

**INTERIM REPORT ON
VIABILITY CRITERIA FOR
WILLAMETTE AND LOWER COLUMBIA BASIN
PACIFIC SALMONIDS**

WILLAMETTE/LOWER COLUMBIA TECHNICAL RECOVERY TEAM

MARCH 31, 2003

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ABBREVIATIONS AND ACRONYMS

BRT	biological review team
CWT	coded-wire tag
DIP	demographically independent population
EDT	ecosystem diagnosis and treatment
ESA	Endangered Species Act
ESU	evolutionarily significant unit
HPVA	habitat population viability analysis
λ_{JOM}	JOM growth rate
JOM	juvenile outmigrant
NWIFC	Northwest Indian Fisheries Commission
NMFS	National Marine Fisheries Service (also referred to as NOAA Fisheries)
PCC	population change criteria
PFC	properly functioning conditions
PVA	population viability analysis
QET	quasi-extinction threshold
TRT	technical recovery team
VSP	viable salmonid population
WDFW	Washington Department of Fish and Wildlife
WLC	Willamette/Lower Columbia

1. INTRODUCTION

In 1995, the National Marine Fisheries Service (NOAA Fisheries) announced that it would initiate a series of coastwide status reviews of anadromous salmonids in the states of Washington, Idaho, Oregon, and California. These status reviews resulted in the listing of several evolutionarily significant units (ESUs) of salmonids as threatened or endangered under the U.S. Endangered Species Act (ESA). Listed ESUs were organized into geographically proximate units, called recovery domains, as part of a multispecies approach that could address common regional recovery issues. This report focuses on the Willamette/Lower Columbia (WLC) domain.

The WLC domain contains five listed ESUs and one candidate ESU:

- Columbia River chum salmon (listed as threatened, 1999),
- Lower Columbia River steelhead (listed as threatened 1998),¹
- Lower Columbia River chinook salmon (listed as threatened 1999),
- Upper Willamette River steelhead (listed as threatened 1999),¹
- Upper Willamette River chinook salmon (listed as threatened 1999),
- Lower Columbia River coho salmon (candidate species 1997).

To obtain advice on technical issues related to recovery planning, NOAA Fisheries convened technical recovery teams (TRTs) in each recovery domain. The TRTs are composed of scientists from NOAA Fisheries; other federal, tribal, state and local agencies; academic institutions; and private consulting firms. A complete description of the TRT composition, tasks, relationship to ESA recovery planning, and operating principles can be found in the NMFS document *Recovery Planning Guidance for Technical Recovery Teams (TRTs)* (<http://research.nwfsc.noaa.gov/cbd/trt/about.htm>). The Willamette/Lower Columbia Technical Recovery Team (WLC-TRT) was established in May 2000. One of its first tasks was to provide technical information to support the development of delisting criteria. This report is a response to that task. The main text of this report is a consensus product of the TRT. The report contains a number of appendices in support of the main text, which are not TRT consensus products. The appendix authors are identified at the beginning of each appendix. Most of the appendices include individual TRT members as authors; the appendices were produced in coordination with and in support of the TRT.

Under the ESA, NOAA Fisheries must identify measurable and objective delisting criteria as part of recovery planning. The delisting criteria must describe the conditions under which a listed species or ESU is no longer in danger of extinction (endangered) or likely to become so in the foreseeable future (threatened). We define a viable ESU as one that is unlikely to be at risk of extinction. Ultimately, the crafting of delisting criteria requires the consideration of technical analyses relating to viability, which are contained in this document, and policy decisions such as acceptable levels of risk, which are not. This document presents the WLC-TRT's viability criteria guidelines. As with any scientific conclusions, it is anticipated that the recommendations in this document may be revised in the future based on new data or analysis. In

¹ Both anadromous forms of *Oncorhynchus mykiss* (steelhead trout) and resident forms *O. mykiss* (rainbow trout) often occur in the same river systems. The genetic and demographic relationships among these two life history types are poorly understood. In this document, we concentrate on criteria related to anadromous *O. mykiss*.

addition, the criteria need to describe viability conditions in a way that is usable by managers, thus revised viability criteria may be developed in the future in response to interaction with managers developing recovery goals.

The listed unit under the ESA for Pacific salmon is the ESU, and this is the unit that must be considered for delisting. Thus, delisting criteria must ultimately address the overall extinction risk of the ESU. In approaching the development of criteria for delisting ESUs we have relied on the language in the ESA, information described in the listing decision, concepts outlined in a report on viable salmonid populations (VSPs) by McElhany et al. (2000), which can be found online at <http://www.nwfsc.noaa.gov/pubs/tm/tm42/tm42.pdf>; and in published research describing salmon populations and their past or potential responses to changes in climate and ocean conditions (e.g., Bradford and Irving 2000).

The ESA lists five potential factors for decline that must be considered in species listing decisions (ESA Section 4.2.1):

1. the present or threatened destruction, modification, or curtailment of its habitat or range;
2. overutilization for commercial, recreational, scientific, or educational purposes;
3. disease or predation;
4. the inadequacy of existing regulatory mechanisms;
5. other natural or manmade factors affecting its continued existence.

The NMFS identified all five factors as contributing to the endangerment of Pacific salmonids. In considering how viability criteria might inform population delisting requirements, the TRT also considered all five factors for decline.

The TRT approach evaluates the extinction risks facing an ESU by assessing the viability of the individual populations within that ESU. The TRT identified population-level viability criteria based on:

1. a combination of the four population parameters identified in the VSP document—productivity, abundance, spatial structure, and diversity;
2. information about the habitat requirements of the listed salmon; and
3. the need to separate population responses to freshwater and estuarine habitat conditions from population responses to fluctuating marine and climatic conditions.

Building from these population-level criteria, the WLC-TRT developed the ESU criteria framework in Figure 1.1.

The approach depends first on identifying historical, demographically independent populations within each ESU. Population identification focuses on demographically independent units because many of the processes affecting extinction risk operate on this scale. (This concept is discussed in more detail in McElhany et al. 2002) A draft WLC-TRT document (Myers et al. 2002) estimates historical population boundaries for all five listed ESUs in the WLC domain. The populations identified in Myers et al. are used in this report.

The overall approach we have taken to establishing ESU viability criteria is outlined in Figure 1.1. In Section 2, we develop the ESU-level viability criteria by first dividing the ESU into groups of populations called strata. The strata are based on major life-history characteristics (e.g., spring versus fall chinook) and ecological zones. The ecological zones are relatively large

scale, with the Lower Columbia being divided into three ecological zones and the Willamette consisting of a single ecological zone. The strata represent major diversity components of the ESUs, and populations in the different strata are likely to be subject to different catastrophic events. Therefore, it is important for ESU viability to ensure a reasonably high probability of persistence for each stratum, so the ESU-level viability criteria are crafted as a function of the persistence probability of each stratum. The persistence probability of each stratum is in turn a function of the viability of its component populations, and in Section 2 we develop an algorithm for estimating how many and which populations need to have a given persistence probability in each stratum.

This approach requires some way to assess the overall persistence probability of individual populations. In assessing individual populations, the WLC-TRT developed guidelines for criteria about five attributes:

1. adult productivity and abundance,
2. juvenile outmigrant (JOM) growth rate,
3. within-population diversity,
4. habitat, and
5. within-population spatial structure.

In order for a population to be considered viable, it would have to meet the criteria for all five attributes. There is necessarily some redundancy built into these criteria guidelines. In a simple world, one criterion would suffice, but there are many potential scenarios in which any four of the above criteria might lead to a false conclusion that a population's extinction risk was low enough for it to be considered viable. For example, in a scenario in which adult salmon escapements are increased under favorable ocean conditions some criteria may be met (e.g., adult productivity and abundance, within-population spatial structure, within-population diversity, and habitat), yet JOM criteria would indicate that actual freshwater production was not yet high enough to delist. Alternatively, habitat criteria might not be met when all four fish performance criteria are met, indicating that populations were in a period of favorable ocean and climatic conditions, but that freshwater and estuarine habitats were not yet of sufficient quality to support the population during less favorable ocean and climate conditions.

In Section 3, we propose several approaches for integrating each individual attribute into an overall assessment of population persistence probability. In Sections 4 through 8, we describe criteria associated with each individual population attribute.

This report does not describe what actions need to be taken to restore salmonid ESUs. It is limited to describing measurable and objective attributes of VSPs and ESUs. For example, some reasons that ESA-listed salmonid populations may be threatened with extinction include the following:

- Density-independent survival is too low for populations to replace themselves.
- The carrying capacity of the population is low enough for density-dependent processes to keep the population at critically low abundance.

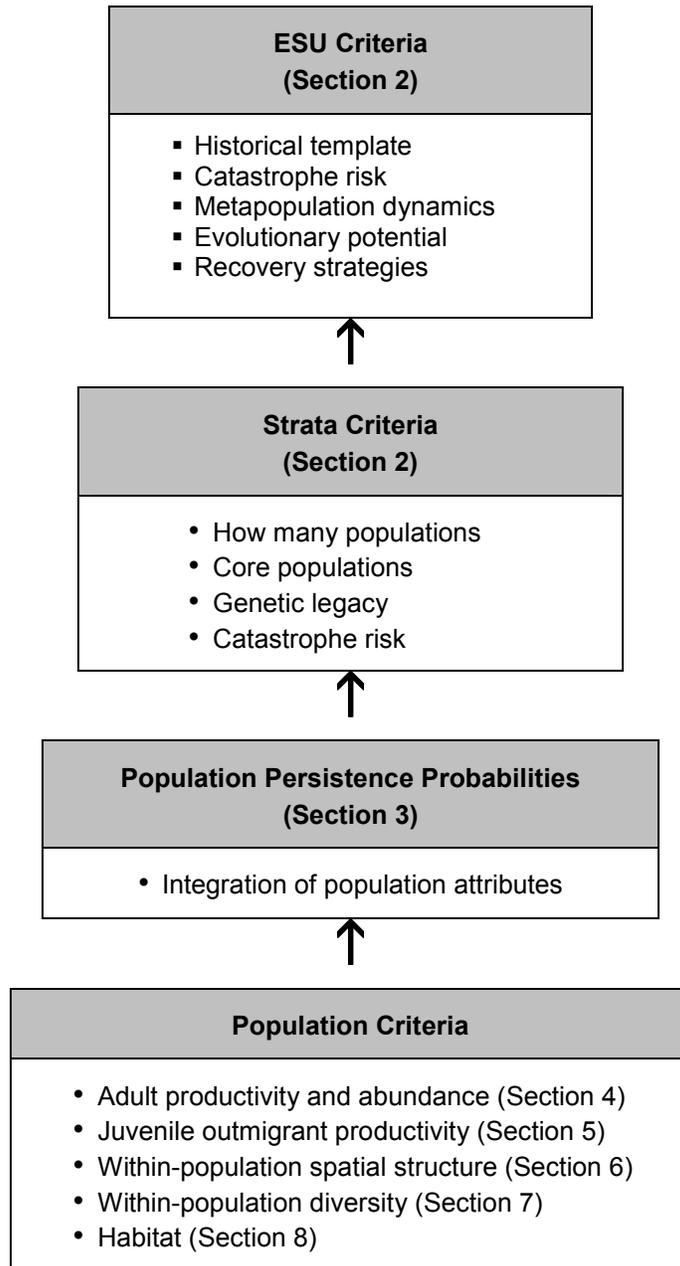


Figure 1.1 Approach to ESU criteria. The bullets list key considerations involved in each criterion. The section numbers refer to the section of this document that addresses each issue.

- The population is subject to extinction from catastrophic events.
- The population is experiencing genetic degradation.
- The habitat is experiencing progressive degradation.

We considered each factor but worked to develop criteria that could define viable populations and ESUs without regard to which factors are causing a population to be at risk. We did not attempt to determine the primary risk factor currently acting on any particular population or ESU.

The extinction risk factors can be subdivided into specific factors that have led to population and ESU decline. For example, if a population is at risk because density-independent survival is too low, the proximate cause may be poor water quality, excessive harvest, high hydrosystem passage mortality, or predation by exotic species, to name a few possibilities. In general, the salmon viability criteria do not attempt to partition the sources of mortality. For example, adult productivity and abundance criteria examine the spawning population after the fish have experienced all sources of mortality. If a population is currently at risk of extinction because survival is too low, the criteria allow us to evaluate whether survival has improved; however, the criteria do not presuppose what needs to be fixed to improve survival. In this respect, the productivity and abundance criteria may be referred to as “mortality-source neutral.” To address a specific factor of concern, the criteria may be considered “harvest neutral” in that the criteria do not stipulate a specific harvest level. In combined consideration of all mortality sources, any harvest strategy that allows the criteria to be achieved would be considered possible in order to achieve a viable status.

Although the salmon attribute criteria are not intended to identify specific actions required for recovery, the ability to achieve different criteria will clearly be affected differently by different potential factors for decline. For example, the spatial structure and diversity criteria within a population are heavily affected by habitat structure, and the criteria described below reflect this fact. Again, the criteria do not specifically address what factors need to be addressed in any particular population.

Some of the population attribute criteria described in this report—notably the spatial structure, diversity, and habitat criteria—will require additional analysis at finer spatial scales than have been undertaken by the WLC-TRT so far. The criteria on these topics in this report essentially amount to guidelines; population-specific criteria will need to be developed so that concrete goals can be established.

2. ESU-LEVEL VIABILITY

ESU-LEVEL CRITERIA GUIDELINES
1. Every stratum (life history and ecological zone combination) that historically existed should have a high probability of persistence.

STRATA CRITERIA GUIDELINES
1. Individual populations within a stratum should have persistence probabilities consistent with a high probability of strata persistence.
2. Within a stratum, the populations restored/maintained at viable status or above should be selected to: <ol style="list-style-type: none">Allow for normative metapopulation processes, including the viability of “core” populations, which are defined as the historically most productive populations.Allow for normative evolutionary processes, including the retention of the genetic diversity represented in relatively unmodified historical gene pools.Minimize susceptibility to catastrophic events.

ESU-LEVEL RECOVERY STRATEGY CRITERIA GUIDELINES
1. Until all ESU viability criteria have been achieved, no population should be allowed to deteriorate in its probability of persistence.
2. High levels of recovery should be attempted in more populations than identified in the strata viability criteria because not all attempts will be successful.

Overview

As the unit listed under the ESA, the ESU is also the unit that must be considered for delisting. Part of the process for developing ESU delisting criteria involves describing the biological attributes of a viable ESU, which is defined as one with a high probability of persistence. The persistence probability is the complement of the extinction risk (i.e., persistence probability = 1 – extinction probability), and both terms are used in this document. The ESU viability criteria proposed in this report provide some flexibility in deciding which populations need to be restored to what status. Finalization of a viable ESU scenario will require policy/technical interaction.

To develop the viability criteria we applied the VSP approach outlined in McElhany et al. (2000). The basic strategy is to identify historically independent populations, develop criteria

describing viable independent populations (i.e., VSPs), then determine how many and which populations need to be at a particular status relative to the VSP criteria for the ESU as a whole to have an acceptably low extinction risk. Elsewhere in this document we describe the population-level viability criteria for the attributes of productivity, abundance, juvenile outmigrants, diversity, habitat, and spatial structure. In this section, we address the question of how many and which populations need to be in what viability status.

Clearly the most precautionary approach—the one that would give the highest probability of ESU persistence—would be for all historical populations to meet or exceed the viable population criteria. However, several ESUs historically contained a relatively large number of populations (Table 2.1) and it is possible that a subset of the historical populations can provide an adequate probability of ESU persistence. For example, the Lower Columbia chinook ESU is estimated to have consisted of 31 demographically independent populations. As supported by intuition and simple probability modeling (below), the probability of extinction for an ESU with 30 of the 31 historical populations in viable condition is not likely to be much different than the probability of extinction for a population with all 31 historical populations in a viable condition. In either case, the probability is low. If we allow that not all historical populations need to be viable for the ESU to be viable, we are confronted with the questions exactly how many are needed and does it matter which ones.

McElhany et al. (2000) provides seven guidelines for determining how many and which populations are needed for a viable ESU.

1. The ESU should contain multiple populations.
2. Some populations within the ESU should be geographically widespread.
3. Some populations should be geographically close to each other.
4. Populations should not all share the same catastrophic risk.
5. Populations that display diverse life histories and phenotypes should be maintained.
6. Some populations should exceed VSP guidelines.
7. Evaluations should take into account uncertainty about the ESU-level process.

These guidelines are motivated primarily by concern about catastrophic risks, metapopulation dynamics, and long-term evolutionary dynamics. If an ESU contained only a single population, there is a possibility that it could be driven extinct by a single catastrophic event. This necessitates multiple viable populations within a viable ESU. The risk of ESU extinction from

Table 2.1 Estimated number of historical demographically independent populations.

ESU	Historical Populations
Lower Columbia chinook	31
Lower Columbia steelhead	23
Columbia River chum	16
Upper Willamette chinook	7
Upper Willamette steelhead	4

Source: Myers et al. (2002)

catastrophic events can be further reduced by careful consideration of which populations are restored or maintained at viable status. Appendix K is an exploration of the spatial distribution and frequencies of potential catastrophic events affecting Pacific salmonid populations in the WLC. For reasons discussed in the appendix, it is difficult to predict catastrophic risks to salmon populations, but several general conclusions relevant to setting viability criteria are possible.

- Extinction risk is reduced if viable populations are spatially distributed throughout the ESU.
- Populations that utilize different types of environments experience different catastrophic risks. Having populations in different environments reduces the likelihood that a single catastrophic event would affect every population in an ESU.
- Because of the spatio-temporal patterns of catastrophic events, fish with different life histories that share the same river basin may be affected differentially by the same catastrophic event.

As discussed in the section on within-population diversity, genetic and life-history diversity helps buffer a population from extinction. Different genotypes and life histories are likely to be favored under different environmental conditions, and, as a consequence, diverse populations have a higher probability of persistence. As at the population level, diversity at the ESU level can increase the persistence probability of the ESU. If an ESU contains populations with different genetic or life-history types, it is less likely to go extinct because not all populations would respond to the environment in the same way. Conditions that cause one population to decrease in abundance may not affect another population at all, or may actually cause it to increase. In fact, this buffering effect can occur simply as a result of spatial diversity, in which different populations respond differently to conditions as result of their spatial dispersal.

Restoring and maintaining populations with different genetic and life-history types is also important for maintaining the evolutionary processes that are a part of any functioning biological system. The environment will change in the future and the existence of genetic diversity is essential if the ESU is to respond evolutionarily to that change and persist. The ESU concept is based on the premise of protecting the “evolutionary legacy” of an ESU (Waples 1991), and part of the evolutionary legacy of an ESU is the diversity within it. The concept of an evolutionary response to change is particularly relevant in the face of directional environmental change caused by humans. Some of the most significant long-term changes to affect salmon could be effects of global climate change as a result of the “greenhouse effect.” It is difficult to predict with confidence which genotypes or life-history types will be favored under any future changes in the environment. Thus to ensure that at least some genotypes exist that will be favored in the future, the ESU-level criteria incorporate diversity considerations.

