567 ,,,,	JPSURV	0.7						
1	JPSURV	0.6						
1,2,3,4,5,6,7	ESURV	0.3	0.4	0.5	0.6	0.7	0.8	0.9’
1,2,5,6,7	ESURV	0.2						
1,2,6,7	PSURV2	0.9						

Table A-7. Slopes derived from the minimum and maximum value of the input parameter and their associated response of wild spawners after 50 year simulations.

VARIABLE	W0	W1	W3	W5	W5I	W1SC	W1SI
CC	0	0	0	0	0	0	0
ICCC	0	0	-1	0	0	0	0
RWSC	0	-45	-270	-86	-224	-12	-4
EPFT01	0	0	0	0	0	0	0
EPFT02	1	1	1	1	1	1	1
EPFT03	0	0	1	0	0	0	0
EPFT04	0	0	0	0	0	0	0
E.FSURVTO	11512	10545	8416	5599	10197	10541	10899
F.PSSURVT0	117'47	10679	8332	5128	9783	10785	1 1 1 2 6
PS.SSURVTO	11749	10698	8400	5313	9884	10790	11127
S.SSURV	13187	12063	9582	6006	11246	12153	12656
JPSURV	21863	20819	18649	16331	19861	20788	21335
ESURV	81610	82417	82493	80467	81137	81345	81554
PSURV1	1511	1525	2254	450	1361	1491	1518
PSURV2	13689	12568	10087	6 6 2 8	11707	12855	13158
PSURV3	11209	10312	7708	3562	9476	10473	10868
PSURV4	462	4 5 1	565	133	439	470	472
MiHR SELECT		-77	2666	5350	172	45	-368
MiHR RAND		-6917	-3205	-1949	-6194	-7077	-7609
ADTOM1	978	871	267	282	1431	1635	1665
ADTOM2	1020	914	277	277	1546	1741	1749
ADTOM3	-2202	-1964	-763	-594	-3248	-3698	-3755
ADTOF1	90	298	-232	-23i	271	1814	1718
ADTOF2	529	213	158	178	682	305	438
ADTOF3	-1073	-843	-85	-85	-1516	-2466	-2537
ADT3M1		-31	-36	-36	-296	-193	-70
ADT3M2	--	-11	-17	-17	-105	-69	-25
ADT3M3	--	41	50	50	384	251	91
ADT3F1	--	-79	-227	-227	-51	-55	-143
ADT3F2	--	3	8	8	1	1	4
ADT3F3	--	67	193	193	4 4	47	123
IRSMTO	0	0	0	0			
IRSFTO	0	0	0	0			
IRSMT3I		--	0	0			
IRSFT3I		--	0	0			
Mi%NBS	--	-284	-1459	387	0	-842	-611
Mx%UNR	--	-73	-3613	-3613	0	-1	-1
Mx%UTR		-40	-2888	-2888	0	-1	-1
Mx%T3E	--	1	521	521	-3	0	-1
FFT1		267	520	520	371	1242	3539
FFT2	--	4	115	115	1	10	75
FFT3		59.	61	61	238	0	0
FFI	--	0	0	0	0	1058	2273
FFa	--	--	--	--	0	0	0
FFc	--	217	4138	1085	638	1396	0
FFi	--	--	--	--	--		2273
RELSURVf	--	-125	910	425	-3659	0	
RELSURVs	--	0	0	0	--	-486	1073
PINNs	--	--	--		--		108
Mx%CCE	0	0	0	0	0	0	0
PCCB2	0	0	0	0	0	0	0

Table A-8. The relative ordering of the effect of each input parameter on wild spawners after 50 year simulationos based on the rank order of the absolute value of the slope from greatest to least.