Establishing ESU-level viability criteria is hampered by our limited understanding of many of the processes that operate at the ESU scale. For example, ESUs may operate as a metapopulation at large spatial and temporal scales, with populations naturally experiencing periodic extinction and recolonization (Levins 1969, Hanski and Gilpin 1997). This suggests that metapopulation modeling could be used to help determine ESU-level viability criteria. However, accurate estimates of the key parameters needed for quantitative metapopulation modeling, such as dispersal rate and local extinction probabilities, are simply not available. Although the concepts of metapopulation theory informed our thinking about ESU-level criteria, we conducted only very limited quantitative modeling (see “Number of Populations per Stratum,” page 11).

Rather than rely on quantitative modeling, we focused on the principles suggested by considering the importance of catastrophic events and among-population diversity to develop the general framework of the viability criteria. We also relied on the general concept that the historical ESU was viable and that it provides the only known template of a functioning ESU. As noted above, it may not be necessary for every historical population in an ESU to be at viable status for the ESU to be viable. However, confidence in ESU viability can be enhanced if the populations restored and maintained at VSP status recreate the basic structure of the historical template. Reference to the historical template motivates several components of the ESU-level viability criteria.

In addition to the biological concerns about ESU persistence, answering the questions how many and which populations are needed to delist an ESU must be informed by the language of the ESA itself. The ESA states that a species may be listed if it is threatened or endangered in "... all or a significant portion of the range." Since the ESU is functionally considered a "species" for the purposes of the ESA, presumably an ESU could only be delisted if it is no longer at risk of extinction in a significant portion of its range. The word significant is not defined in the ESA, and it is not clear whether "a significant portion of the range" would constitute more of the range than is required for species viability. In this document, we focus on viability and do not rely on the "significant portion of the range" language of the ESA in developing criteria.

Viability criteria describe a set of conditions, which, when met, would indicate that a population or ESU has a high probability of persistence. We have generally focused on the desired future conditions and have not discussed actions or strategies for reaching these goals in developing the viability criteria in this document. However, we did consider it important to include reference to two "recovery strategy guidelines" regarding the ESU viability criteria. These guidelines are included because presenting the viability criteria alone could suggest recovery strategies that would be inconsistent with actually reaching the criteria goals.

Viability Criteria Approach

In considering all the concepts discussed above to develop the viability criteria, the TRT partitioned the populations in an ESU into a number of different strata, then specified a risk evaluation system for deciding how many populations within each stratum should be at what status (Figure 1.1). The strata are defined based on two factors: (1) major life-history differences and (2) ecological zones (Table 2.2). The partitioning based on ecological zones also results in a partitioning based on spatial distribution. If the ESU contains populations in each stratum, it will have a relatively low extinction risk from catastrophic events, correlated environments, and loss of diversity. In addition, the ESU will have some semblance of its historical structure, which increases confidence in ESU viability. Attributes of the different strata are described briefly below and in more detail in Appendix A.

Table 2.2 Estimated number of populations in different strata in the Willamette/Lower Columbia domain.

ESU	Ecological Zone ^a	Run Timing ^a	Historical Populations ^b
Lower Columbia chinook	Coast Range	Fall	7
	Cascade	Fall	9
		Late fall	2
		Spring	7
	Columbia Gorge	Fall	4
		Spring	2
Lower Columbia steelhead	Cascade	Summer	4
		Winter	14
	Columbia Gorge	Summer	2
		Winter	3
Columbia chum	Coast Range	Fall	7
	Cascade	Fall	7
	Columbia Gorge	Fall	2
Upper Willamette chinook	Willamette	Spring	7
Upper Willamette steelhead	Willamette	Winter	4
Total			81

^a Each run timing and ecological zone combination is a separate stratum.

^b The historical number of populations is based on Myers et al. (2002).

The life-history factors defining the strata are based on major differences that are the basis of some population designations (Myers et al. 2002). Lower Columbia chinook salmon are partitioned into spring, fall, and late-fall runs. Lower Columbia steelhead are partitioned into summer and winter runs. Populations of the three other listed ESUs in the WLC domain, Columbia chum salmon, Upper Willamette chinook salmon, and Upper Willamette steelhead, each consist of a single major life-history type and were not partitioned by run timing. While the different life-history types are named by run timing, each run type exhibits a number of different, presumably coadapted, life-history characteristics. Differences between the Lower Columbia chinook and steelhead life-history types are described in some detail in the TRT document identifying populations in the WLC domain (Myers et al. 2002). Loss of major life-history types was considered significant during decisions to list Lower Columbia River ESUs under the ESA. Myers et al. (1998) indicated that the Lower Columbia River chinook salmon ESU was listed, in part, because the biological review team (BRT) was unable to identify a single healthy spring-run chinook salmon population. Busby et al. (1996) indicated that one of the reasons the BRT listed Lower Columbia River steelhead as threatened was concern over the status of summer steelhead in this ESU.

Ensuring that populations persist in each ecological zone reduces risk of ESU extinction from catastrophic events and loss of diversity. Ecoregions defined by the U.S. Environmental Protection Agency (EPA) (Omernik 1987) were used to help define ecological zones for the WLC ESUs. The EPA ecoregions were designated for the contiguous United States based on

soil, topography, climate, potential vegetation, and land use (see Appendix B). Hughes et al. (1987) noted a strong link between ecoregions and freshwater fish assemblages. Salmon and steelhead populations in the Lower Columbia River ESU primarily cover the Coast Range, Cascade Range, and Columbia Gorge (East Cascades) ecoregions (Myers et al. 1998, Busby et al. 1996, and Johnson et al. 1997). Spring-run chinook salmon and winter steelhead in the Willamette ESU occupy the Cascade and Willamette Valley ecoregions (Busby et al. 1996, Myers et al. 1998). The EPA ecoregions were modified slightly to create more salmon-appropriate “ecological zones” (Appendix A). Because the climate, geology, and ecological processes in each ecological zone are different, it is expected that different ecological zones are unlikely to be affected by the same catastrophic event (Appendix E). The ecological zones represent distinct selective environments, and the persistence of populations in each zone is expected to preserve much of the ESU’s diversity.

Number of Populations per Stratum

Given the value in restoring and maintaining viable populations within each stratum, we need to decide how many and which populations should be at what status within a stratum. This section addresses “How many?” and the next section addresses “Which ones?” It is important to note that we are not striving for a zero extinction risk for each stratum. The unit listed under the ESA, the focus of the viability criteria described in this section, is the ESU. However, ESU viability is more likely if each stratum has a relatively low probability of extinction.

As one approach to considering how many populations are needed per stratum, we estimated the probability that there would be no populations remaining in a stratum after some period of time, given an initial number of populations and an independent, identical, per-population extinction rate. Under these assumptions, the stratum extinction risk declines exponentially with the initial number of populations as

$$\phi = \theta^\eta$$

where

ϕ is the probability that all the populations in a stratum will be extinct within y years,

θ is the probability that a single population will go extinct in y years, and

η is the number of initial populations in the stratum.

The probability of stratum extinction for a number of different per-population extinction risks when $y = 100$ years is shown in Figure 2.1. To really parameterize this equation, we would need to know the per-population extinction risk. This is not something we can estimate with any degree of precision. Meeting all population-level viability criteria is likely to result in a low probability of extinction from processes internal to the population, but we cannot calculate exactly how low. In addition, populations are subject to extinction from external catastrophic events, and for reasons discussed in Appendix K, it is difficult to quantify the per-population catastrophe risk. The calculation also makes the critical assumption that population extinction risks are independent. This is most certainly not the case, because correlated environments and catastrophic risks increase the likelihood that multiple populations can go extinct at the same time. The probability calculations indicate that, in general, having 2 to 3 populations with a low extinction risk in a stratum provides a relatively significant reduction in risk compared to a single

population, but having four or more populations does not greatly reduce the risk. There is a continuous exponential decline in extinction risk as more populations are added; however, the practical increase in risk reduction shows diminishing returns. Because the simple model is likely to underestimate extinction risk, we concluded that it is potentially useful in defining a lower bound on the minimal number of populations, but not informative beyond that limited application. Based on this simple probability analysis and professional judgment about the point of diminishing returns, the TRT concluded that a viable ESU should contain at least two viable populations per strata, but that additional considerations are needed to estimate how many more than two are required.

We approached the stratum risk criteria from the perspective of the historical template. The approach is based on the principle that the historical population structure of the strata produced a relatively low risk of extinction, and the closer the population structure is to that historical structure, the lower its extinction risk. Conversely a population structure that deviates greatly from the historical structure would be considered at high risk. Although this general argument is logically sound, it does not allow the identification of a “bright line” viability threshold for stratum criteria. How close to historical is good enough? Below, we present a stratum evaluation system with some suggested benchmarks for criteria. However, it must be recognized that these benchmarks are based on professional judgment of high, moderate, and low risk categories.

Another limitation of the simple stratum risk calculation presented above is the

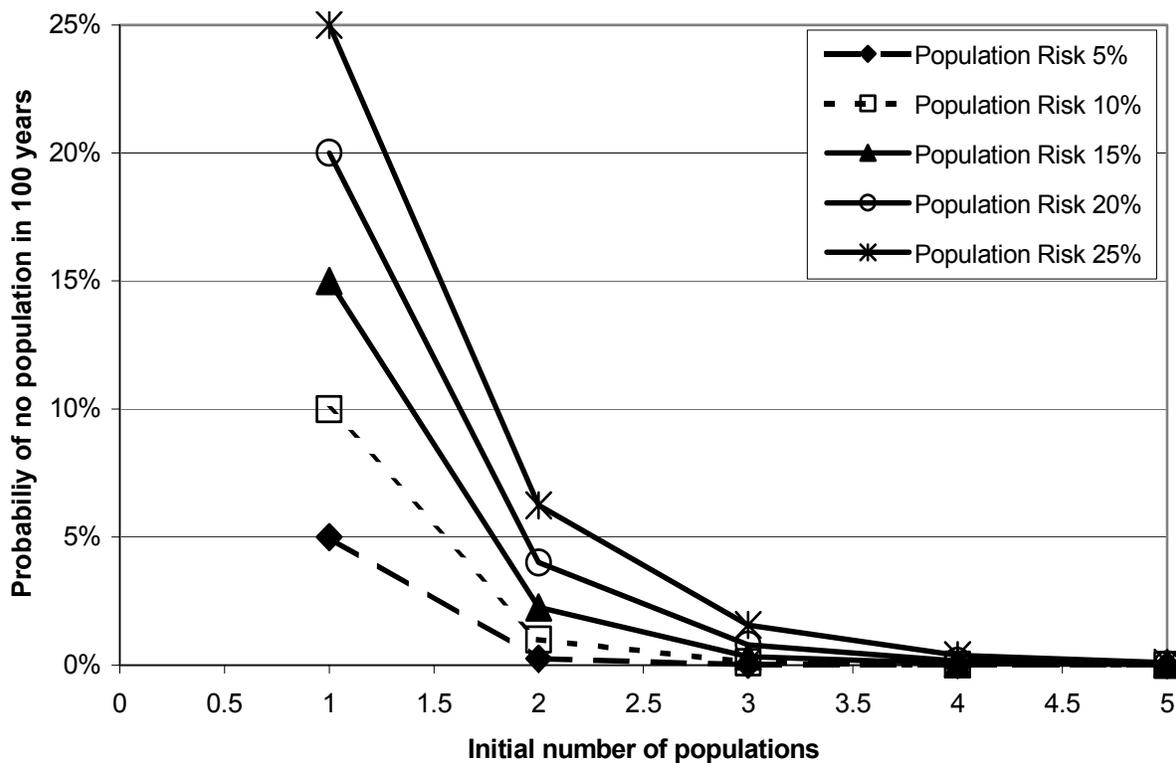


Figure 2.1 Probability of losing all the populations in a stratum within 100 years as a function of the initial number of populations, assuming populations are independent. Each curve represents a different per-population probability of extinction in 100 years.

assumption that all populations will have the same extinction risk. In fact, population extinction risks vary by population and a viable ESU scenario is likely to contain populations at different risk levels. This complication makes development of a quantitative metapopulation model that predicts viable ESU scenarios even more challenging. In a previous draft of this document (May 2002), we developed stratum criteria based primarily on consideration of a single risk level, that of a viable population as defined in McElhany et al. 2000 (i.e., negligible risk of extinction in 100 years). In the earlier draft, we specified the number of populations needed to meet or exceed VSP status. A second, higher risk level was also discussed (i.e., that associated with an effective population size of 500 spawners). This earlier approach failed to consider the entire range of potential population risks in a viable ESU scenario. Some populations may have a much lower risk of extinction than that defined in McElhany et al. 2000, and others may have a much higher risk. Because of issues related to population connectivity and metapopulation dynamics, populations at all risk levels have the potential to contribute to ESU viability, and the challenge is to identify the combination of populations at different risk levels that leads to a viable ESU.

Although population persistence probability is a continuum from near 100% (at least in 100-year time frames), to near 0% (or even already extirpated), there is limited precision in persistence probability estimates. Thus, to develop ESU-level criteria, we have divided the continuum into five categories (Table 2.3). Population risk assignment is limited to five categories because a continuous scale could impart a false sense of precision regarding the estimates. With some hesitation, we provide quantitative persistence probabilities associated with each qualitative persistence category in Table 2.3. Simply stating the quantitative thresholds implies that persistence can be measured with some degree of precision. Again, we do not believe it possible to accurately estimate persistence probability. However, it is possible to provide rough quantitative estimates of persistence probabilities associated with population productivity and abundance (Section 4), and Table 2.3 aids in associating such estimates with the persistence categories. The majority of sections in this document (Sections 2–8) address the establishment of criteria for assigning populations to risk categories. In Section 3 (“Integrating Population Risk”), we present an approach for combining information on individual population attributes (productivity, abundance, diversity, habitat, and spatial structure) into one of these five risk categories.

Using the categories described in Table 2.3, we have developed an approach for describing how many populations need to be at what status in each stratum. The approach uses

Table 2.3 Description of population persistence categories.

Population Persistence Category	Probability of Population Persistence in 100 Years	Description
0	0–40%	Either extinct or very high risk of extinction.
1	40–75%	Relatively high risk of extinction in 100 years.
2	75–95%	Moderate risk of extinction in 100 years.
3	95–99%	Low (“negligible”) risk of extinction in 100 years (viable salmonid population).
4	>99%	Very low risk of extinction in 100 years.

the average risk category of the populations in the stratum. The average is based on the historical number of populations, not the current number (e.g., if an historical population is extirpated, it is not ignored but is entered into the average as a 0.) Taking the metric of stratum extinction risk as an average of the individual populations risks allows the stratum metric to be scaled to the historical number of populations (i.e., strata that historically contained more populations would need more populations in a low-risk category than strata with few historical populations). This will result in viable ESU scenarios that resemble the historical population structure in terms of the number of populations and are consistent with the historical template concept. Using an average approach also recognizes that having some populations that exceed the VSP population criteria (i.e., category 4) can help mitigate the risk from populations with higher risk categories (i.e., categories 0–2). In examining stratum averages, we developed the general guidelines for stratum risk shown in Table 2.4. We considered, but did not provide, quantitative persistence probabilities associated with each stratum persistence category. We have no way of providing quantitative estimates of stratum persistence, and did not want to impart a false sense of precision.

The professional judgment for the thresholds was made after considering the averages of all the possible combinations of population values that could occur in a stratum. As a rough guide, the TRT identified averages that produced combinations considered functionally similar to the strata criteria developed in the previous draft of this document (i.e., the greater of 2 populations or 50% of the historical populations in a stratum should be at viable status or higher, and all extant populations should have an effective population size of at least 500). The new averaging approach provides more flexibility in defining viable ESU scenarios, but should describe similar levels of risk as those in the previous draft. Tables showing the averages of all possible combinations of populations are available on the WLC-TRT Web site at http://research.nwfsc.noaa.gov/cbd/trt/trt_wlc/viability_report.htm.

The average population risks in Table 2.4 are proposed as thresholds for the strata criteria guideline related to the number of populations.² The reliance on professional judgment for the

Table 2.4 Stratum persistence categories based on averages of individual population risks. The category thresholds are based on *professional judgment*.

Stratum Persistence Probability Category	Average of Population Risks
Low persistence	Average < 2
Moderate persistence	2 ≤ Average < 2.25; at least two populations ≥ 3
High persistence	Average ≥ 2.25; at least two populations ≥ 3

² Note on the mathematical properties of the average population risk: The strata average does not indicate the expected value of the persistence probability for populations in the strata. There is a nonlinear relationship between the population persistence probabilities and the population persistence categories. That is, some population persistence categories are associated with very wide ranges (e.g., category 1 has a range of 40%) and other population persistence categories are associated with more narrow ranges (e.g., category 3 has a range of 10%). The population average is used as a metric of stratum persistence probability, not as an expected value. The nonlinearity in the population categories does not reduce the utility of the metric.

establishment of these stratum average thresholds is in many ways unsatisfying. However, the inability to quantitatively model the relevant processes leads to a reliance on professional judgment for decisions about stratum risk.

Selection of Populations in a Stratum

Within a stratum, careful selection of the populations restored or maintained at a high persistence probability status (i.e., category 3 or 4) can increase the probability of ESU persistence. Within a stratum, the populations restored or maintained at viable status should be selected so as to:

- Allow for normative metapopulation processes, including the viability of “core” populations, which are defined as the historically most productive populations.
- Allow for normative evolutionary processes, including the retention of the genetic diversity represented in relatively unmodified historical gene pools.
- Minimize susceptibility to catastrophic events.

Metapopulation Processes

A metapopulation is a group of relatively independent populations that interact through the movement of individuals among them. Individual populations within the metapopulation may be extirpated (or nearly so) by internal or external processes and subsequently be recolonized (or “rescued”) by migrants from neighboring populations. In a stable metapopulation, the natural rate of population extirpation is matched by the natural rate of recolonization (see McElhany et al. 2000 for discussion of metapopulations and Pacific salmonids). On relatively large temporal and spatial scales, the populations in an ESU are expected to act as a metapopulation, within which the exchange of migrants among populations has an important impact on the ESU’s long-term persistence. Section 6 (“Within-Population Spatial Structure Criteria”) discusses these issues at smaller spatial and temporal scales.

Simply having enough populations is one important consideration for metapopulation persistence. The stratum average approach discussed above is an effort to identify an adequate number of populations as a function of the historical number. In addition to sheer numbers, other issues may be important, such as the distribution of populations and the particular dynamics involved. Source-sink dynamics are one type metapopulation process in which some populations are consistently more productive than others. These source populations can serve as a source of migrants to recolonize neighboring, less productive (sink) populations that are periodically extirpated or depressed in abundance. A key strategy in conserving a source-sink metapopulation is to protect the source population (McElhany et al. 2000).