W0	W1	W3	W5	W5I	W1 SC	W1SI
ESURV	ESURV	ESURV	ESURV	ESURV	ESURV	ESURV
JPSURV	JPSURV	JPSURV	JPSURV	JF'SURV .	JPSURV	JPSURV
PSURV2	PSURVZ	PSURVZ	P S U R V Z	PSURVZ	PSURVZ	PSURVZ
S.SSURV	S.SSURV	S.SSURV	S.SSURV	S.SSURV	S.SSURV	S.SSURV
PS.SSURVTO	PS.SSURWO	E.FSURWO	E.FSURVTO	E.FSURVTO	PS.SSURVTO	PS.SSURVTO
F.PSSURVTO	F.PSSURWO	PS.SSURVTO	MiHR SELECT	PS.SSURVTO	F.PSSURVTO	F.PSSURVTO
E.FSURVTO	E.FSURWO	F.PSSURVTO	PS.SSURWO	F.PSSURVTO	E.FSURWO	E.FSURVTO
PSURVB	PSURV3	PSURVB	F.PSSURVTO	PSURV3	PSURVB	PSURV3
ADTOM3	MiHR RANDOM	FFc	Mx%UNR	MiHR RANDOM	MiHR RANDOM	MiHR RANDOM
PSURVI	ADTOM3	Mx%UNR	PSURVB	R E L S U R V f	ADTOM3	ADTOM3
ADTOF3	PSURVI	MiHR RAND'OM	Mx%UTR	ADTOM3	ADTOF3	FFT1
ADTOM2	ADTOMZ	Mx%UTR	MiHR RANDOM	ADTOMZ	ADTOFI	ADTOF3
ADTOMI	ADTOMI	MiHR SELECT	FFc	ADTOF3	ADTOMZ	FFi
ADTOF2	ADTOF3	PSURVI	ADTOM3	ADTOM1	ADTOMI	FFI
PSURV4	PSURV4	Mi%NBS	Mx%T3E	PSURVI	PSURVI	ADTOMZ
ADTOFI	ADTOFI	RELSURVf	FFT1	ADTOF2	FFc	ADTOFI
	Mi%NBS	ADTOM3	PSURVI	FFc	FFT1	ADTOM1
	FFT1	PSURV4	R E L S U R V f	PSURV4	m	P S U R V I
	FFc	Mx%T3E	Mi%NBS	ADT3M3	Mi%NBS	RELSURVs
	ADTOF2	FFT1	ADTOM2	FFT1	RELSURVs	Mi%NBS
	RELSURVf	ADTOM2	ADTOMI	ADT3M1	PSURV4	PSURV4
	ADT3F1	RWSC	ADTOFI	ADTOFI	ADTOFZ	ADTOFZ
	MiHR SELECT	ADTOMI	ADT3F1	FFT3	ADT3M3	MiHR SELECT
	Mx%UNR	A D T O F I	ADT3F3	RWSC	ADT3M1	ADT3F1
	ADT3F3	ADT3F1	ADTOFZ	MiHR SELECT	ADT3M2	ADT3F3
	FFT3	ADT3F3	PSURV4	ADT3M2	ADT3F1	PINNs
	RWSC	ADTOFZ	FFT2	ADT3F1	ADT3F3	ADT3M3
	ADT3M3	FFT2	RWSC	ADT3F3	MiHR SELECT	FFT2
	Mx%UTR	ADTOF3	ADTOF3		RWSC	ADT3M1
	ADT3M1	FFT3	FFT3		FFT2	ADT3M2
	ADT3M2	ADT3M3	ADT3M3			
		ADT3M1	ADT3M1			
		ADT3M2	ADT3M2			
		ADT3F2	ADT3F2			

Table A-9. Slopes derived from the minimum and maximum value of the input parameter and their associated response of total spawners after 50 year simulations.