Under historical conditions, not all salmon populations had the same productivity. Myers et al. (1998) demonstrated that some salmon populations were more productive than others. Using a life-cycle model for coho salmon, Nicholson and Lawson (2000) indicated that in periods of low ocean productivity only salmon inhabiting the best rivers or reaches survived. Population abundance is not the same as productivity, but variation in abundance or density

among populations provides some indication of variability in productivity. As an example of this variability, the lower Cowlitz River fall chinook salmon population is estimated to have historically consisted of 54,000 fall chinook spawners in a 441-square-mile drainage area, giving a density of 122 spawners per square mile. In contrast, there were an estimated 5,000 fall chinook spawners historically in the 98-square-mile Coweeman River drainage, yielding a density of 51 spawners per square mile (Appendix J). Historical population estimates for summer steelhead also indicate similar levels of among-population variability in abundance, with the East Fork Lewis River spawner abundance estimated to be 400 fish, while the Wind River spawner abundance was estimated at 2,300.

We define the historical salmon populations that were the center of productivity and abundance for a stratum as core populations. Note that this definition of core potentially differs from other uses of the term in conservation biology and natural resource management. Some researchers and managers have used the term core to describe current population strongholds or to identify areas for intensive restoration or protection. Our definition is based on historical fish performance and may or may not correspond to current status or management strategies. Based on the historical ESU template concept, having at least some core populations with a high probability of persistence is likely to provide the highest probabilities for ESU persistence. The recovery of core populations is likely to create an ESU with a strong resemblance to the historical structure. The basis of the historical template concept is that the historical ESU was viable, and the more an ESU resembles the historical structure, the more confidence we have that it will be viable. In Appendix B, we identify core populations in the WLC domain.

Evolutionary Processes

As discussed in more detail in Section 7, the genetic variability within a salmon population allows salmon to adapt to a changing environment. Given that genetic traits underlie the productivity and ecological potential of a population, conservation biologists have placed a high priority on protecting this diversity because it is a key to species survival. In fact, the intent of the ESA is to protect the ESU, which is defined as representing “an important component in the evolutionary legacy of the species.” Human transfer of salmon between basins has been widespread for more than 100 years, and many of the current populations differ genetically from the historical populations, resulting in a loss of diversity. In deciding which populations to restore and maintain at viable status it is important to include populations that still represent the historical diversity. Appendix B of this document and Appendix C of Myers et al. (2002) describe the genetic and life-history relationships between current and historical populations; the information in these appendices can help identify current pools of diversity. Maintaining these pools of diversity should be a key consideration when populations are ranked or prioritized to achieve viability goals.

Catastrophic Risk

The presence of viable populations in each stratum is expected to substantially reduce the risk of extinction of the ESU from catastrophic events. Careful selection of populations within a stratum can further reduce the extinction risk due to catastrophic events. For example, the Lower

Columbia River ESUs will be less vulnerable to catastrophic loss if viable populations exist on both sides of the Columbia River. As another example, multiple salmon populations could be impacted by the same volcanic event, and the existence of viable populations in watersheds that are not entirely located on the same volcano can increase ESU viability. Appendix L describes the spatial distribution of some potential catastrophic events that could affect salmon populations. This information can be used for ranking or prioritizing which populations should be restored and maintained at viable status. In an effort to minimize risk from catastrophic events, the populations within a stratum will generally be geographically widespread.

Approach to Selecting Populations

From a biological perspective, determining which populations in a stratum should be restored and maintained at viable status requires simultaneous consideration of metapopulation processes, evolutionary processes and catastrophic risk. Because of the many contingencies involved, we recommend that the evaluation of proposed stratum viability scenarios be conducted using professional judgment. The appendices listing core populations and genetic legacy populations provide guidance on the selection of populations for viable stratum scenarios. However, it may not be necessary for all of the core populations and genetic legacy populations to be viable for the stratum and ESU to be viable. Determining exactly whether a particular population is needed for a functioning metapopulation or to reduce risk from catastrophic events depends on which other populations are at viable status. Since the number of potential combinations of populations at viable status is potentially very large, we did not find it feasible to develop a simple mathematical algorithm for determining which populations to select and instead rely on professional evaluation based on the relevant biological principles.

ESU-Level Viability Criteria and Strata Persistence

A precautionary approach to ESU viability would require all strata to have a high probability of persistence. A less precautionary approach might consider a mixture of strata with high and moderate persistence probabilities. We suggest that a viable ESU should have all strata in the high-persistence category.

How precautionary to be in setting delisting criteria at the ESU scale is ultimately a policy decision. However, the appropriate attribute threshold (e.g., stratum average) associated with each persistence category is a scientific question. Unfortunately, it is not a question that can be answered with precision, and there is ample room for scientific debate. For several reasons, we have not attempted to associate qualitative descriptions of ESU persistence (e.g., high, low) with quantitative thresholds (e.g., a high persistence is a 99% probability in 100 years). Such associations rely on societal and policy perceptions of high and low and the relation of these perceptions to the ESA. In addition, scientific estimates of persistence probability at the ESU scale are even less precise than at the population and stratum scales. The imprecision associated with each assessment level (population attribute → population summary → stratum → ESU) is propagated up to the ESU level to create a very uncertain estimate. If policy makers were to supply an explicit acceptable probability of ESU persistence, we could provide a professional judgment estimate of criteria thresholds. However such estimates would be extremely imprecise,

thus relying on qualitative advice, such as describing potential ESU scenarios as “more precautionary” or “high risk,” may be the best the TRT can provide without implying greater precision than actually exists.

Recovery Strategy Criteria

The viability criteria in this document describe scenarios that, if observed, would indicate a population or ESU has a high probability of persistence. These criteria should be clearly distinguished from a strategy for how to actually recover the ESU. The viability criteria describe a future desired state. Given that some efforts to recover populations will inevitably not be successful, a prudent recovery strategy would require attempting to recover more populations to a higher status than is stipulated simply by the viability criteria. As a simple example, imagine that the target viability criteria required that three populations in a stratum be at VSP status (i.e., category 3). If there is an 80% chance that any given population recovery effort will be successful, there is only a 51% probability that three populations will be recovered if recovery is only attempted in three populations (Table 2.5). In this example, to have a greater than 95% probability of achieving the target of three populations, recovery would need to be attempted in at least six populations.

In this document, we do not assess the probability that any given recovery strategy will be successful. This probability depends on the recovery strategy selected. Information on the likelihood of success for different recovery strategies will need to be developed as action plans are created. However, no population recovery strategy is guaranteed to be successful, and it will be important to “overshoot” the number of populations in which recovery is attempted.

Another issue related to the distinction between viability criteria and a recovery strategy involves the protection of extant populations. Viable ESU criteria may allow for extirpated populations. Although this may describe an acceptable end state, it would be highly risky to allow current populations to decline in the short term. As noted in the previous paragraph, it is important as a recovery strategy to overshoot the goal, and striving for an exact target is likely to fail. As a practical matter, high recovery levels likely will need to be attempted in most, if not all, current natural production areas. Recovery strategies should consider the fact that we do not know *a priori* which population recovery attempts will be successful. There is a particular danger in writing off any extant populations, which might permanently remove options for ESU

Table 2.5 Probability of achieving recovery of at least three populations if the probability of a successful population recovery attempt is 80%. The probability of success for each population recovery attempt is considered independent.

Number of Populations in which Recovery Is Attempted	Probability of Recovering at Least Three Populations
3	51%
4	82%
5	94%
6	98%

recovery. Until all ESU viability criteria are met with regard to all populations, no population should decline from its current status.

Examples of Viable ESU Scenarios

The best way to explore the ESU viability criteria is through examples. In this section, we work through two example ESU scenarios that are consistent with the proposed criteria. In order to examine the criteria at the extremes, one of the examples involves the ESU with the most populations and strata (i.e., Lower Columbia chinook salmon), and the other involves the ESU with the fewest populations and strata (i.e., Upper Willamette steelhead). It is important to emphasize that these are EXAMPLES and NOT RECOMMENDATIONS for viable ESU scenarios.

To generate these example scenarios, a random collection of population persistence categories was selected for each stratum, such that the stratum average was between 2.25 and 2.5, and the stratum contained at least two populations of category 3 or higher (Table 2.6). Restricting the collections to an average of 2.25 to 2.5 puts all strata just barely above the high-persistence threshold. Strata with a higher average would also be considered at high persistence, but the behavior of the criteria near the threshold is likely to be of most interest. Strata with only two populations are the exception. In order to have at least two populations of category 3 or greater, the minimum possible average is 3. Random selection of the collection of population categories was considered the best way to develop an EXAMPLE. In practical application, target population persistence categories will not be selected at random but instead will consider the feasibility of restoration and other policy issues.

Once the collection of population persistence categories was selected, we considered metapopulation processes (e.g., core population), the evolutionary processes (e.g., populations that represented the genetic legacy) and the issues of catastrophic risk to decide which populations would be most important to be category 3 or higher (Table 2.7). These decisions relied on the information in Appendix B (core populations) and Appendix K (catastrophic risk), and (from Myers et al. 2002) Appendix C (genetic legacy). The key information from those appendices are summarized in Table 2.7. The prioritization we developed is not necessarily the only possibility, but it is an EXAMPLE that is consistent with the criteria principles.

Table 2.6 Random collection of population persistence categories used for example viable ESU scenarios.

ESU	Stratum	Number of Populations	Random Collection of Population Persistence Categories ^a	Average Population Persistence Category
Lower Columbia chinook salmon	Coastal fall	7	4,4,4,3,2,0,0	2.43
	Cascade fall	9	4,3,3,3,2,2,2,2,1	2.44
	Cascade late fall	2	3,3	3.00
	Cascade spring	7	3,3,3,3,2,1,1	2.29
	Gorge fall	4	3,3,2,1	2.25
	Gorge spring	2	3,3	3.00
Upper Willamette steelhead	Willamette	4	3,3,2,2	2.50

^a The collections were selected to have a stratum average between 2.25 and 2.5 and to contain at least two populations of category 3 or higher. The two strata with only two historical populations are an exception, with a stratum average of 3.0.

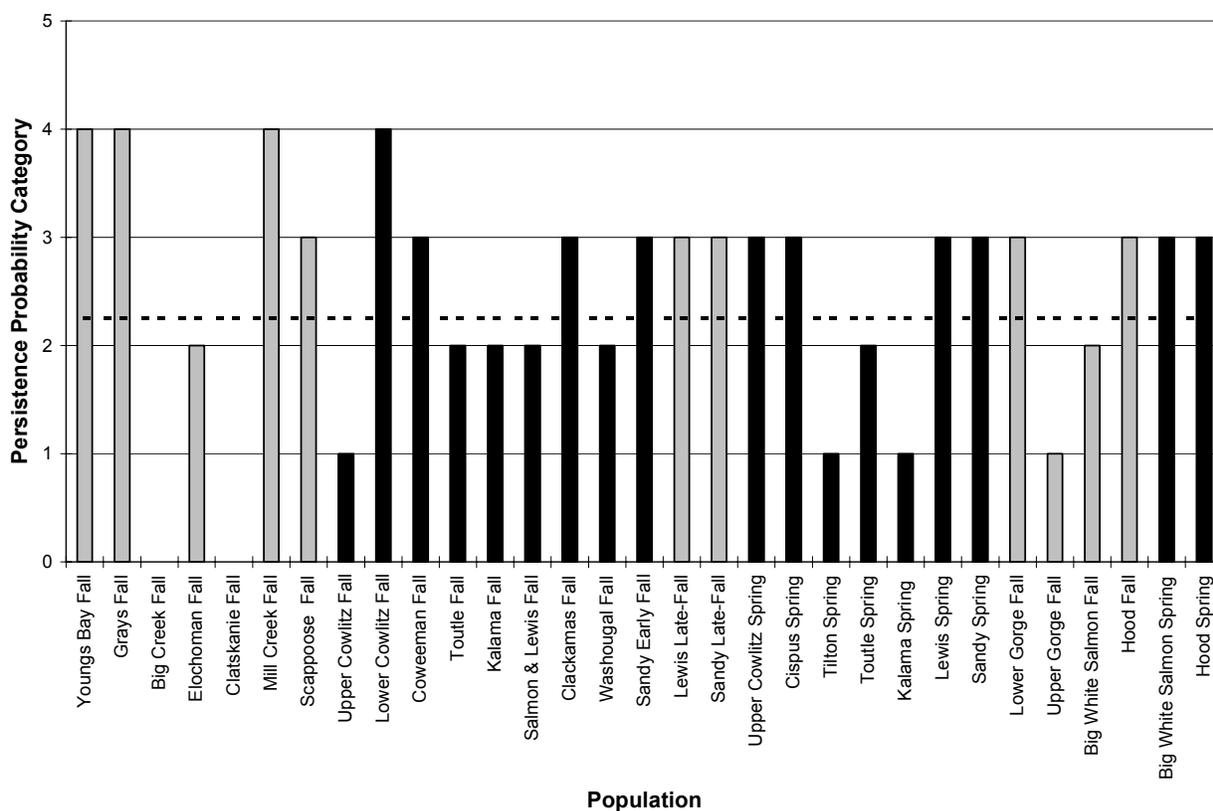


Figure 2.2 EXAMPLE Lower Columbia chinook salmon ESU scenario. The gray and black bars distinguish separate strata. Population risk categories were randomly selected from all of the strata combinations with an average of 2.25–2.5 (i.e., all strata are just above the low-risk threshold), except strata with only two populations. The dashed line indicates the 2.25 average persistence probability threshold for a high-persistence stratum.

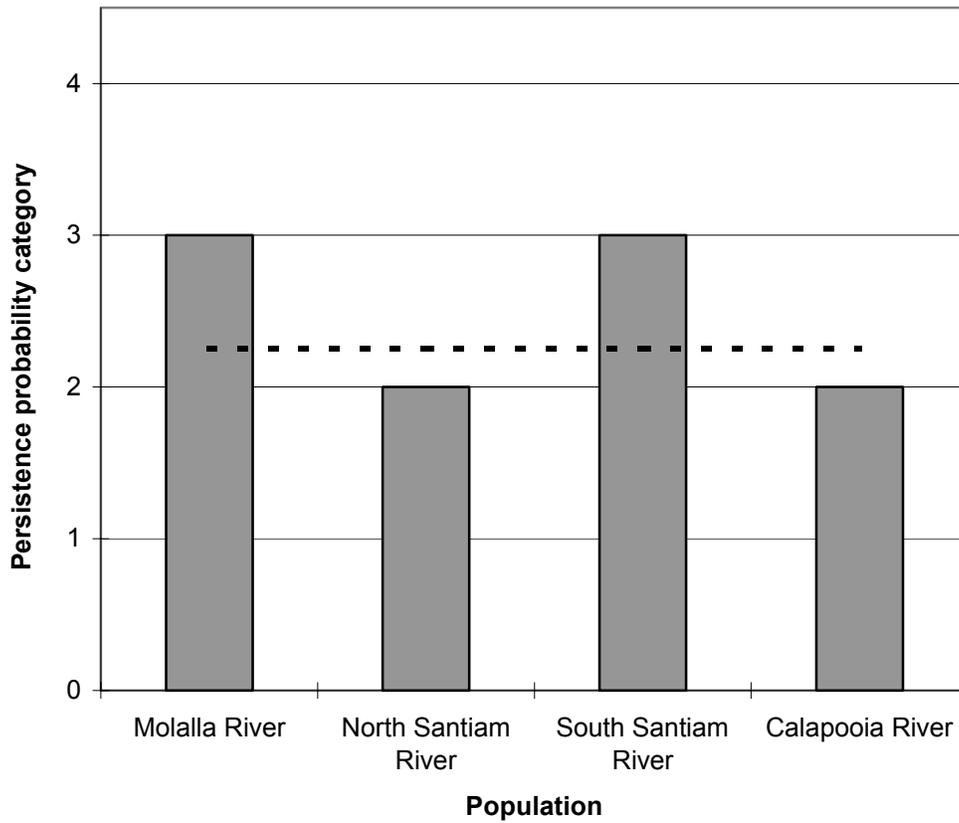


Figure 2.3 EXAMPLE Upper Willamette steelhead viable ESU scenario. This ESU consists of a single stratum. Population risk categories were randomly selected from all strata combinations with an average of 2.25–2.5 (i.e., all strata are just above the low-risk threshold). The dashed line indicates the 2.25 average persistence probability threshold for a high-persistence stratum.

Willamette/Lower Columbia Salmonid Viability Criteria

Table 2.7 EXAMPLE selection of populations needed above persistence category 3 for example viable ESU scenarios (continued on facing page).

ESU	Stratum	Core Populations	Genetic Legacy Populations
Lower Columbia chinook salmon	Coast fall	Elochoman Big Creek	
	Cascade fall	Lower Cowlitz Toutle Clackamas	Coweeman Salmon Creek-Lewis
	Cascade late fall	Lewis Sandy	Lewis Sandy
	Cascade spring	Upper Cowlitz Cispus Lewis Sandy	Upper Cowlitz Sandy
	Gorge fall	Lower gorge tributaries Upper gorge tributaries	
	Gorge spring	Big White Salmon River	
Upper Willamette steelhead	Willamette	North Santiam South Santiam	North Santiam South Santiam

Table 2.7 cont.