VARIABLE	TO	T1	T 3	T5	T5I	T1SC	T1SI
cc	0	0	0	0	0	0	0
ICCC	0	0	-1	- 1	0	0	0
RWSC	0	-45	-262	-12'1:	-225	-12	-4
EPFT01	0	0	0	0	0	0	0
EPFT02	1	1	1	1	1	1	1
EPFT03	0	0	1	0	0	0	0
EPFT04	0	0	0	0	0	0	0
E.FSURWO	11512	10673	8840	6430	10633	11228	11928
F.PSSURWO	11747	10869	8953	6342	10423	11471	12155
PS.SSURVT0	11749	10888	9020	6519	10524	11476	12157
S.SSURV	13187	12253	10196	7201	11893	12999	13926
JPSURV	21863	21009	19241	17364	20520	22024	23188
ESURV	81610	82419	82822	81224	81251	85006	87046
PSURV1	1511	1545	2268	731	1434	1611	1698
PSURV2	13689	12761	10710	7824	12362	13527	14465
PSURV3	11209	10497	8319	4817	9870	11238	12016
PSURV4	462	452	555	167	435	483	492
MiHR SELECT		-230	2080	4433	-341	-504	-1192
MiHR RANDOM	--	-7108	-3919	-2854	-6832	-7694	-8536
ADTOM1	978	873	279	273	1432	1643	1677
ADTOM2	1020	906	258	258	1512	1713	1708
ADTOM3	-2202	-1961	-769	-599	-3226	-3690	-3742
ADTOF1	90	156	-577	-577	461	1170	752
ADTOF2	529	258	207	227	623	495	723
ADTOF3	-1073	-758	158	158	-1634	-2060	-1927
ADT3M1	--	37	175	175	-53	51	296
ADT3M2	--	13	58	58	-19	18	106
ADT3M3	--	-48	-225	-225	69	-66	-384
ADT3F1	--	-2	-46	-46	208	212	258
ADT3F2	--	25	83	83	75	81	1 2 2
ADT3F3	--	-30	-04	-64	-282	-292	-386
IRSMTO	0	0	0	0			
IRSFTO	0	0	0	0			
IRSMT3I	--	--	0	0			
IRSFT3I	--	--	0	0	--		
Mi%NBS	--	-127	-892	650	0	-489	-216.
Mx%UNR	--	-63	-3178	-3178	0	-1	-1
Mx%UTR	--	-35	-2496	-2496	0	-1	-1
Mx%T3E	--	1	994	994	-3	0	19
FFT1	--	262	682	682	352	1242	3 5 3 9
FFT2		4	147	147	1	10	75
FFT3	--	59	88	88	238	0	0
FFI	--	0	0	0	0	1059	2273
FFa	--	--			0	0	0
FFc	--	214	4004	1415	618	1396	0
FFi	--	--	--				2273 ,
RELSURVf	--	5 6 4	2654	1682	-1280	0	
RELSURVs		0	0	0	--	5616	6837
PINNs			--				657
Mx%CCE	0	0	0	0	0	0	0
PCCB2	0	0	0	0	'0		0

Table A-10. The relative ordering of the effect of each input parameter on total spawners after 50 year simulations based on the rank order of the absolute value of the slope from greatest to least.

T0	T1	T3	T5	T5I	T1SC	T1SI
ESURV	ESURV	ESURV	ESURV	ESURV	ESURV	ESURV
JPSURV	JPSURV	JPSURV	JPSURV	JPSURV	JPSURV	JPSURV
PSURV2	PSURV2	PSURV2	PSURV2	PSURV2	PSURV2	PSURV2
S.SSURV	S.SSURV	S.SSURV	S.SSURV	S.SSURV	S.SSURV	S.SSURV
PS.SSURVT0	PS.SSURVT0	PS.SSURVT0	PS.SSURVT0	E.FSURVT0	PS.SSURVT0	PS.SSURVT0
F.PSSURVT0	F.PSSURVT0	F.PSSURVT0	E.FSURVT0	PS.SSURVT0	F.PSSURVT0	F.PSSURVT0
E.FSURVT0	E.FSURVT0	E.FSURVT0	F.PSSURVT0	F.PSSURVT0	PSURV3	PSURV3
PSURV3	PSURV3	PSURV3	PSURV3	PSURV3	E.FSURVT0	E.FSURVT0
ADT0M3	MiHR RANDOM	FFc	MiHR SELECT	MiHR RANDOM	MiHR RANDOM	MiHR RANDOM
PSURV1	ADT0M3	MiHR RANDOM	Mx%UNR	ADT0M3	RELSURVs	RELSURVs
ADT0F3	PSURV1	Mx%UNR	MiHR RANDOM	ADT0F3	ADT0M3	ADT0M3
ADT0M2	ADT0M2	RELSURVf	Mx%UTR	ADT0M2	ADT0F3	FFT1
ADT0M1	ADT0M1	Mx%UTR	RELSURVf	PSURV1	ADT0M2	FFi
ADT0F2	ADT0F3	PSURV1	FFc	ADT0M1	ADT0M1	FFI
PSURV4	RELSURVf	MiHR SELECT	Mx%T3E	RELSURVf	PSURV1	ADT0F3
ADT0F1	PSURV4	Mx%T3E	PSURV1	ADT0F2	FFc	ADT0M2
	FFT1	Mi%NBS	FFT1	FFc	FFT1	PSURV1
	ADT0F2	ADT0M3	Mi%NBS	ADT0F1	ADT0F1	ADT0M1
	MiHR SELECT	FFT1	ADT0M3	PSURV4	FFI	MiHR SELECT
	FFc	ADT0F1	ADT0F1	FFT1	MiHR SELECT	ADT0F1
	ADT0F1	PSURV4	ADT0M1	MiHR SELECT	ADT0F2	ADT0F2
	Mi%NBS	ADT0M1	ADT0M2	ADT3F3	PSURV4	PINNs
	Mx%UNR	RWSC	ADT0F2	FFT3	Mi%NBS	PSURV4
	FFT3	ADT0M2	ADT3M3	RWSC	ADT3F3	ADT3F3
	ADT3M3	ADT3M3	ADT3M1	ADT3F1	ADT3F1	ADT3M3
	RWSC	ADT0F2	PSURV4	ADT3F2	ADT3F2	ADT3M1
	ADT3M1	ADT3M1	ADT0F3	ADT3M3	ADT3M3	ADT3F1
	Mx%UTR	ADT0F3	FFT2	ADT3M1	ADT3M1	Mi%NBS
	ADT3F3	FFT2	RWSC	ADT3M2	ADT3M2	ADT3F2
	ADT3F2	FFT3	FFT3		RWSC	ADT3M2
	ADT3M2	ADT3F2	ADT3F2		FFT2	FFT2
		ADT3F3	ADT3F3			Mx%T3E
		ADT3M2	ADT3M2			
		ADT3F1	ADT3F1			