Catastrophic Risk Issues	Number of Populations in Random Collection of Category >= 3 (See Table 6)	Populations Selected To Be of Category >= 3
<ul style="list-style-type: none"> ▪ Earthquakes—low probability/high impact ▪ Landslides—from steep slopes, stream channels ▪ Disease from hatcheries—17.5 million hatchery fish raised and released in system ▪ Transportation oil spills—negligible to medium density 	4	<ul style="list-style-type: none"> ▪ Youngs ▪ Grays ▪ Mill ▪ Scappoose
<ul style="list-style-type: none"> ▪ Volcanoes—Mount St. Helens, Mt. Adams, Mt. Rainier, Mt. Hood ▪ Landslides—from volcanoes, steep slopes, and channels ▪ Disease from hatcheries—49.3 million hatchery fish raised and released in system ▪ Transportation oil spills—high density in urban areas 	4	<ul style="list-style-type: none"> ▪ Lower Cowlitz ▪ Coweeman ▪ Clackamas ▪ Sandy
<ul style="list-style-type: none"> ▪ Volcanoes—Mount St. Helens, Mt. Hood ▪ Landslides—from volcanoes, steep slopes, and channels ▪ Disease from hatcheries—10 million hatchery fish raised and released in system 	2	<ul style="list-style-type: none"> ▪ Lewis ▪ Sandy
<ul style="list-style-type: none"> ▪ Volcanoes—Mount St. Helens, Mt. Adams, Mt. Rainier, Mt. Hood ▪ Landslides—from volcanoes, steep slopes, and channels ▪ Disease from hatcheries—21.3 million hatchery fish raised and released in system ▪ Transportation oil spills—high density in urban areas 	4	<ul style="list-style-type: none"> ▪ Upper Cowlitz ▪ Cispus ▪ Lewis ▪ Sandy
<ul style="list-style-type: none"> ▪ Volcanoes—Mt. Adams, Mt. Hood ▪ Landslides—from volcanoes, steep slopes, and channels ▪ Disease from hatcheries—45.9 million hatchery fish raised and released 	2	<ul style="list-style-type: none"> ▪ Lower gorge ▪ Hood
<ul style="list-style-type: none"> ▪ Volcanoes—Mt. Adams, Mt. Hood ▪ Landslides—from volcanoes, steep slopes, and channels ▪ Disease from hatcheries—0.38 million hatchery fish raised and released 	2	<ul style="list-style-type: none"> ▪ Hood ▪ White Salmon
<ul style="list-style-type: none"> ▪ Landslides—from steep slopes, stream channels ▪ Disease from hatcheries—11.4 million hatchery fish raised and released ▪ Transportation oil spills—high density in urban areas 	2	<ul style="list-style-type: none"> ▪ South Santiam ▪ Mollala

3. INTEGRATING ATTRIBUTES AND ASSESSING POPULATION RISK OF EXTINCTION

Overview

The basic strategy for setting ESU viability criteria uses a hierarchical system to relate population scale attributes to ESU criteria (population attributes → population persistence probabilities → strata persistence probabilities → ESU criteria; Figure 1.1.) The population scale attributes are indicators of a population’s extinction risk (or conversely, a population’s persistence probability). McElhany et al. (2000) identified four important indicators of population extinction risk: productivity, abundance, spatial structure, and diversity. Working within the VSP framework as a starting point, the WLC-TRT developed the following general categories of indicators:

- adult productivity and abundance,
- juvenile out-migrant (JOM) productivity,
- population diversity,
- habitat, and
- spatial structure.

Subsequent sections of this document explore how each attribute can be used as an indicator of population extinction risk. In this section, we address the challenging task of integrating information on each attribute into an overall assessment of population extinction risk.

In Section 2, we introduced the approach of describing population persistence probability on a 0–4 qualitative scale, with 0 indicating a population with a low probability of persistence, and 4 indicating a population with high probability of persistence (Table 2.3). This 0–4 population scoring system is used as the basis for the ESU-level criteria. Because it is critical to this section, Table 2.3 is repeated here as Table 3.1.

Table 3.1 Description of population persistence categories.

Population Persistence Category	Probability of Population Persistence in 100 Years	Description
0	0–40%	Either extinct or very high risk of extinction
1	40—75%	Relatively high risk of extinction in 100 years.
2	75—95%	Moderate risk of extinction in 100 years.
3	95—99%	Low (negligible) risk of extinction in 100 years (VSP).
4	>99%	Very low risk of extinction in 100 years

Approach to Integrating Population Attributes

The proposed approach to integrating population attributes involves first evaluating the status of each population attribute separately on a 0–4 scale, then integrating the individual attribute values into an overall assessment of population status. The population attribute scores are based on the persistence category descriptions provided in each attribute section of this document, somewhat similar to those found in Table 3.2. For example, the population spatial structure would be evaluated based on whether it is consistent with a persistence probability that is high, low, or somewhere in between and assigned a 0–4 value accordingly. For some criteria (e.g., adult productivity and abundance and JOM growth rate), it may be possible to provide more quantitative thresholds associated with each level on the 0–4 scale. For other attributes (e.g., within-population diversity), it may not be possible to identify *a priori* quantitative thresholds, and more reliance on professional judgment will be required to determine the appropriate category. Issues related to the characterization of the individual attributes are discussed in the chapter on each attribute.

The TRT considered a number of possible procedures. Ideally, attribute persistence levels could be determined in a highly quantitative manner; however, in almost all cases the quantity and quality of available information necessary to derive such formulae were lacking (and will continue to be deficient under existing monitoring programs). Furthermore, the biological relationships among population characteristics are poorly understood. Data quality was a major concern for the TRT, and it was generally agreed that any population attribute measure needed to include some accounting for uncertainty due to poor data quality, in contrast to uncertainty due to environmental stochasticity. Furthermore, adjustments for poor data quality needed to be precautionary in nature and should be distinct from evaluations of the biological parameters.

A summary population profile table is a convenient way to view the status of populations in an ESU (Table 3.2). A table like this retains information on each individual attribute as well as the estimate of the overall population persistence category.

Table 3.2 Example “summary population profile table.”^a

Population	Population Attribute Persistence Categories					Population Persistence Category
	Growth & Abundance	JOM Growth	Spatial Structure	Diversity	Habitat	
A	3	1	1	1	1	2
B	4	ND ^b	3	3	3	4
C	0	0	0	0	0	0
D	2	1	ND	1	2	1
E	3	3	2	3	2	3
F	2	2	1	2	2	2

^a All values are completely made up and the individual attributes were arbitrarily integrated into an overall population persistence category.

^b ND = No Data. Indicates missing information; see Appendix C for TRT approach to missing data.

The TRT discussed a number of issues related to assigning values for each individual attribute and to assigning an overall persistence category for a population. Some of the key issues are as follows:

- *How much the procedure should rely on quantitative algorithms versus professional judgment.* Quantitative algorithms are potentially less subjective, but the majority of data will be qualitative, and professional judgment might provide the most accurate assessment of population status.
- *How to elicit professional judgment.* A number of procedures have been proposed for forming expert panels and eliciting professional opinion. It is important to capture diverse views within any expert panel.
- *How to incorporate uncertainty into the assessment.* There is uncertainty associated with each population attribute because of inherent variation in biological processes, scientific uncertainty about biological relationships, and uncertainty about data quality and measurement error. These different sources of uncertainty need to be explicitly identified and communicated during the risk assessment process.
- *How to handle attributes for which no information is available.* For some attributes, there may be no data available. For example, few locations currently have facilities to assess JOMs, and it is unlikely that JOMs can be assessed for every population. The assessment process needs to consider any additional risk associated with ignorance about a particular attribute.
- *How to account for the inherent correlation among all the population attributes.* All population attributes are expected to be correlated with one another to some extent. For example, the abundance of a population is correlated with its diversity, because processes like genetic drift are a function of population size. Habitat attributes are expected to be highly correlated with all the other attributes, particularly spatial structure (see Section 8). It is useful to consider each attribute separately because each one provides some independent information, but the correlations must be taken into account in weighting the value of each attribute into an integrated population persistence category.

In Appendix C we describe our approach to assigning persistence categories to populations. We intend to apply the method by assessing the current status of WLC populations. As the approach is applied, it may be modified as more is learned about the integration process.

4. POPULATION PRODUCTIVITY AND ABUNDANCE CRITERIA

ADULT POPULATION PRODUCTIVITY AND ABUNDANCE CRITERIA GUIDELINES

1. In general, viable populations should demonstrate a combination of population growth rate, productivity, and abundance that produces an acceptable probability of population persistence. Various approaches for evaluating population productivity and abundance combinations may be acceptable, but must meet reasonable standards of statistical rigor.
2. A population with a non-negative growth rate and an average abundance approximately equivalent to estimated historical average abundance should be considered to be in the highest persistence category. The estimate of historical abundance should be credible, the estimate of current abundance should be averaged over several generations, and the growth rate should be estimated with an adequate level of statistical confidence. This criterion takes precedence over criterion 1.

Overview

Key Issues

If a population experiences an unabated decline, it will eventually go extinct. This is true no matter how large the initial population or the cause of the decline. Thus, one of the primary metrics of population viability is an estimate of the long-term growth rate of the population. However, even if a population is not experiencing a long-term decline, there is some probability that it can go extinct. A population that is, on average, stable or increasing can go extinct as a result of stochastic (i.e., random) factors, which operate most strongly at small population sizes or as a result of catastrophic or other environmental events that may be independent of population size. The likelihood that a nondeclining population will go extinct is a function of the population's productivity.³ In these population productivity and abundance criteria, we focus on the processes that can lead to extinction of small populations. We address issues of size-independent catastrophic risk in the context of habitat criteria and in the context of ESU-level criteria.

The unit to which productivity and abundance criteria are applied can be very important. The appropriate unit for the criteria we have developed is a demographically independent population as described in McElhany et al. (2000). The demographically independent population concept is applied in the WLC domain in the draft TRT document identifying populations (Myers et al. 2002). The population units described in that document are used for the productivity and abundance criteria that follow.

³ The term intrinsic productivity refers the number of recruits per spawner that would occur at very low spawner abundance (i.e., if there were only a single pair of spawners). In this section, we use the more generic term productivity to refer to the general tendency of a population to return to dynamic equilibrium abundance if perturbed below that abundance. A population with high productivity would be considered resilient and have a relatively low risk of extinction.

As described below, a number of approaches can be used to set productivity and abundance criteria. Each approach is limited by its own critical assumptions and data requirements. The TRT recommends using the population change criteria (PCC) approach as a default method for setting productivity and abundance viability criteria. However, the default method involves only a general approximation of extinction risk and should be replaced with more detailed analyses when such analyses are supported by the data.

Approaches Considered

The TRT considered three basic approaches to estimating minimum population size. One approach relied on population viability analysis (PVA) modeling, in which minimum size thresholds were determined by estimating extinction risk as a function of the population size and other parameters. The other two approaches relied on estimation of historical abundance. The first of these was estimates of the historical population abundance based on broad-scale habitat-capacity analysis. The second historical approach was habitat productivity viability analysis (HPVA) modeling, as conducted by the Washington Department of Fish and Wildlife (WDFW) and the Northwest Indian Fisheries Commission (NWIFC). HPVA also uses habitat information, but makes productivity and capacity inferences based on fish-habitat relationships. For reasons explained below, we relied more on PVA than on the historical approaches in setting viability criteria.

In the PVA modeling, we focused on the role of environmental variation in identifying the minimum population size criteria. The risks confronting small populations include demographic stochasticity, environmental stochasticity, Allee effects, and genetic problems associated with inbreeding or the accumulation of deleterious mutations. Theoretical evidence suggests that in many cases the primary factor limiting the viability of small populations with nonnegative growth rates will be environmental stochasticity or catastrophes (Lande 1988 and 1993). Environmental stochasticity refers to the fluctuations in survival and fecundity associated with random environmental events. Even if a population is, on average, not declining, a chance sequence of bad years may drive a small population extinct, whereas a larger population would persist. Salmon are recognized as being highly variable in abundance, suggesting an important role for environmental stochasticity in setting minimum viable population sizes. Another key factor affecting extinction risk is a population's productivity or resilience, defined as its tendency to return toward equilibrium if pushed to low abundance.

The sections below and several appendices provide details on the PVA models, including the relationships between productivity, abundance, variability, and extinction. Specifically, we focus on two PVA-based analyses: the PCC approach and a two-life-stage recruit per spawner model. The PCC is considered the more precautionary of the two approaches.

We also evaluated to what extent historical abundance information could be used to develop viability criteria and to inform viability criteria developed by other methods. If we define historical as the time of pre-European settlement, most populations are assumed to have been viable at historical abundances and large enough to persist in the presence of natural environmental variability. Therefore, historical abundance could generally be used as a precautionary viability criterion. However, some populations, as defined in Myers et al. (2002), were relatively small, inhabited relatively unstable environments, and historically may have not have met the criteria of a viable population. For the majority of populations that were historically

viable, it is difficult to know whether historical abundance represents a minimum viability threshold. It is quite conceivable that a population below historical abundance levels would not be in danger of extinction. Allowing that populations below historical abundance may be viable, we explored the possibility of a viability criterion based on some specified fraction of historical abundance. The difficulty of this approach is that there is no clear way to link a fraction of historical abundance to viability except for the general (unquantifiable) statement that the closer a population is to historical abundance the more likely it is to be viable. It is also difficult to link historical abundance to viability, because simply looking at abundance does not provide information about resilience. Because there is no clear link between the fraction of historical abundance and viability, we relied primarily on the PVA modeling to obtain quantitative abundance viability criteria.

Estimates of historical abundance do, however, play an important role in the viability criteria by providing an upper bound on abundance criteria. As described in more detail below, a great deal of uncertainty is associated with the PVA modeling-based criteria. If the PVA modeling suggests a viable threshold abundance that exceeds the estimated historical abundance, the criteria use the historical abundance. This is because the thresholds established by PVA modeling (at least the population change criteria) are largely generic criteria applied to all populations in an ESU, and the circumstances in any given individual population may have allowed persistence at lower abundance than that suggested by the more generic standard. Although the PVA modeling threshold was considered generally appropriate, if credible historical analysis suggests that a population persisted at a lower abundance, the historical abundance was adopted as the viability criteria. Historical abundance was estimated based on a broad-scale habitat analysis (page 38 and Appendix I) and HPVA modeling (page 39 and Appendix J). Limited data based on historical surveys were also available for some populations, but in general these provided poor quantitative estimates of historical abundance (Myers et al. 2002).

The third approach considered in determining population abundance criteria was the HPVA modeling, as conducted by WDFW and the NWIFC and as described in Puget Sound TRT documents (PS-TRT 2002). HPVA is a specific application of the ecosystem diagnosis and treatment (EDT) method (Lichatowich et al. 1995, Mobernd et al. 1997) currently used in recovery planning. It uses up to 45 habitat and landscape attributes to predict the abundance, productivity, spatial distribution, and diversity of a population under particular habitat conditions. This approach does not identify a population viability threshold, but rather describes fish population attributes that would be expected under given habitat conditions. Because this analysis is not clearly related to extinction risk, we did not use HPVA analysis to establish viability criteria except as it informs the estimates of historical abundance. The EDT model can be evaluated under estimated historical habitat conditions to provide an estimate of historical population abundance. Although EDT documentation cautions against using the model as a predictive tool, HPVA results can produce qualitative information on historical abundance. HPVA for the WLC domain are provided in Appendix J. Although of limited application regarding productivity and abundance viability criteria, the HPVA analysis may be useful for developing other recovery planning goals. For example, HPVA information is being used to develop recovery targets for Puget Sound salmon species (Shared Strategy 2002).

PVA Modeling

Overview

This section provides a brief description of the PVA modeling approaches for setting productivity and abundance criteria. For a more complete explanation of conceptual underpinnings, assumptions, parameter estimation techniques, caveats, and references see Appendices D-H on PVA models.

A population with an unabated long-term decline will eventually go extinct. Thus, an intuitive viability threshold is the point at which a population replaces itself every generation and there is no long-term decline. This intuition is supported by PVA models, which indicate that long-term growth rate is one of the most informative predictors of population extinction risk. The median annual growth rate of a population, λ , can be estimated from an abundance time series as:

$$\hat{\lambda} = e^{\mu},$$

$$\mu = \text{mean} \left(\ln \left(\frac{N_{t+1}}{N_t} \right) \right)$$

where N_t is the population abundance at time t . The critical value occurs where λ equals 1. If λ remains less than 1, the population will eventually go extinct. If λ remains greater than 1, the population will increase. Since the growth rate and minimum-size criteria are intertwined, they are discussed together in the material below.

Even if a population is, on average, not declining, there is still some probability that it will go extinct because of chance fluctuations in population abundance. The environment is variable, and a chance sequence of bad years may drive a population, particularly a small population, to extinction. The probability that a population “bounces” to extinction because of environmental variation depends on the size of the population, the amount of variation, and the population’s resilience, that is, its tendency to return toward an equilibrium value if pushed to low abundance. Resilience can be estimated as the intrinsic productivity of the population: intrinsic productivity is defined as the number of returning fish per spawner that would be produced if the population were at very low abundance. All else being equal, a population with higher intrinsic productivity has a lower extinction risk than a population with low intrinsic productivity. This is because a population with a high intrinsic productivity is likely to return to high abundance if pushed to low abundance by environmental variation, whereas a population with a low intrinsic productivity is more likely to stay at lower abundance, making it more susceptible to extinction during the next period of poor environmental conditions. Although a convention of population biology, the term intrinsic productivity may be somewhat misleading in that it suggests the value is an inherent property of a species, when in fact it is a function of both the species’s biology and the environment (which can change).

A generic approach to identifying a viable productivity-abundance criterion is to estimate extinction risk using a population dynamics model and determine the threshold at which productivity and abundance parameters just yield an acceptable risk. The results of these sorts of analyses can be plotted in a viability curve, on which every point represents a productivity-abundance combination with identical extinction risk (Figure 4.1). Two key issues in developing

a specific method from this generic approach are defining the form of the population dynamics model used to estimate extinction risk and determining the method for estimating the model parameters. We explored a number of different functional forms for the population projection model and methods of estimating parameters (Appendices D–H). All the projection models we examined are variations of a spawner-recruit model. Spawner-recruit models use a relatively simple function to predict the average number of recruits produced by a given number of spawners. Recruits can be defined in terms of different life stages (e.g., JOM, pre-harvest, returning spawners). Figure 4.2 illustrates a number of different potential spawner-recruit relationships. The slope of the curve at the origin (near 0 spawners) is considered the intrinsic productivity of the population as defined above and is of critical importance in estimating extinction risk. A central distinction among the different approaches we explored to set criteria is the method used to estimate this productivity parameter. Our analysis suggests criteria not be based on a single method, but rather on a hierarchical approach to parameter estimation that is driven by the information content of the data. Where the data allow, an approach that involves fitting spawner recruit curves may be more appropriate; where the data are sparse, the PCC approach may be most appropriate. Both approaches are described below.

In using PVA models to define a viability curve (Figure 4.1), we attempt to identify threshold conditions that just produce an “acceptable extinction risk.” A statement of acceptable risk may be phrased as “an X% probability of declining to lower threshold of spawners in Y years.” The lower threshold could be either true extinction (i.e., 0 fish) or a quasi-extinction threshold (QET). The QET represents an abundance below which the population should not go because it would experience a greatly elevated extinction risk as the result of processes other than environmental stochasticity, or because uncertainty about population behavior is highly elevated. Two factors contributing to highly elevated extinction risk at very low abundance are demographic stochasticity and increased risk of permanently losing genetic variability. The X and Y values in the risk statement are largely policy decisions about what is legally and socially acceptable. Guidance from NOAA Fisheries suggests a 5% probability in 100 years is appropriate for defining a viable population threshold (*sensu* McElhany et al. 2000). A number of different time periods are discussed in the context of these criteria (Table 4.1).