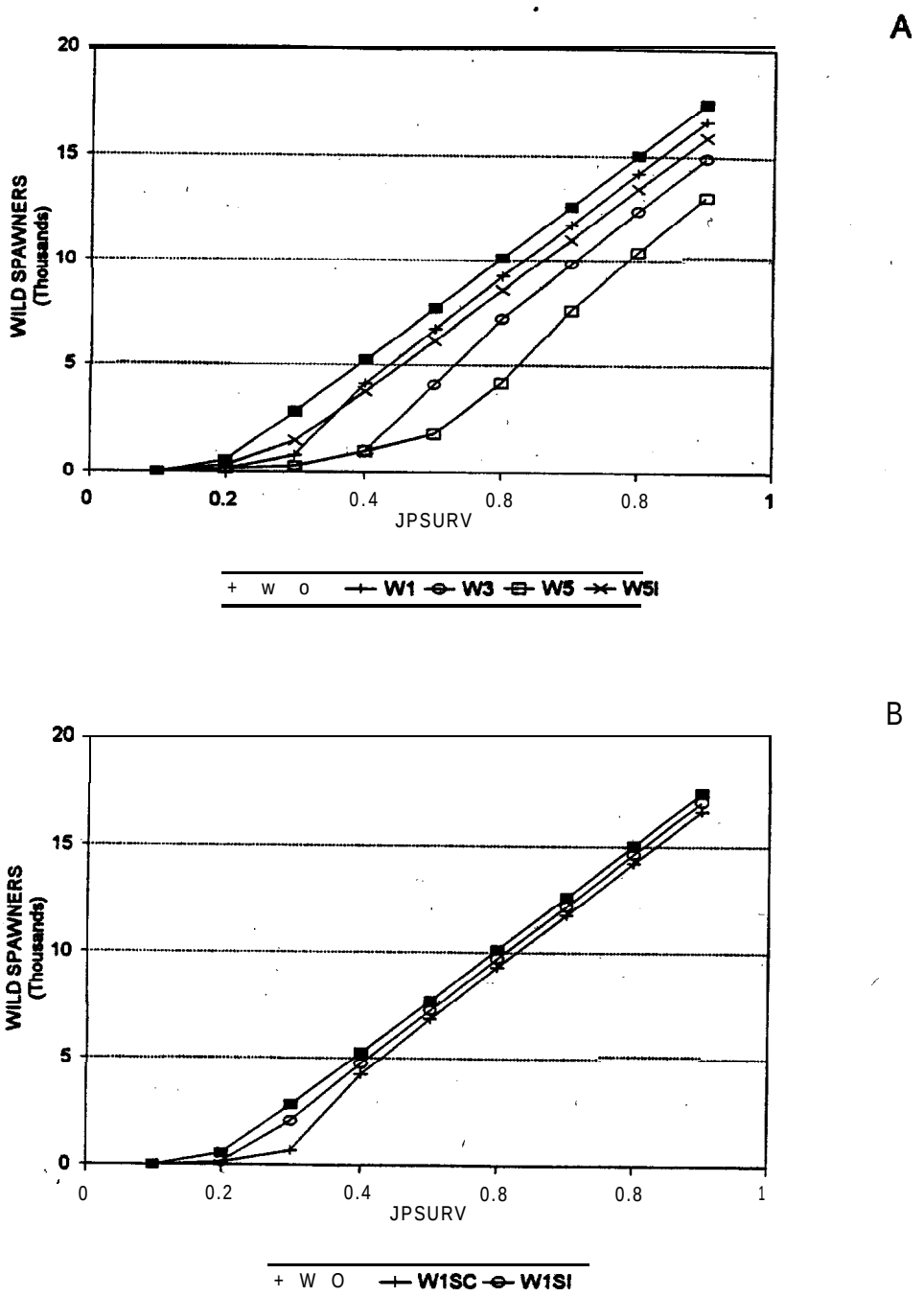
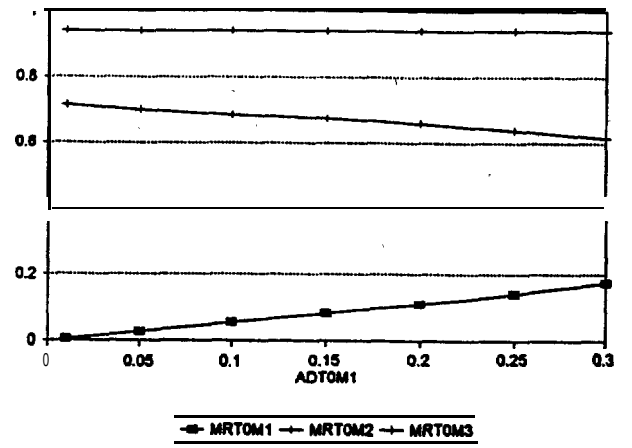
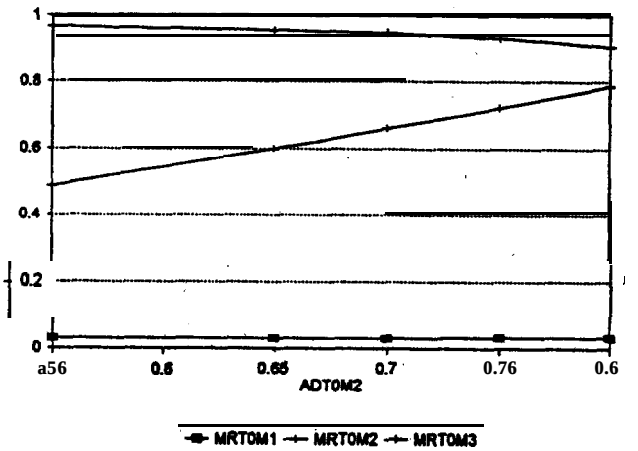


Figure A-l. **Curvature in the response function of juvenile passage survival and the number. of wild spawners after a 50 year simulation.**





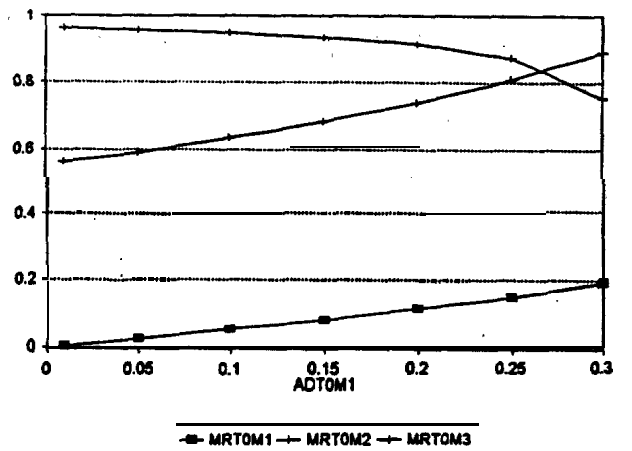


Figure A-2. Maturity rate for age classes 1, 2, and 3 as a function of the age distribution input parameters.

ECOSYSTEM DIAGNOSIS AND TREATMENT MODEL AS APPLIED TO SUPPLEMENTATION

APPENDIX B
DISAGGREGATION OF THE BEVERTON-HOLT EQUATION

The EDT planning model assumes that the underiying relationship between spawning stock size and subsequent production can be described by the Beverton-Holt **equation. This** stock-production (S-P) relation is highly suited to multi-life stage modeling because of how it can be disaggregated into separate functions for each life stage. Each separate function is then described by a Beverton-Holt equation, consisting of a productivity and capacity parameter. This disaggregation procedure provides an analytical framework for conceptualizing the basic environmental and biological mechanisms that regulate the abundance of a salmonid population.

The basis of the disaggregation approach comes from Beverton and Holt (1957) and Moussalli and Hilbom (1986). The approach is also discussed by Hilbom and Walters (1992).

The aggregated form of the Beverton-Holt equation is

$$R_n = \frac{P_n S}{1 + \frac{P_n S}{C_n}} \qquad \text{(B-1)}$$

where R_n = the number of individuals surviving through the nth stage, P_n = the composite **of** productivities expressed as density-independent survival for n successive stages, C_n = cumulative capacity through stage n, and S = the number of individuals at the start of the first stage (or the number of eggs deposited).

The number of fish at the start of each life stage can then be described by

$$R_{i+1} = \frac{p_i S_i}{1 + \frac{p_i S_i}{c_i}} \qquad \text{(B-2)}$$

where R_{i+1} = the number of individuals at the start of the $(i + 1)$th life stage, p_i = *the* productivity between stage i and $i + 1$ expressed as density-independent survival for this life stage, c_i = the capacity for life stage i, and S_i = the number of individuals at the start of stage i.

The composite of productivities (P_n) for the n stages is

$$P_n = \prod_{i=1}^{n} p_i \qquad \text{(B-3)}$$

which is simply all productivities multiplied together. For a three stage life cycle, for example, $P_n = P_3 = p_1 * p_2 * p_3$. The parameter P_n is referred to as S_0 or the low density egg to smolt survival rate in the Systems Planning Model (NPPC 1989).