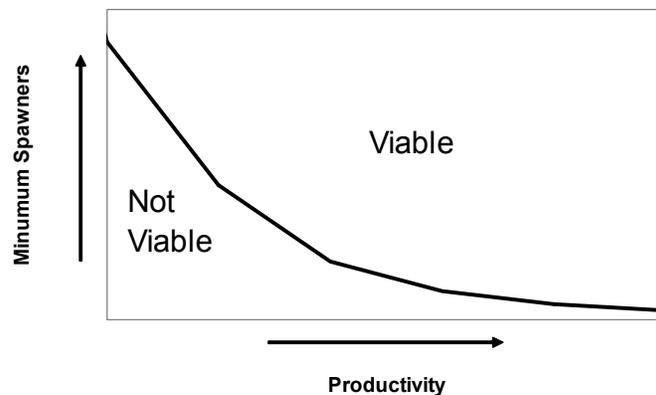


Figure 4.1 Conceptual graph of the relationship between productivity, population size, and extinction risk. The curve represents combinations of size and productivity that exactly have the acceptable extinction risk.

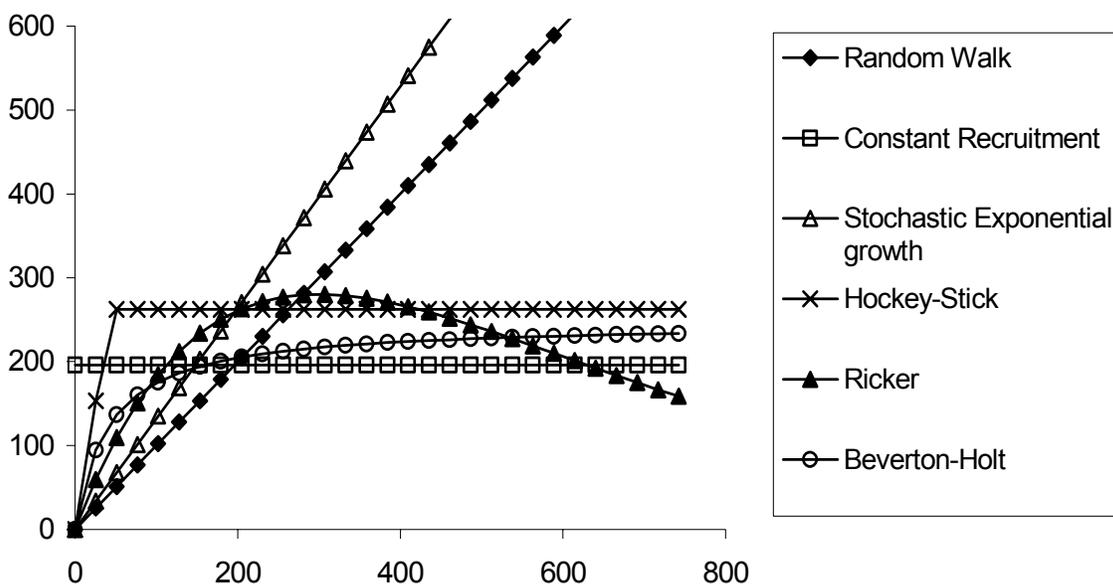


Figure 4.2 Different types of spawner-recruit curves.

Table 4.1 Definitions of time intervals used in discussion of population productivity and abundance criteria.

Time Interval or Period	Definition
Historical period	Period just prior to Euro-American impact on salmon populations and habitat.
Recent time series	Period encompassing recently collected time series of abundances. Most time series start after the 1960s.
Observation period	This is the period over which a population will be evaluated to determine if it is viable. For delisting decisions, this is likely encompasses the period from the present to some point several decades in the future.
Extinction risk time horizon	This is the period over which we expect the population to persist with some probability. For PVA modeling, we evaluated periods of 100 years into the future
Running sum length	In setting the population change criteria, the exact method used relies on a running sum of the abundance data. The length of the running sum used for this analysis was four years. The current size and target size for the population change criteria are reported as the four-year average, not a running sum.

Fitting Spawner Recruit Curves

In fisheries biology, a common approach to estimating the parameters of spawner-recruit models is to statistically “fit” spawner-recruit curves to abundance data. Spawner-recruit data can be visualized by plotting the number of recruits against the number of spawners. Table 4.2 shows sample spawner-recruit data and a number of different curves fit to that data. To use a spawner-recruit analysis to estimate extinction risk, it is necessary to determine which, if any, recruitment functions provide an adequate approximation of the data and to determine the degree of confidence in the parameter estimates. In Appendix G, we attempt to fit a number of different potential recruitment functions to recent spawner-recruit data from salmon populations in the WLC, where recruits are defined as either returning spawners or preharvest adults. A key conclusion of this analysis is that the examined abundance data provide very little statistical power to estimate spawner-recruit relationships. That is, the data are not very informative about either the form of the recruitment function or parameters such as intrinsic productivity. This is unfortunate, because an accurate description of the spawner-recruit relationship, particularly the relationship at low abundance, would greatly aid in assessing population extinction risk.

The poor fit of the recruitment functions is likely due to a combination of factors including measurement error, environmental stochasticity (especially in the ocean), the lack of contrast in spawning escapement due to the constant infusion of hatchery spawners, and uncertainty about the reproductive success of hatchery spawners. One response to the problem of a poor fitting spawner-recruit curve is to try to improve the fit by collecting better data. Part of the reason that fitting spawner-recruit curves may be so uninformative in many populations is the high levels of measurement error in the abundance or age structure estimates. If the data had fewer errors, the spawner-recruit parameters could be estimated with better accuracy and precision. However, lower measurement error may not solve all the problems of fitting recruitment functions. Accurate parameter estimation requires a relatively large number of data points from a stationary time series, with adequate “contrast” in the spawner abundance. These issues are discussed in more detail in Appendix G.

Given that it may not be possible to precisely estimate productivity from fitting spawner-recruit curves with adult data for many populations, we considered several alternatives.

- It has been suggested that an average recruit per spawners value calculated using the low spawner abundance data points could provide important information about the resilience of a population (Chilcote⁴). This method does not fit a spawner-recruit curve and does not estimate “true” intrinsic productivity, but could provide a precautionary estimate of its value. The statistical properties of this approach, and the conditions under which it could be deployed, have not been rigorously explored, but the approach holds promise for development into a viability metric.
- By partitioning the projection model into multiple life stages, extinction risk may potentially be better assessed. Below and in Appendix G, a two-life-stage model is explored that partitions the life cycle into freshwater and marine life stages. Some variability that contributes to the poor fit of adult spawner-recruit curves can be accounted for in a multi-life-stage model, therefore parameters may be better estimated. Evaluating extinction risk with this type model requires accurate

⁴ Mark Chilcote, Oregon Department of Fish and Wildlife, Portland Oregon, personal communication, February 2003.

abundance estimates at multiple life stages (e.g., both adult spawners and juvenile outmigrants).

- Observed population growth rate can provide a precautionary estimate of the productivity of a population. This concept was developed into the PCC described below and in Appendices D–F. Although the method does not estimate the true spawner-recruitment relationship, it can be applied to any time series of abundance, and the statistical properties of the approach are reasonably well understood.

Two-Life-Stage Projection Model

Extinction risk is largely determined by the productivity or resiliency of the stock. Analysis of Columbia River chinook salmon marine survival patterns indicates that marine survivals do not randomly vary but follow a pattern at the decadal scale; that is, decades of high and low marine survival. This indicates that extinction risk is not likely to occur at random, but during periods of low marine survival. Therefore, extinction modeling using recruitment functions should be developed with marine survival, an index of marine survival, and/or another measure of ocean productivity. Appendix H explores an approach to setting viability criteria in which density dependence is assumed to occur in the freshwater life stage, and marine survival is considered a density-independent factor driven by the environment. Criteria developed using this approach would likely demonstrate that, based on the model, a population has sufficient freshwater productivity and capacity to persist in the face of hypothesized future marine survival patterns. With this approach, there is no single freshwater productivity and capacity target, as multiple combinations of productivity and capacity could produce identical extinction risks. Instead of a single *a priori* target, the approach could potentially be used retrospectively to evaluate whether a population has improved enough to have an acceptably high probability of persistence.

In Appendix H, the approach is applied to evaluate the current status of the Wind River steelhead population. Model parameters were fit using the spawner and smolt data, and a forward project of abundance was modeled under a number of hypothesized future ocean survival patterns. The Wind River data have not yet been analyzed using a formal model selection procedure like that described in Appendix I. The current Wind River data set consists of only seven data points, and it would not meet the standards of statistical rigor required for extinction analysis. However, as more data are collected, this approach could be used.

Population Change Criteria

Overview

The PCC approach is a novel method of developing viability criteria. With this approach, productivity is estimated from the observed growth rate of the population, not from fitting spawner-recruit curves. If a population grows at a given rate, it is assumed in the PCC approach that its average productivity is at least as high as the growth rate estimate. Because of the potential influence of density dependence, the population's intrinsic productivity may actually be higher than the observed growth rate, so the approach is precautionary in applying the criteria

and is unlikely to result in prematurely concluding that a population is viable. This approach addresses the question, “Given the current population size, what growth rate does the population need to exhibit over a given number of years to just achieve an acceptably low extinction risk?” The approach is a performance metric for assessing viability. Details on the approach are provided in Appendix D and a computer program to calculate the criteria is available on the Web at http://research.nwfsc.noaa.gov/cbd/trt/trt_wlc/viability_report.htm.

The forward projection model used for the PCC approach is a hockey-stick recruitment model. The PCC approach involves identifying the average growth rate for the population over Z years that just produces an acceptable extinction risk. As illustrated in Figure 4.1, the extinction risk of a population is a function of both the productivity and abundance of the population. As a consequence, the target growth rate (productivity) is a function of the population’s initial size. To calculate the extinction risk associated with a given combination of current abundance and growth rate, we must have estimates of all the parameters needed as input to the extinction risk model: environmental variance, QET, time horizon, initial size, productivity, and capacity. The environmental variance for a population is estimated from recent time series; the QET is set at 50 spawners, based on demographic and genetic concerns; and the time horizon was evaluated at 100 and 200 years. The estimate of productivity is based on the estimate of population growth rate. By knowing a population’s current size and how big it gets in a given amount of time, its target size, we can estimate its growth rate. The initial size parameter in the population extinction model is the target size of the PCC. The model is parameterized so that if the population achieves the growth rate target in the specified time, it would not need to continue growing but would still be considered viable if it stabilized at the final abundance. Calculating the target size requires estimating the environmental variance and the growth rate of populations. These parameters are estimates; there is uncertainty about their true value. This uncertainty is incorporated into the calculation of extinction risk by using the parameters’ probability distributions, not the point estimates. In this way, the target sizes and associated growth rate explicitly include parameter uncertainty. The criteria estimated with the PCC approach can be expressed either as target abundances or as growth rate. For ease of communication and because it better reflects the key parameter of the analysis, we present results in terms of observed growth rate.

The PCC is a population performance test rather than a statement of how many fish are needed for viability, and is in many ways different from other approaches the TRT considered. Understandably, a number of concerns were raised about the PCC approach; they are addressed in Appendix F.

Complications in Estimating Productivity Addressed with PCC

In the PCC approach, productivity is estimated as the change from the current population size to target size in a given amount of time (i.e., growth rate). This is a relatively straightforward calculation for a population of natural spawners. However, if hatchery-origin spawners are present in the population, the approach must be modified to estimate the natural productivity of the system. For a given acceptable level of risk, the target sizes are often substantially higher if hatchery spawners are part of the system than if they are not.

In the base calculations, we assume that the productivity, estimated as a change from the population’s current size to target size, is typical of the long-term average productivity. However, salmon respond to “regime shifts” in productivity, in which several decades of higher-

than-average marine survival may be followed by several decades of lower-than-average marine survival. To incorporate these regime shifts into the targets, the population productivity estimate is modified by a marine survival factor. This factor is a function of the difference between marine survival over the observation period and the long-term average. If marine survival over the observation period is higher than the long-term average, the target size needs to be higher than if the marine survival over the observation period matches the long-term mean. Because of uncertainties about marine survival patterns, this modification is applied asymmetrically: target sizes are raised if marine survival over the observation period is higher than average, but they are not lowered if the marine survival over the observation period is below the average. The marine survival modifications can only be applied after the observation period has passed, which makes it difficult to fix the target size at the outset.

Example Output of Population Change Criteria

An example output of the PCC approach is shown in Table 4.3. It is important to note that the growth rate targets are a function of the length of the observation period. The example in Table 4.3 uses an observation period of 20 years. Given the need to estimate population parameters with confidence, and the decadal scale shifts in marine survival described above, 20 years of data may be required before robust conclusions about viability can be made. A computer program for calculating population change criteria based on user-provided input is available on the Web at <http://www.nwfsc.noaa.gov/crri/programtest/salmonmodels.htm>.

In Tables 4.2 and 4.3, the extinction probabilities are the probability of declining to a four-year annual average of 50 spawners; they are calculated using population prediction intervals with 20 degrees of freedom for the variance estimate. The point estimate of the variance

Table 4.2 Growth and abundance viability criteria expressed as growth rate. The percent risk is the probability of declining to a four-year annual average of 50 spawners within 100 years.

Starting Population Size ^a	Average Growth Rate Observed Over 20 Years ^b			
	60% Risk (Persistence Category 1)	25% Risk (Persistence Category 2)	5% Risk (Persistence Category 3 (VSP))	1% Risk (Persistence Category 4)
<150	200 spawners	400 spawners	800 spawners	1,400 spawners
150–500	2%	6%	11%	15%
500–1,000	–1%	4%	9%	13%
1,000–1,500	–2%	2%	8%	12%
1,500–2,000	–3%	2%	7%	12%
2,000–3,000	–3%	2%	7%	11%
3,000–4,000	–3%	1%	7%	11%
4,000–6,000	–4%	1%	6%	11%
6,000–8,000	–4%	0%	6%	11%

^a The starting population size is estimated at the beginning of the period being evaluated for viability.

^b The productivity viability metric is the average annual productivity that would need to be observed over a 20-year observation period. Modification of the productivity would be required if hatchery fish are present or if the observation period occurred during a period of higher than average marine survival.

Table 4.3 PCC productivity criteria for conditions where hatchery fish are present or marine survival over the observation period differs from the long-term average.^a

Starting Population Size ^b	Average Growth Rate of Natural-Origin Spawners Observed over 20 Years ^c			
	Effective Fraction of Hatchery-Origin Spawners ^d			Assuming Ocean Survival Is Twice Long-Term Average ^e
	5% Hatchery	10% Hatchery	30% Hatchery	
<150	1,400 spawners	2,900 spawners	>3,000 spawners	1,300 spawners
150–500	15%	20%	>21%	14%
500–1000	13%	19%	>21%	13%
1000–1500	13%	18%	>21%	12%
1500–2000	12%	17%	>21%	11%
2000–3000	12%	17%	>21%	11%
3000–4000	11%	16%	>21%	11%
4000–6000	11%	16%	>21%	10%
6000–8000	10%	15%	>21%	10%

^a The extinction risk associated with these criteria are 5% in 100 years, the same as in column four in Table 4.2.

^b The starting population size is estimated at the beginning of the period being evaluated for viability.

^c The productivity viability metric is the average annual productivity that would need to be observed over a 20 year observation period.

^d If hatchery fish are present and effectively spawning, the observed growth rate needs to be higher because of hatchery masking effects.

^e If the marine survival over the observation period is higher than the long-term average marine survival, the observed growth rate needs to be higher to provide an equivalent long-term extinction risk.

used to generate these targets is 0.05. The current abundance values for WLC populations are shown in Appendix D. The growth rates in Table 4.2 assume that 0 hatchery-origin spawners are present in any of the populations in the next 20 years. (If hatchery-origin fish are expected, see Table 4.3 for examples). The targets also assume that the average of the marine survival index in the next 20 years is equal to long-term average marine survival.

Conclusions Regarding PVA Modeling Approaches

We recommend a data-driven approach to PVA-based viability criteria. Where data are sufficient, fitting spawner-recruit curves can provide a good retrospective analysis of population viability. Since a number of potential spawner-recruit curves could potentially be viable, we are not recommending a single curve as a viability target. In many cases, the collection of data on multiple life stages could provide a better estimate of population viability than a spawner-recruit curve that concentrates only on adults. Again, evaluation of viability would be retrospective, and we are not recommending a single set of parameters for a multi-life-stage model as criteria. The approach of estimating productivity and abundance target combinations based on estimates of average recruits per spawner using low-abundance data points has promise, but is not yet fully developed. The PCC have the least data requirements and can be estimated in advance to provide target criteria for most all populations. However, the PCC may be overly precautionary in some cases, and an effort should be made to apply one of the other methods if data are adequate. Since

the PCC can be applied to all populations based on current information, and viability with the other approaches will likely be only evaluated retrospectively, we recommend that the PCC serve as default criteria.

Historical Abundance

Historical Abundance Estimates Using Broad-Scale Habitat Analysis

Historical abundance can potentially be estimated from a study of historical habitat quantity and quality. Such analyses are likely to produce results with a high level of uncertainty because they require estimating both historical habitat conditions and associating fish abundance with habitat condition. Nevertheless, historical habitat analysis can inform viability criteria by suggesting some upper bounds on target abundances. The HPVA discussed below attempts this type of calculation using a relatively large number of habitat variables that require estimating a relatively large number of quantitative relationships between habitat attributes and population response. The broad-scale analyses conducted by Steel and Sheer (Appendix I) estimates fish densities implied by a range of population viability criteria for both currently and historically available habitats. These analyses are based on relatively few habitat attributes, which can be estimated from available data.

The approach to broad-scale analysis undertaken taken by Steel and Sheer partitions the WLC domain into different habitat types based on remotely sensed data and on digitally available and spatially referenced field data. These data allow habitat partitioning based on features such as accessibility, stream gradient, stream width, etc. It would be theoretically possible to estimate historical abundance of a population by multiplying an estimate of the fish density associated with each habitat type by the quantity of that type available, then summing all the different habitat types. However, such an approach would require good estimates of the species densities associated with each habitat type, and the analysis could become very complex as issues of density dependence at different life stages are introduced.

Rather than estimate historical abundances per se, we have taken the approach of estimating population targets via demographic modeling, then evaluating whether the targets would be associated with reasonable historical fish densities. In attempting to identify reasonable fish densities, we can divide fish density into three categories: (1) clearly historically achievable, (2) clearly historically unachievable, and (3) historical achievability unknown. It should be possible to identify these regions without having to specify all the parameters needed to generate an estimate of historical abundance. The regions could be identified based on observations of currently “healthy” populations. If the population targets developed by demographic modeling fall into category 1, we will accept the demographically derived target as the criteria. If the target falls into category 2, we may need to look more carefully at the demographic modeling assumptions. If the target falls into category 3, further analysis will be required to evaluate the historical abundance of the population.

Thus far, habitats throughout the WLC domain have been categorized into types based on a number of features. Tables were developed that estimate the densities associated with some example population targets, based on channel gradient and on currently and historically accessible stream lengths. We have not yet evaluated whether these densities are reasonable. Furthermore, the process of categorizing the habitat is undergoing refinement. As the approach

develops, it may ultimately be possible to provide the “credible estimates of historical abundance” described in the viability criteria for situations in which the historical abundance may have been lower than the demographically established target.

Historical Abundance Estimates Using HPVA

Habitat population viability analysis (HPVA) is a specific application of the ecosystem diagnosis and treatment (EDT) method (Lichatowich et al. 1995, Mobrand et al. 1997) currently used in recovery planning. It uses up to 45 habitat and landscape attributes to predict abundance, productivity, spatial distribution, and diversity of a population under particular habitat conditions. The basic method for running an HPVA of a watershed for a particular species is as follows:⁵

1. Stream reaches are defined by delineating the geographic scope, describing environmentally homogeneous reaches, and coding the basin hydrography, indicating the direction of water flow and the spatial relationship of tributaries in such a way that it can be understood by a computer program.
2. Information on the species’ life-history parameters is incorporated into the model. These include juvenile age at migration, juvenile migration pattern (spring or summer migrant, etc.) adult age at return, run-timing, ocean distribution, harvest rate and location, fecundity, and number of females by age.
3. As many as 45 habitat attributes known to affect salmonid performance are included in the database. Attributes include percent habitat types, stream substrate, channelization level, riparian condition, water quality and quantity, percent fine sediment, toxic substances, exotic species present, food, large woody debris, and many others. If measured data are not available, either professional opinion is used or the attribute is ignored altogether. In current analyses used by Washington State and tribal co-managers, four tiers of attributes are used: current conditions, PFC conditions, PFC+ conditions, and historical conditions. PFC conditions are attribute ratings based on the properly functioning condition values in the Matrix of Pathways and Indicators (NMFS 1996). PFC guidance for estuarine and marine habitats does not yet exist. The condition of these habitats was set at current for one analysis of otherwise PFC conditions (called HPVA_{PFC}), and at fully functional (historical) for another (called HPVA_{PFC+}).
4. The model is now run. Trajectories are used to estimate fish survival from egg incubation all the way through adult spawning. Briefly, a trajectory starts out in identified spawning reaches, then is moved through time and space by life stage as determined by the species’ biology. Hundreds of these trajectories are sent from a basin to determine its survival landscape. Randomness is included in the trajectories so that the full range of environmental conditions present in the stream is encountered. The model calculates and tracks the productivity and capacity of each trajectory through each stream reach. Trajectories that have productivity less than 1.0 are nonviable, thus are considered not to be used by the fish population being

⁵ Modified from a description by Bruce Watson of Mobrand Biometrics, Inc.

modeled. The productivity and capacity values of all trajectories are combined to determine the productivity and capacity values for the population, assuming a Beverton-Holt relationship. The difference in the number of successful trajectories under various conditions (e.g., historical versus current) is used to calculate a diversity index for the population. A run is done for each of the four tiers of habitat attributes, so productivity, capacity, and diversity are estimated for current, PFC, PFC+, and historical conditions.

Output from analyses run on Lower Columbia River populations are shown in Appendix H. HPVA data are only available for populations in Washington, therefore complete coverage is not available for any of the WLC ESUs. Moberland Biometrics, Inc. cautions against using the EDT model for predictive purposes: they state that its intended application is hypothesis generation. Therefore, although no confidence metrics are provided, values provided in the table should be considered highly uncertain. However, they do provide some hypotheses about historical abundance against which to compare the PVA model estimated targets.

Risk Characterization

Using PVA models provides the greatest opportunity to quantitatively relate any of the criteria to the 0–4 population persistence categories. For example, Table 4.2 shows how PCC could be related to persistence categories. If data are available, the other PVA models discussed above could also be used to calculate persistence probabilities. In addition to the PVA model approaches discussed above, other data, such as presence-absence information, could inform an evaluation of the risk status of a population. However, the other types of data generally have greater uncertainty regarding their relationship to viability, and we are not recommending their use as primary criteria. Any risk characterization that utilized metrics not clearly related to viability would likely result in the population being considered in a lower category because of increased uncertainty. As described in the criteria bullets, the estimate of historical abundance could be important in assigning the persistence category.

5. JUVENILE OUTMIGRANT GROWTH-RATE CRITERIA

JUVENILE OUTMIGRANT PRODUCTION CRITERIA GUIDELINES

1. The abundance of naturally produced juvenile outmigrants should be stable or increasing as measured by observing a median annual growth rate or trend with an acceptable level of confidence.

Definitions

Juvenile outmigrants (JOMs) are fish that are leaving a watershed. These are not necessarily smolts; the exact life stage depends on species and life history.

JOM abundance is based on cohort age for populations with multiple age classes in the outmigrating population. Abundance may be an estimate of total abundance or a standardized index of abundance.

JOM growth rate (λ_{JOM}) is the annual change in cohort-to-cohort abundance (whole population or index), estimated with a four-year running sum or a fitted trend (slope).

Overview

The TRT strongly supports the inclusion of JOM growth-rate criteria for assessing the viability of salmon populations. The criteria will contribute important information about the status of a population that cannot be obtained by exclusively monitoring adults. JOM monitoring has multiple benefits and should be a priority in all ESUs, particularly for populations in which freshwater habitat improvements are a major management goal. However, it is not clear whether all populations in an ESU need to be extensively monitored or meet the JOM growth-rate criteria. JOM monitoring should, at a minimum, be part of recovery planning for all populations designated to attain VSP status in an ESU.

Viability criteria based purely on abundance and spawner trends are problematic. Spawner numbers fluctuate for a variety of reasons, including harvest management, the influence of hatchery spawners, and long-period ocean productivity cycles that affect smolt-to-spawner survivorship. Populations may increase over a relatively short period due to good ocean conditions, even while freshwater productivity declines. This factor is particularly important for short-term recovery assessment, because ocean conditions are currently favorable for many populations and the number of returning spawners may increase rapidly. Spawner counts also give a poor indication of how well management actions are improving survival at various life stages. Efforts to improve freshwater habitat and survival will be difficult to evaluate without a benchmark at some other point in the life history. JOM production can serve as this benchmark and must meet minimum standards *in addition to* population growth and abundance criteria set for adults.

Several studies have shown a relationship between salmonid abundance or ocean survival rates and periodic shifts in the physical and biological characteristics of the North Pacific, such as the Pacific Decadal Oscillation (PDO) (Hare et al. 1999; McFarlane et al. 2000; Hobday and Boehlert 2001). Patterns in ocean survival can have a profound effect on the number of returning spawners with periods of rapid population increase that can mask changes in freshwater capacity and productivity (Lawson 1993; Bisbal and McConaha 1998; Tschaplinski 2000). Figure 5.1 illustrates how spawners and JOMs might vary in a population experiencing cycles in marine survival. Measures of JOMs and adult spawners may provide different types of information that are critical for assessing the long-term viability of populations. While JOM abundance should track adult abundance when the population is below carrying capacity, changes in freshwater habitat quantity or quality are better assessed by JOM productivity.

JOM monitoring is required for estimates of marine survival rates. Because the productivity and abundance criteria (Chapter 4) require a correction for ocean survival rate, a minimum number of populations must be monitored to ensure that the correction factor is

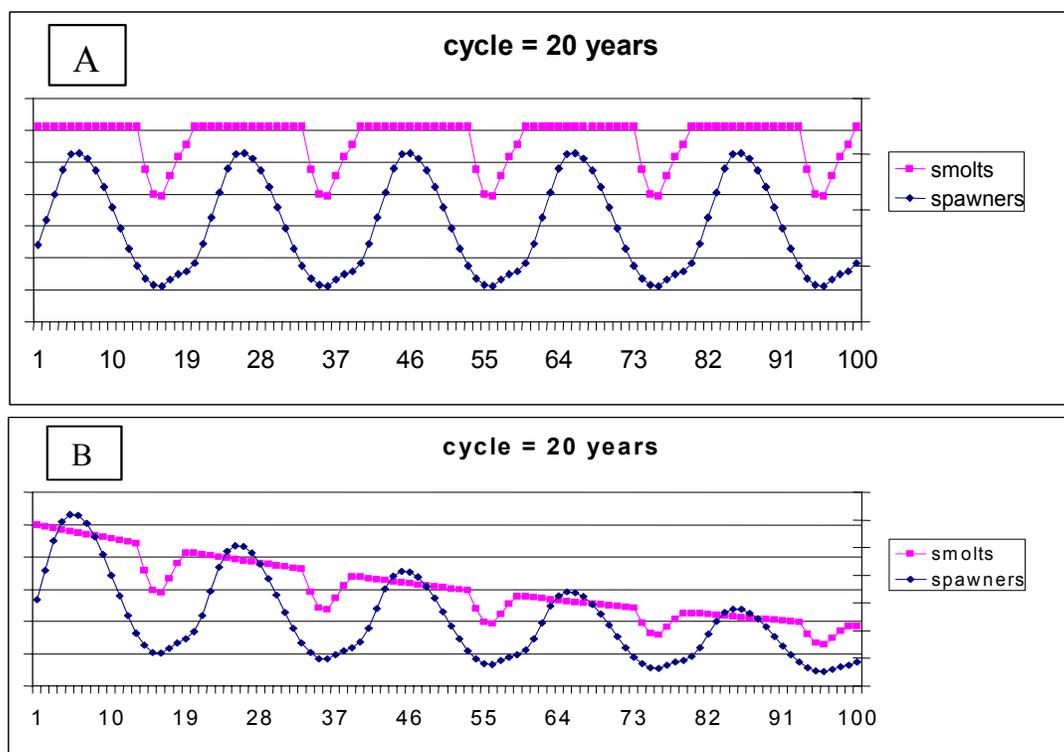


Figure 5.1 Hypothetical changes in spawner and smolt abundance in a 20-year cycle (sine-wave) of ocean survival. To make this example easy to interpret, no variability was added to the simulation. A hockey-stick, smolts-per-spawner function was applied. A. Freshwater capacity is constant through time. B. Freshwater capacity is declining at 1% per year. Note that the spawner growth rate remains positive for a much longer interval than the JOM growth rate; the difference depends on how quickly the recovering population reaches carrying capacity.

relevant to a given population. Currently, marine survival rates are primarily calculated with hatchery fish returns; this is insufficient, unless we are certain that marine survival rates for hatchery and wild fish are comparable. Likewise, because marine survival encompasses survival in the mainstem Columbia and estuary, we should expect that the rates would vary by stratum ecoregion and life-history type within an ESU. JOM monitoring in multiple populations is thus a critical part of population assessment and an important indicator of ESU viability.

Approaches Considered

The production of JOMs is an indicator of freshwater habitat productivity and capacity (Nickelson and Lawson 1998; Bradford et al. 2000; Sharma and Hilborn 2001). Although environmental factors and measurement error make JOM abundance highly variable from year to year, it is critical to assess the JOM growth rate and confirm that productivity is not decreasing in recovered populations. A decreasing trend in JOM abundance over a long period suggests deteriorating habitat quantity or quality. An exception to this would be a decrease in JOMs due to declining spawner abundance; in that case, a population would not be considered viable under the spawner growth and abundance criteria. Additionally, JOM abundance could decline if there was a decrease in the average age (and size) of spawning females. Under any of these three scenarios, a long-term decline in JOM abundance indicates a nonviable population. In computer simulations that include cycles of ocean survival rates, the JOM growth rate is consistently the best metric for correctly assessing changes in freshwater productivity and capacity when compared to other potential metrics, such as JOM/spawner or absolute JOM abundance (two-stage model, Appendix H). However, as with spawner abundance and growth, this metric of population health and recovery is only an accurate indicator when calculated over a relatively long period. This is because growth rate estimates and spawner abundance are both variable and are correlated.

Based on our current understanding of ocean productivity cycles, a minimum of 20 years of JOM abundance estimates are considered necessary to obtain an accurate assessment of population viability. Longer time series of λ_{JOM} should also increase confidence that a decline in productivity, freshwater capacity, or juvenile survival is not occurring.

Several other criteria for juvenile production were considered, including a minimum JOM/spawner, a minimum JOM population size (JOM_{min}), and a requirement for $\lambda_{\text{JOM}} \geq \lambda_{\text{spawner}}$. JOM/spawner may provide valuable information during early stages of recovery, when rearing habitat is below full seeding capacity. If freshwater habitat capacity and productivity are not in decline, we would expect no change in JOM abundance if spawning escapement is high enough to seed habitat to capacity, or an increase if spawning escapements have been lower than seeding levels. However, JOM/spawner may decrease dramatically as the juvenile population reaches freshwater carrying capacity; this may or may not indicate a problem in the freshwater habitat. If the JOM abundance is declining, then it is likely at least one of the following is occurring: (1) freshwater habitat quality or quantity is declining, (2) seeding levels (number of adult spawners) are declining below the level needed to produce the maximum JOM abundance, and/or (3) a Ricker relationship holds and high seeding levels are causing a decline in JOM abundance. If JOM are declining *and* JOM/spawner is declining, the most likely cause is a decline in freshwater habitat quality and quantity. However, at this time, the TRT feels that λ_{JOM} is the best

metric because of uncertainty about the effects of ocean cycles on adult survival rates and assumptions regarding the current and future carrying capacity of our watersheds. While JOM/spawner may be a valuable metric during the early stages of population recovery and restoration, density-dependent changes in survival can drastically alter this relationship over time. An accurate estimate of JOM/spawner may also be difficult to obtain and highly variable due to measurement error and monitoring locations.

Additional simulation exercises and population-specific productivity data may make it possible to develop more specific JOM criteria in the future. Many managers are predicting that both management actions and improving ocean conditions will lead to increases in adults and juveniles over the next few years. By monitoring JOM production, we will be better able to separate the causes of population change and evaluate habitat restoration activities. More generally, delisting criteria and population assessments for JOMs are the first steps toward monitoring and evaluation of the entire salmon life cycle. JOM counts are already conducted at a number of sites. While JOM surveys are difficult and potentially costly, they are feasible for many populations, and may ultimately save resources by improving our ability to assess both salmon populations and management actions.

Strategies Selected

The abundance of juvenile outmigrants in viable populations should be stable or increasing with an acceptable level of confidence. For populations with life histories that include multiple age classes in the annual JOM count, abundance should be determined by cohort year rather than the sum of JOM from multiple cohorts. The JOM growth rate can be estimated as:

$$\hat{\lambda}_{JOM} = e^{\mu_{JOM}},$$

$$\mu_{JOM} = \text{mean} \left(\ln \left(\frac{N_{t+1}}{N_t} \right) \right)$$

where N_t is a 4-year running average of JOM abundance, which may be an estimate of total JOM produced in a cohort year or an index of abundance that has been standardized for all populations within the ESU. The JOM growth rate should be determined by a running sum of 4 years to reduce variability caused by cohort strength. For example, if the assessment period is 20 years, only 16 estimates of N_t are used to determine the growth rate λ_{JOM} . In viable populations, λ_{JOM} should be ≥ 1.00 .

Alternatively, a trend in JOM abundance can be determined by regression analysis or a time-series analysis that incorporates autocorrelation. Each method will result in different confidence intervals and should be standardized within the ESU. A trend analysis may result in an acceptable level of confidence for $\lambda_{JOM} \geq 1$ in less than 20 years. However, we strongly advise long time intervals for assessment, due to the potential for decadal changes in marine survival rates.

If sufficient monitoring is in place to estimate spawner and JOM abundance by cohort year, a marine survivorship rate can be calculated simply as:

$$\text{marine survivorship} = \frac{\text{Spawners}}{\text{JOM}}$$

This marine survivorship estimate requires cohort-specific estimates of actual abundance, rather than indices of abundance. The productivity and abundance criteria require an estimate of marine survivorship at some level for an ESU, preferably for each stratum and optimally for each population, as populations vary in the amount of time spent in the ocean and estuary.

Critical Uncertainties

JOM abundance and growth rates may indicate freshwater habitat conditions, but the mechanisms of this relationship are still poorly understood. JOMs respond to habitat quality or quantity and environmental variability in unpredictable ways. The relationship between habitat quality and juvenile survival or other population-level metrics has not been assessed for most populations. Finally, most assessments of population response to density and habitat quality have been done in recent years, when stocks were declining or severely depleted. Improved ocean survival rates may drastically alter the number of returning spawners; management efforts that improve freshwater habitat quality may require new analyses of density-dependent relationships and changes in JOM productivity.

Computer simulations were used to evaluate a number of different JOM delisting criteria, including JOM/spawner minima and JOM abundance criteria. The goal of these exercises was to determine how often a given model correctly advises delisting under a wide range of “real life” scenarios, such as cyclical ocean conditions and various forms of density dependence. These exercises include a range of stock-recruit functions and other assessments of uncertainty, but they need to be improved and updated with new information. The simulations should include measurement error and explore the optimum criteria for a range of life-history types. Measurement error may be high for JOM monitoring, except in the rare cases where dam passage allows complete counts (Bradford et al. 2000; Phillips et al. 2000). Managers will need to develop appropriate monitoring and extrapolation methods that can be standardized within a population and, ideally, for all populations within the ESU. This will be a difficult task, as salmon life histories can be extremely complex. For example, several major life-history trajectories have been identified for spring- and fall-run chinook salmon. Chinook salmon and steelhead JOMs monitored at the mouth of a Lower Columbia River tributary will be from multiple cohorts due to the multiple life-history pathways in these species. Monitoring will require subsampling of JOMs to verify age-class and relate JOM abundance to cohort strength. This may be difficult if both fall and spring chinook JOMs are present in a watershed.

Monitoring and Evaluation

Population monitoring is an essential part of recovery planning and assessment. The TRT recognizes the potential difficulties of monitoring JOM production in all watersheds. These recommendations may be modified for each ESU, but represent our best professional judgment for general guidelines.

1. JOM abundance should be assessed annually in at least one population per stratum.

Monitoring should be integrated with efforts to assess changes in population diversity, habitat quality, and within-population spatial distribution, as well as efforts to monitor effects of restoration activities. This monitoring need not be restricted to JOM trapping; alternative mark-recapture estimates or other indices of abundance can provide good trend estimates, provided that methods are standardized among years.

Currently, JOMs are not censused in most populations. This lack of information reduces our confidence in stratum and ESU risk characterization, and will be reflected in the integration of population attributes used for population, stratum, and ESU assessment (Appendix C). The TRT strongly recommends the establishment of JOM monitoring at some level in all watersheds.

2. Methods for JOM assessment must be standardized within populations.

Rigorous monitoring and assessment methods for JOMs need to be established. There are three sources of variability to consider:

1. interannual variability, primarily due to environmental factors,
2. intra-annual variability among sites within a population, and
3. variability in estimate of JOMs at a given site due to methodology (e.g., mark-recapture estimation).