The cumulative carrying capacity (C,,), or smolt carrying capacity as used in the EDT model, i s

$$C_n = \frac{P_n}{\sum_{i=1}^{n} \frac{P_i}{c_i}} \qquad \text{(B-4)}$$

Unlike the simple product in equation B-3, the cumulative capacity C_n depends both on the stage-specific capacity and stage-specific productivity terms. ,

A three stage model for egg to smolt (as used in the EDT model) results in the following equation for smolt carrying capacity

$$C_n = \frac{p_2 p_3}{\frac{1}{c_1} + \frac{p_2}{c_2} + \frac{p_2 p_3}{c_3}} \qquad \text{(B-5)}$$

where c_1 = capacity of egg incubation stage, c_2 = capacity of summer rearing stage, c_3 = capacity of the overwintering stage, p_2 = productivity of the summer rearing stage, and p_3 = productivity of the overwintering stage. The term p_1, productivity of the egg incubation stage, factors out of the equation and does not affect cumulative capacity,

The model described by equation B-5 illustrates that smolt carrying capacity varies in relation to the capacities of all individual life stages and the productivities of the latter two life stages. Thus smolt carrying capacity can be altered by changing productivity of the summer or overwintering stages or capacity of any of the three stages. The relative effect of altering one

parameter on cumulative capacity will depend on its relative contribution to the total. Equation B-S can be used to perform a limiting habitat analysis '(see Lestelle et al. 1993).

Equation B-5 also provides the avenue for estimating the capacity of each of the three stages using a ratio of **capacities**

The capacity of the second stage (c_2) is described by

$$c_2 = \frac{p_2 Z \cdot p_2 p_3}{\frac{p_2 p_3 Z}{C_n} - \frac{Z}{c_1}} \qquad \text{(B-6)}$$

where Z is the ratio c_3/c_2.

The capacity of the third stage (c_3) is then simply

$$c_3 = Zc_2 \qquad \text{(B-7)}$$

The capacity of the first stage (c_1) is described by

$$c_1 = WC_n \qquad \text{(B-8)}$$

where W is the ratio c_1/C_n.

The value of Z (this is the same as ***RWCSC***; see Table 6 **in** Part III) is an index of the relative contribution of winter and summer habitat to the overall smolt carrying capacity. A very small Z (i.e., winter capacity, c_3, is small compared to summer capacity, c_2) indicates that winter is the principal limitation to smolt carrying capacity, while a large Z indicates that summer tends to be the dominant limitation. A **continuum** exists. for Z, illustrating that each stream's carrying capacity is uniquely influenced by the relative amounts of summer and winter habitat that exists there. Lestelle et al. (1993) concluded that streams with Z values $\leq$ 0.25 are limited more by overwintering habitat; streams with values $>$ 0.25 are limited more during summer. The higher the Z **value** the more strongly summer habitat would limit smolt population size.

Values of W (this is the same as ***RICCC***; see Table 6 in Part III) higher than about 200 would indicate virtually no density-dependent mortality during the egg to fry stage and

generally that spawning habitat is adequately abundant to seed the available rearing area when sufficient spawnersarrive on the spawning grounds.

Estimates of the ratios Z and W can be based on empirical data, as described-in Lestelle et al. (1993), or can be assumed. Biologists who, have worked on a particular stream will almost always have some knowledge about the relative amount of spawning and overwintering habitat.

Estimation of C_n, smolt carrying capacity, can be drawn from reported information, or data files used for the Systems Planning Model. To disaggregate P_n, start with an estimate of p_1, based on literature, existing studies or an assumption.Then let $p_2 = p_3$ *as* a starting point for modeling, or use estimates drawn from literature or studies.

The model should be used to examine the effect of uncertainty in these estimates on outcome.