Estimates of abundance can be determined from mark-recapture of JOMs caught in traps, direct counts at dams, and index abundance measures. Most estimates of JOM are made using a trap efficiency method (Dempson and Stansbury 1991; Thedinga et al. 1994). Methods should be standardized in all cases where data are to be pooled, such as indices derived from multiple tributaries in a watershed, and general methods should be standardized for each ESU to allow statistical comparisons of population status. New statistical methods of smolt trap mark-recapture may be useful for standardizing JOM abundance estimates (Bjorkstedt 2000). Finally, if hatchery fish are present in the monitoring area, they must be marked to provide an accurate assessment of wild fish recovery.

It is unlikely that we can achieve an accurate estimate of total JOM production for an entire population, except in the rare case of a population that must pass through a dam. The best estimates of abundance may be obtained in small tributaries, but they may not be representative of the population. Thus, a pooled index of abundance may be the most feasible option. One approach that may provide good coverage across a stratum, with an adequate level of monitoring for trend estimation, is a rotational monitoring scheme that would measure abundance in multiple populations but staggered over multiple years. It is difficult to anticipate the level of uncertainty and measurement error *a priori* for each population or stratum, as so few populations are currently monitored. It may be possible to select an optimal strategy in the future, using a power analysis for predicting the maximum level of error in abundance that will lead to a detectable trend over various time intervals and number of sites. Figure 5.2 hypothetically illustrates what such a power analysis might look like for two levels of λ_{JOM} .

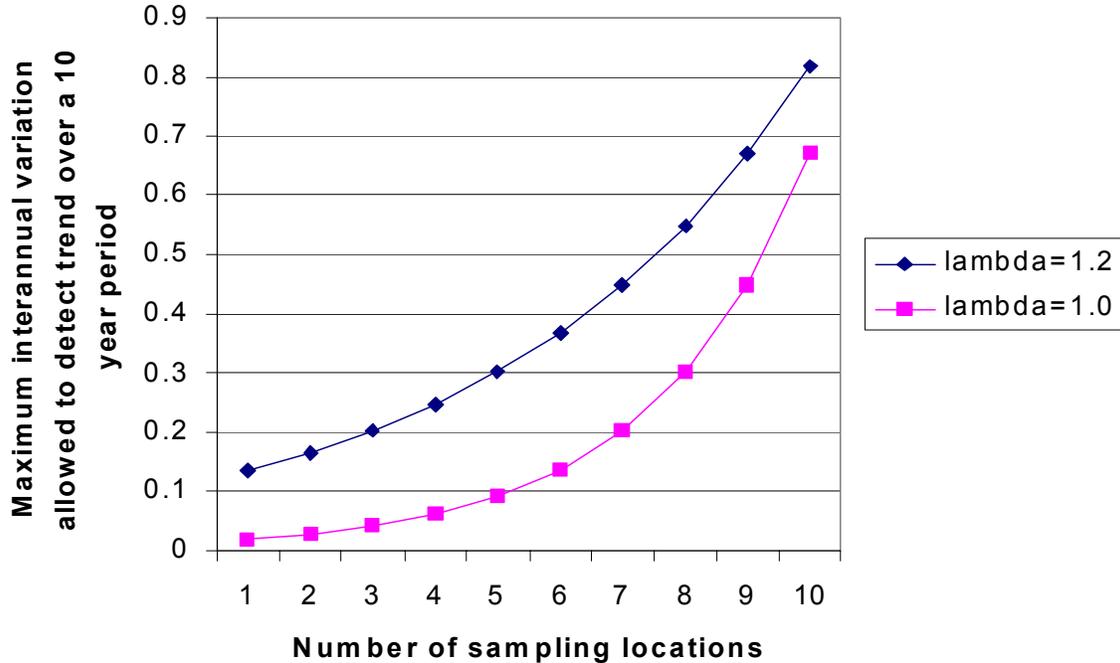


Figure 5.2 Hypothetical changes in the maximum intra-annual variability allowed for detection of λ_{JOM} , given an increasing number of samples. Detectability and confidence will depend on the number of years included in the analysis, as well.

3. An acceptable level of uncertainty in the growth rate estimate should be determined for each population.

Measurement error and year-to-year variability in JOM counts may lead to large confidence intervals for λ_{JOM} . Requirements for the appropriate confidence intervals or λ_{JOM} will depend on data quality and the methods used to determine JOM abundance in each population. Pooled counts from multiple tributaries in a watershed may reduce this variability. Most JOM abundance estimates for listed populations are likely to fall within plus or minus 25% because of the small sample sizes (fish abundance is low because they are listed) and low trap efficiencies (we tend to fish in the lower end of the basin in less flow to estimate the total population, and under these conditions trap avoidance is often high) (Schwartz and Dempson 1994). Within-year variability will be less critical with longer time series.

Figure 5.3 gives an example of three scenarios that might arise in an assessment of λ_{JOM} . For each example, the λ_{JOM} from a running sum and the λ_{JOM} estimated from a regression analysis are given. In Figure 5.3a, data variability within years is extremely high, leading to wide confidence intervals around each annual estimate. Figure 5.3b gives an example where within-year variability is moderate, but the number of years in the assessment is also low, reducing our confidence in λ_{JOM} . Figure 5.3c increases the number of years in the former example, and gives a good estimate of λ_{JOM} .

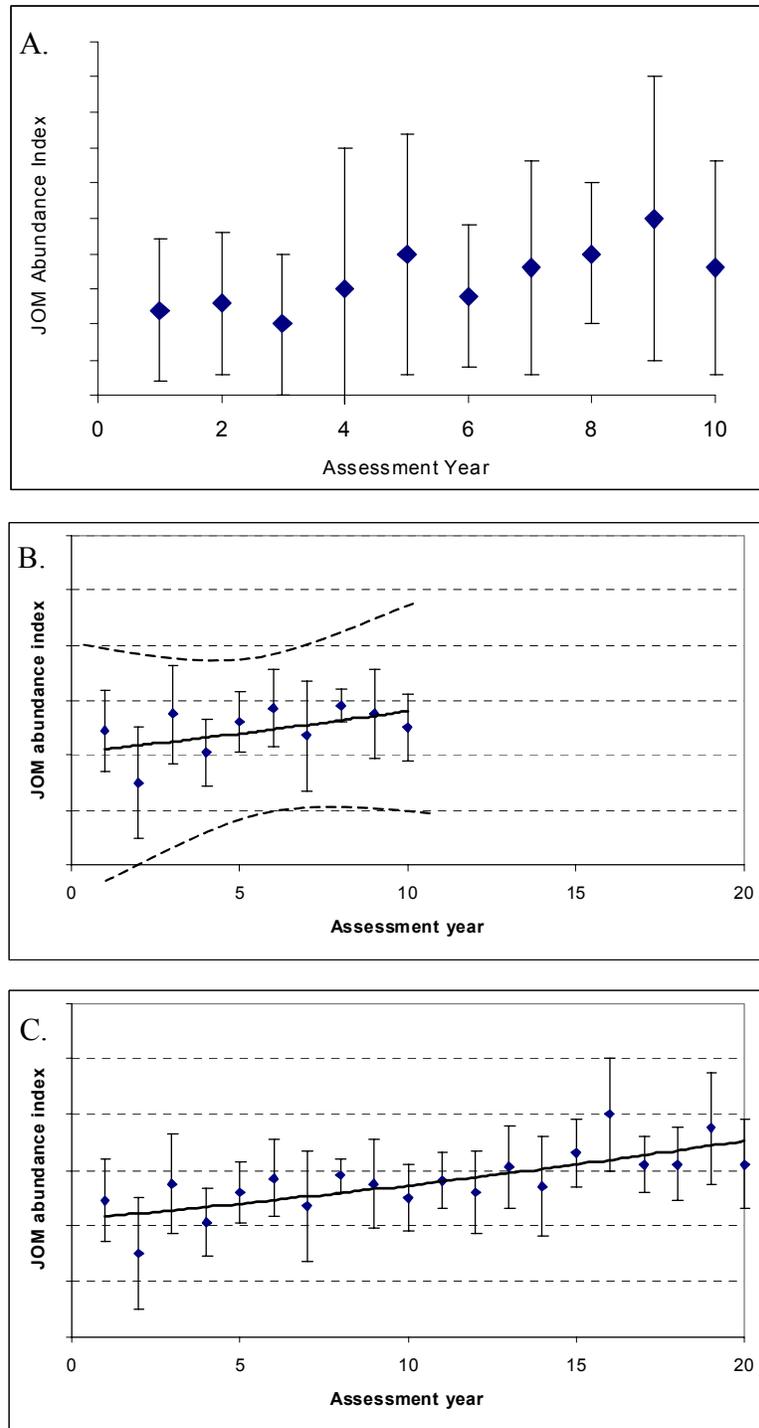


Figure 5.3 Three JOM abundance estimate scenarios, showing the importance of intra-annual variability for trend estimation. A. Visually, an increasing trend, but very high uncertainty in the estimate for each year reduces our confidence—this population could even be decreasing. B. A scenario with greater confidence in the abundance estimate each year, but too few years to be statistically confident in the trend. The dashed lines represent 95% confidence intervals for the slope given by the solid line. C. When additional years are added to scenario B, we are much more confident that the JOMs are increasing for this population.

Once a marine survivorship rate has been calculated for a population, it could be assumed to apply to other populations in that stratum. Thus, given the estimated spawner count by cohort year and a marine survival rate, the number of JOMs produced by a population could be back-calculated as follows:

$$\hat{JOM} = \frac{\text{spawners}}{\text{marine survivorship}}$$

This assumes that (1) the marine survivorship rate for one population in a stratum is the same as for another population in a stratum, and (2) the number of returning spawners in a cohort can be accurately estimated. Because the extrapolation of a marine survival rate to neighboring populations adds uncertainty to the JOM estimate, the JOM criteria score is discounted (see “Integrating with Other Criteria,” below). As more information on JOM trends and marine survivorship become available, a correlation analysis may help determine the validity of extrapolation. Also, we note that there will be a lag of as many as seven years required to estimate chinook marine survivorship, as the rate estimate requires that all potential spawners from a cohort have returned.

Risk Characterization

The relative value of JOM monitoring for evaluation of population status depends on data quality (accuracy) and how well the index or abundance estimate represents the entire population. We recommend that a scoring system for λ_{JOM} incorporate both the quality of the estimate and the predicted growth rate.

Table 5.1 gives an example of how population persistence category could be based on combinations of λ_{JOM} and statistical confidence in λ_{JOM} . The variance in JOM abundance estimates or indices between years due to environmental stochasticity is not related to data quality, but may make us less confident in a trend. The actual confidence levels used to determine population persistence category will depend on the acceptable level of risk.

Table 5.1 Relationship between λ_{JOM} and population persistence category.

Population Persistence Category	λ_{JOM} and confidence
0	Declining with high confidence in slope or extrapolated from other data sources
1	Stable, extrapolated from other data sources
2	Stable or increasing, low confidence in trend or extrapolated from other data sources
3	Stable or increasing, medium confidence in trend
4	Stable or increasing, <u>high</u> confidence in trend

Data quality for population attribute integration (Appendix C) may not be directly related to the confidence interval calculated for λ_{JOM} and should be assessed through professional judgment. Factors to consider include standardization of methods across a watershed, the proportion of the population represented in the index or indices used to estimate λ_{JOM} , and whether λ_{JOM} for the given population was assessed directly or extrapolated from other sources (for example, estimates from neighboring populations or from an adult spawner estimate with a marine survivorship calculated for a neighboring population).

If wild fish marine survivorship can be derived from JOM and returning spawner abundance, it can be used in the productivity and abundance criteria for multiple populations within a stratum (Section 4). Changes in JOM abundance can also serve as quantitative indicators of habitat quality (Section 7).

6. WITHIN-POPULATION DIVERSITY CRITERIA

WITHIN-POPULATION DIVERSITY CRITERIA

1. Sufficient life-history diversity must exist to sustain a population through short-term environmental perturbations and to provide for long-term evolutionary processes. The metrics and benchmarks for evaluating the diversity of a population should be evaluated over multiple generations and should include:
 - a. a substantial proportion of the diversity of a life-history trait(s) that existed historically,
 - b. gene flow and genetic diversity should be similar to historical (natural) levels and origins,
 - c. successful utilization of habitats throughout the range,
 - d. resilience and adaptation to environmental fluctuations.

Overview

Genetic diversity, and the morphological and physiological traits that it determines, defines the life-history characteristics of a population and its ESU. In established populations, this life-history diversity reflects generations of adaptation to local environmental conditions and is fundamental to population sustainability. Similarly, biochemical measures of genetic diversity can reflect historical patterns of reproductive isolation and may be indicative of ancestral phylogenies; however, anthropogenic factors have done much to disrupt historical patterns of genetic diversity. Riddell (1993) states that genetic variation, within and between population levels, and productive habitats are the resource base of Pacific salmon, both for long-term sustainable production and continuing evolutionary processes. Population diversity is not a static attribute, but is representative of dynamic processes involving migration, mutation, genetic drift, and adaptive selection for an equally dynamic environment. The current depressed status of many salmon populations may be due, in part, to the loss of diversity or the disruption of the adaptive relationship between a population's life-history traits and its environment. Dramatic decreases in the abundance of a population, even for one or two generations, can result in the loss of genetic diversity. Local adaptation can be disrupted when nonnative conspecific fish are introduced into the breeding population, or when environmental changes occur at a substantially faster rate than the population can adapt to (especially when the new conditions are outside the normal range).

When considering the criteria for the level of within-population diversity needed to establish sustainable populations, we focus on diversity in major life-history traits and in life-history trajectories or strategies (those that most directly influence an individual's fitness). Consideration should also be given to the status of natural processes that create and maintain life-history diversity. Stearns (1976) defines life-history strategies as a set of co-adapted reproductive traits resulting from selection in a particular environment. Collectively, the expression of life-history traits in an animal allows it to successfully move temporally and

spatially through diverse ecological landscapes during the course of its life. For salmonids, major life-history trajectories include traits such as juvenile utilization of freshwater habitat, time of saltwater entry, age at maturation, and spawn timing and location (main stem, side channel, inlet, beach, etc.).

For example, salmon that spawn in short coastal systems generally need to emigrate before summer conditions (low flow and high water temperatures) render much of the river uninhabitable, or before barrier berms form at the mouths of the rivers. Some juveniles may move rapidly to the ocean, while others may remain in freshwater for weeks or months. Juvenile body size is also positively correlated with successful emigration to the ocean. Larger eggs produce larger juveniles, but females with large eggs have fewer total eggs. Older fish are larger and more fecund, but there are additional risks to remaining in the marine environment for an additional year. Thus, traits such as juvenile emigration timing, egg size, and age at maturation create a matrix of possible life-history options. The success of these options depends on the both the general basin ecology and the specific environmental conditions for that year. In addition, some species of salmonids (for example *Oncorhynchus mykiss* and *O. tshawytscha*) also display variability in anadromy, with both freshwater resident and anadromous phenotypes present in some populations. Whether resident fish are included in population status evaluations needs to be determined on a population by population basis. The U.S. Fish and Wildlife Service (USFWS) and National Marine Fisheries Service (NMFS) are currently developing criteria to evaluate the relationship between resident and anadromous forms within a population.

Sustainability depends on a population's ability to exploit available habitats, to adapt to environmental changes by maintaining multiple life-history trajectories, and to modify life-history trajectories in response to changing environmental conditions. Diversity provides a population with a repertoire of potential life-history trajectories. In this way, a population is able to effectively buffer itself against short-term environmental changes. Life-history diversity in association with the plasticity of life-history trait expression enhances (but doesn't necessarily ensure) a population's ability to remain productive through highly variable environmental conditions. Although there are probably an infinite number of possible life-history trajectories, previous selection and current local habitat conditions define a limited number of successful trajectories. Ecological differences among watersheds may result in differences in the suite of successful trajectories; therefore, there is no single set of diversity criteria that can adequately be applied across strata to all populations in this ESU. Historical indices of life-history diversity provide the most likely benchmark for a recovered population; however, the quality and quantity of historical information available is extremely limited. Examination of existing populations may be useful in defining diversity criteria, although the degradation of habitat conditions and population integrity may have altered or constrained the expression of life-history traits. It is also possible that different approaches to basin management and habitat restoration will result in different but equally sustainable complexes of life-history trajectories. Analysis of both historical and current life-history and habitat information will be necessary to identify those life-history strategies that are fundamental to a population's sustainability. The goal is to reestablish the natural (historical) relationships between habitat and life-history expression, rather than exactly recreate historical diversity patterns.

Developing specific goals for life-history diversity is daunting. It is not realistic to prescribe the relative contribution of any one life-history trajectory; therefore, a more general approach is warranted. A sustainable population needs to exhibit life-history traits (trajectories)

that are adapted to local conditions. Diversity criteria can focus on one or more aspects of the suite of life-history trajectories: the presence of specific life-history trajectories, the relative frequency of these trajectories during any given year, and a population's responsiveness (as measured by changes in the relative frequency of different life-history trajectories) to annual changes in environmental conditions. Regardless of the diversity metric(s) selected, the underlying issue of what level of diversity is sufficient to ensure population viability must be addressed. Although there are some general benchmarks that can be applied (e.g., historical levels), establishing specific recovery levels of diversity for a population will likely require work at the local recovery planning scale.

Approaches Considered

The TRT concluded that monitoring life-history strategies, or trajectories, provides the most useful metric for measuring population diversity. Several other metrics were considered. Biochemical metrics (allozyme or DNA analyses) of genetic diversity are useful for monitoring genetic changes in populations. Declines in genetic diversity for a population can be indicative of increased inbreeding. Monitoring genetic changes can be informative in detecting high rates of gene flow (straying) between populations. Additionally, biochemical measures of diversity between populations are useful in understanding local adaptation patterns. Loss of genetic diversity across an ESU is generally thought to have serious consequences on ESU viability. While biochemical measures of diversity have not been directly linked to specific aspects of a population's adaptability or fitness, changes in diversity can be indicative of changes in effective population size or gene flow between populations. Population census information can also be useful. Changes in the effective population-size thresholds provide another method for the conservation of genetic diversity. WDFW (1997), in its Wild Salmonid Policy, suggests that an effective population size (N_e) of 500 individuals is sufficient to prevent the loss of genetic variability, through inbreeding or population bottlenecks, over a long period. In general, the number of spawning individuals or breeders (N_b) is much larger than N_e . This is because not all adults observed on the spawning ground contribute to subsequent generations. McElhany et al. (2000) discuss the relationship between N_e and N_b and cite several estimates of minimum population (breeder) abundances (417 to 4,170 per year) for the maintenance of sufficient genetic diversity to ensure long-term persistence. Population size provides a relatively simple criterion for ensuring against the loss of genetic variation under specific conditions. Spatial and ecological heterogeneity considerations might result in a larger minimum population size or some degree of geographic structuring of the population. Simply maintaining genetic diversity will not ensure the expression of important life-history traits, nor will expressing life-history traits for which the corresponding habitat no longer exists ensure the population's sustainability.

The criteria for within-population diversity should also provide that the expression of major life-history trajectories within recovered populations will resemble, but not necessarily duplicate, those that occurred historically. The NMFS "Definition of Species" paper (Waples 1991) defines a population as distinct, for ESA purposes, if it (1) is substantially reproductively isolated from conspecific populations and (2) represents an important component of the evolutionary legacy of the species. This definition is important to within-population diversity. Despite substantial reproductive isolation, a population may be part of a larger metapopulation

(Hanski and Gilpin 1997). The diversity expressed within a population may depend in part on how it functions in a metapopulation. The evolutionary legacy of species is the genetic variability that is a product of past evolutionary events and represents the reservoir upon which future evolutionary potential depends. Restoring historical life-history trajectories or restoring the natural processes that affected populations, reestablishes the evolutionary process of populations within an ESU.

Given the plasticity of life-history traits, it may not be feasible to prescribe criteria for the expression of life-history variants. Some life-history trajectories may only be detectable under specific environmental conditions or if specific habitats are available. It is important that the trajectories being evaluated are heritable to some extent and their expression is influenced by environmental conditions. The loss of key habitats for certain life-history trajectories may limit the expression of traits associated with that trajectory. Effects related to the time of sampling complicate monitoring life-history diversity. Only through extensive monitoring of key life-history traits (at multiple life-history stages and over several years) can a useful measure of diversity be obtained. It is envisioned that critical life-history data could be obtained in conjunction with juvenile and adult abundance monitoring, and that representative basins might be selected within major life-history/ecological strata.

While there is limited historical information available to establish life-history diversity benchmarks, it is reasonable to assume that the life-history diversity is strongly correlated with the ecological diversity of habitats utilized by populations. Therefore, the restoration of historical life-history diversity may be best achieved through the restoration of historical habitat diversity. Which elements of historical habitat were critical in maintaining life-history diversity remains to be determined. Historical (baseline) life-history diversity could be derived from the analysis of salmonid populations in pristine habitats, particularly those from similar ecological zones.

Approach Selected

In establishing specific recovery criteria goals, and actions to achieve those goals, it is necessary to identify which life-history trajectories are critical to population viability and how one reestablishes the expression of those trajectories. This requires understanding the suite of life-history trajectories that are possible and how they relate to specific environmental conditions. Where possible, one should identify the current and likely historical life-history characteristics of naturally produced fish within the target population(s) and identify those life-history traits and trajectories that are important to population viability. Local recovery entities should focus on life-history/habitat relationships within their watersheds: where this is not possible, information from other populations within the same life-history/ecological zone stratum should be relevant. In the absence of specific information, management and recovery actions must be based on presumed life-history characteristics. This information will be critical for identifying which life-history strategies historically contributed and are currently contributing to the persistence of a population. Estimates of historical levels of diversity provide an important benchmark for population viability. Historical life-history levels may provide the only proven template for viable populations, although there may be some fraction of historical levels that is sufficient for viable populations. Local recovery entities must consider management actions that can target those habitats that existing strategies rely upon, or actions that restore life-history

strategies that are no longer present. Whether the life-history trajectories are sufficiently diverse is ultimately expressed in a population's sustainability.

Within-Population Diversity Recovery Strategies

This document has focused on defining the criteria that describe a viable population; however, among the population attributes within-population diversity is somewhat different from the others. The diversity characteristics measured reflect adaptation to local environmental conditions, and viability criteria may well differ between populations and certainly between strata. Environmental variability may produce substantial annual variation in character expression, but without any change in population viability. Finally, the only valid measure for evaluating levels of diversity is by monitoring the fitness of subsequent generations. For these reasons, recovery strategies should not focus on producing specific characteristic levels (i.e., specific percentages of yearling migrants), but reestablishing those processes that will result in the expression of appropriate levels of diversity.

1. Maintain or restore conditions that allow for the local adaptation of naturally produced populations.

Historically, established populations were adapted to local habitat conditions. Life-history trajectories evolved over generations of natural selection. If populations have been extirpated or modified through artificial propagation activities, harvest, or habitat degradation, the genetic basis for historical life-history diversity is also lost or modified. In most of these cases, the conditions to which the fish needed to adapt changed at a rate that was too rapid for evolutionary processes to function effectively. Efforts to reestablish locally adapted populations will most likely benefit from the use of founding populations similar to the historical populations. Founding populations may include hatchery populations that may have assimilated elements of the historical population, or geographically proximate populations from ecologically similar basins. The recovery of life-history diversity in existing or reestablished populations will depend on these populations' ability to adapt to local conditions. The pace of local adaptation depends on habitat conditions, the degree of similarity between the historical and founding populations, the continued level of interbreeding between the local population and nonadapted individuals from local or distant hatchery programs or populations, and the intensity of natural selection. While it is not possible to set criteria for the process of local adaptation, it is possible to establish criteria for conditions that facilitate this process. Specifically, one could limit the level of hatchery-origin fish contributing to a naturally spawning population. This permissible level might depend on the genetic similarity between the hatchery and naturally spawning populations. Monitoring biochemical genetic markers in populations is a useful measure of the degree of a population's reproductive isolation and the relative degree of relatedness of different populations. Similarly, harvest regimes can selectively affect portions of a run and should be modified where necessary. It is likely that this process will occur concurrently with habitat restoration efforts. Where the native population has been extirpated or heavily influenced by introduced stocks, judicious selection of a founding population and the effective restoration of local adaptation processes will greatly facilitate recovery efforts.

2. Maintain and restore key historical habitats, with the expectation that populations will exploit ecological opportunities if these areas are recovered through actions such as:

- a. restoration of access to historical habitat (e.g., side-channel and headwater areas) through modification or removal of nonnatural barriers;
- b. restoration of important hydrological processes.

3. Maintain and restore “important” historical life-history trajectories and take actions to establish/restore the necessary habitat pathways for those trajectories.

The expression of specific life-history traits is predicated on the presence of specific habitats. Therefore, it is unlikely that historical life-history diversity can be restored without the restoration of historical habitat, or, at a minimum, those habitat elements that are critical to the expression of life-history trajectories. Where information on historical life-history traits is limited or absent, the restoration of historical habitats may provide a useful surrogate for restoring diversity. Local recovery entities will need to identify distinct habitats that were historically occupied and/or historical life-history trajectories. Where basin-specific information is lacking, it may be necessary to infer similarities between ecologically similar basins. Based on the information available, local restoration efforts can be either life-history or habitat driven.

Critical Uncertainties

When establishing criteria for within-population diversity, there is considerable uncertainty in defining how much life-history diversity is enough to sustain a population at VSP levels. Similarly, there is little information available to establish how much habitat diversity is needed to maintain the necessary level of within-population diversity. Historical life-history traits and trajectories provide us with the template most likely to support viable populations. An examination of historical and current information on life-history traits and historical and existing habitat conditions may provide the necessary insight to identify those life-history trajectories that are fundamental to population diversity and sustainability. Historical information on most populations is sparse, and an understanding of the relationships between life-history traits and habitats is still being developed. In many cases, recovery actions could focus on the restoration of historical habitats, with the assumption that existing populations have retained the appropriate genes necessary to exploit these habitats. It may take some time before managers are able to identify the key habitats necessary to restore life-history trajectories. Alternatively, if a population has gone through a genetic bottleneck it may not be able to express certain trajectories. Under these conditions, actions by local managers may be restricted to recovery efforts with very generalized goals for diversity criteria. It is likely that populations within the same life-history/ecoregion strata would share similar life-history criteria. As monitoring programs develop and our understanding of biological systems improves, more specific criteria will be developed.

It is not possible to definitively identify the spectrum of life-history trajectories necessary to provide enough diversity for population sustainability and long-term evolution. Historical information is useful, but often too limited to assist in prioritizing life-history or habitat types.

Criteria based solely on historical characteristics would ignore the dynamic nature of salmon populations, salmon habitat, and environmental conditions. Habitat restoration activities may also affect the expression of life-history traits. In fact, the responsiveness of life-history traits to environmental fluctuations could be a useful measure of adequate diversity. Life-history diversity, like salmon habitat, is dynamic. Furthermore, there are probably a number of different permutations of life-history trajectories that will ensure a population's sustainability. Recovery criteria need to reflect the functional aspects of life-history diversity, exploitation of multiple habitats, and buffering against environmental variability.

Monitoring and Evaluation

The design and implementation of a monitoring program for life-history diversity within populations is daunting. First, any monitoring effort would have to be tailored to the specific criteria metric established. There are a large number of life-history traits that can be monitored at an equally large number of geographic locations at various points in a fish's life cycle. Monitoring is somewhat facilitated by the association of multiple traits within a life-history trajectory and the relationship between life-history trajectories and specific habitats. Sampling a more limited suite of traits closely related to major life stages may be sufficient. For example:

- smoltification—age at downstream emigration, marine entry (from direct observation or inferred from adult scales);
- age at maturation—from adult scales or juvenile marks (e.g., CWT, otolith marks, etc.);
- run and spawn timing—direct observation of marked fish captured in terminal fisheries or adults observed on the spawning ground.

Furthermore, monitoring traits at these life-history stages could be coordinated with juvenile and adult abundance monitoring. In some cases, monitoring the same trait through different means may provide useful information about the contribution of different trajectories. For example, the age at outmigration can be measured by monitoring juveniles as they leave freshwater systems, or scale patterns from returning adults can be examined to estimate the time of seawater entry. Both types of information are needed to estimate the relative contribution of different emigration strategies. Furthermore, monitoring over an extended time period (years) should demonstrate that a population is capable of expressing a variety of life-history types. Monitoring key life-history traits provides one measure of a population's diversity; alternative methods might include quantifying the diversity of habitat utilized or the responsiveness (degree of change in life-history trajectory composition) to environmental variation. Alternatively, EDT analysis (Mobrand Biometrics Inc., 1996) provides a method of estimating the historical and present life-history trajectories based on habitat conditions. EDT examines the relationship between life-history trajectories and the habitats on which they depend. By evaluating the quality and quantity of the habitats necessary to complete any one pathway under existing and pristine conditions, one can estimate the relative proportion of potential life-history strategies that are currently occupied. Additionally, it may be possible to identify which habitats limit life-history diversity. For this reason EDT analysis may be useful in identifying recovery actions in a watershed. There was some concern, however, that EDT only verifies the existence of habitat pathways for life-

history trajectories and does not actually verify that fish are utilizing those pathways. Furthermore, EDT life-history trajectories are based on estimated movements spatially and temporally through the watershed (with potentially hundreds of permutations), rather than considering major life-history strategies.

An alternative approach to monitoring life-history diversity would combine elements of spatial structure and juvenile/adult monitoring. The presence of fish in specific habitats can be used to infer that the life-history traits necessary to exploit that habitat are present. This may be especially true when fish are observed in newly restored or reconnected habitats.

Extensive monitoring might not be necessary for all populations within an ESU. Sampling a limited number of populations within each life-history/ecozone stratum could be sufficient to characterize the diversity for each stratum. Furthermore, if this extensive monitoring of a selected collection of populations were combined with less-intensive monitoring or the monitoring of correlated characteristics (i.e., habitat diversity as a proxy for life-history diversity) for the other populations in the strata, it may be possible to evaluate the status of life-history diversity throughout the ESU.

In addition to life-history monitoring, both naturally spawning populations and hatchery populations should be regularly monitored for genetic variation using allozymes and/or DNA analysis. While there are a number of monitoring programs currently under way, these activities should be expanded to include all relevant populations and coordinated to maximize efficiency.

Risk Characterization

The approach we have taken to integrating information from all population attributes requires that populations be characterized on a 0–4 scale for all attributes. Within-population diversity is difficult to quantify because there is a vast suite of life-history traits that can be monitored, in addition to numerous less-direct measures of diversity (for example, habitat utilization, biochemical measures of genetic variability, and population effective size). In addition to direct and indirect measures of diversity, consideration should be given to the processes involved in local adaptation (which maintain and restore appropriate diversity to populations). Of these processes, considerable information is available on gene flow. The migration of adult fish across population boundaries, whether of natural or hatchery origin, reduces the efficiency of local adaptation. Within a population, the presence of relatively large numbers of hatchery-origin fish, especially those of nonlocal origins, within a population should be scored as having negative diversity consequences. Other anthropogenic factors (harvest, hydropower flow programs, timing of irrigation withdrawals, etc.) also affect life-history diversity and should be considered in evaluating the persistence category for diversity. Based on the guidelines presented in this section, the following system will be employed until the relationship between specific life-history traits and population viability is better understood and can be more quantitatively approached. Information related to within-population diversity can be assigned to one of three equally important attribute elements: (1) life-history phenotypes, (2) genetic variability or effective population size measures, and (3) local adaptation processes. Professional judgment will be used to evaluate each element relative to the presumed historical levels for that species and population. Similarly, it is necessary to employ professional judgment to weigh the importance of life-history traits being monitored (directly or indirectly) in relation to the ecological conditions that the population experiences. As discussed earlier, the expression

of variation in life-history traits depends on the ecological opportunities that exist at any point in time. Any evaluation should include observed changes in life-history traits over time in response to environmental fluctuations. The ability of a population to respond to environmental perturbations provides a definitive measure of adequate levels of diversity. Where a population's response to such perturbations has not been observed, more reliance needs to be placed on genetic variation/effective population and local adaptation element evaluations.

We expect considerable refinement of the risk characterization to occur in the future, especially with respect to the quantitative levels. Given the existing status of listed ESUs in the WLC recovery domain, it is unlikely that the component populations would achieve VSP persistence levels for some time. Improvements in the quantity and quality of monitoring over the next few years will provide the necessary information to develop a more quantitative approach to risk categorization. In the near term, risk categorization will be most useful in helping recovery entities focus their activities on the limiting components of population attributes.

Table 6.1 Risk characterization for within-population diversity.^a

Population Persistence Category	Within-Population Diversity
0	All four diversity elements ^b are well below predicted historical levels, extirpated populations, or remnant populations of unknown lineage.
1	At least two diversity elements are well below predicted historical levels. Population may not have adequate diversity to buffer the population against relatively minor environmental changes or utilize diverse habitats. Loss of several major presumed life-history phenotypes is evident; genetic estimates indicate major loss in genetic variation and/or small effective population size. Factors that severely limit the potential for local adaptation are present.
2	At least one diversity element is well below predicted historical levels; population diversity may not be adequate to buffer strong environmental variation and/or utilize available diverse habitats. Loss of life-history phenotypes, especially among important life-history traits, and/or reduction in genetic variation is evident. Factors that limit the potential for local adaptation are present.
3	Diversity elements are not at predicted historical levels, but are at levels able to maintain a population. Minor shifts in proportions of historical life-history variants, and/or genetic estimates, indicate some loss in variation (e.g., number of alleles and heterozygosity), and conditions for local adaptation processes are present.
4	All four diversity elements are similar to predicted historical levels. A suite of life-history variants, appropriate levels of genetic variation, and conditions for local adaptation processes are present.

^a Guidelines for incorporating uncertainty due to incomplete or poor data quality are presented in Section 3 and Appendix C.

^b The four diversity elements of the criterion are (1) life-history diversity, (2) gene flow and genetic diversity, (3) utilization of diverse habitats, and (4) resilience and adaptation to environmental fluctuations.

7. HABITAT CRITERIA

GENERAL HABITAT CRITERIA GUIDELINES

1. **The spatial distribution and productive capacity** of freshwater, estuarine, and marine habitats should be sufficient to maintain viable populations identified for recovery.
2. **The diversity of habitats** for recovered populations should resemble historical conditions given expected natural disturbance regimes (e.g., wildfire, flood, volcanic eruptions, etc.). Historical conditions represent a reasonable template for a viable population; the closer the habitat resembles the historical diversity, the greater the confidence in its ability to support viable populations.
3. **At a large scale, habitats should be protected and restored, with a trend toward an appropriate range of attributes for salmonid viability.** Freshwater, estuarine, and marine habitat attributes should be maintained in a nondeteriorating state.

Overview

Habitat, as used here, comprises the myriad environmental components and processes operating over time and space that affect the growth, behavior, distribution, and survival of individual salmonids and therefore the viability of salmonid populations. Delisting criteria will need to address the freshwater and estuarine habitat characteristics necessary for persistence and recovery of a species. The importance of habitat is one of the primary purposes of the ESA [Section 2(b)]: “to provide a means whereby the ecosystems upon which threatened and endangered species depend may be conserved.” Habitat criteria help ensure that recovery is not ephemeral. Inherent time lags occur between certain types of habitat modification and fish population response. For example, the negative effects of removing a riparian buffer may only be observed during infrequent extreme weather events. The dynamics of a fish population in the interval between weather events may suggest that it is viable. However, a broader evaluation, one which included habitat status, might reach a different conclusion about long-term risks facing the population. Thus, evaluating habitat provides unique information about a population’s status. A delisting decision based solely on a fish population’s performance may be short-sighted if the fundamental habitat problems that led to the initial listing are not solved or if new habitat degradation is not prevented.

Habitat criteria also provide a check on viability criteria developed through demographic models. A key assumption of the demographic modeling used to develop biological viability criteria is stationarity, the assumption that the behavior of the population over the observation period will continue into the future. Projecting the future dynamics of relevant habitat features with long temporal responses, such as river sediment dynamics, can provide an important check on the validity of the stationarity assumptions. Habitat criteria have the potential to provide an additional predictive element, which augments our ability to provide for salmonid persistence and recovery into the future. Habitat criteria will help to prevent a delisting decision based on demographic models for which assumptions are no longer valid.

Developing habitat criteria will involve technical analyses that are, in many ways, more complex than the ones needed to develop the criteria that describe salmon population attributes. The challenge will be to determine the habitat conditions the listed salmon species needs to persist throughout its full range and all its life stages. As recovery planning progresses to move beyond the already challenging task of defining viable habitat characteristics, it will be necessary to describe the processes that have led to their deterioration. An additional challenge facing the development of habitat criteria is identifying appropriate temporal and spatial scales. The watershed, including the estuary, is the basic ecological restoration unit of the WLC domain. Land- and water-use practices within watersheds are intimately tied to the condition of the streams or rivers that drain them. Habitat conditions in the mid and upper Columbia River watersheds will impact the estuarine and nearshore conditions experienced by listed fish in the WLC domain. Habitat criteria will necessarily consider entire watersheds within and related to the WLC domain.

Strategies Selected

For all WLC listed salmon ESUs, habitat loss and destruction was identified at the time of listing as one of the major five factors for decline. VSPs require an abundance of high-quality habitat, distributed throughout entire watersheds, including freshwater and estuarine areas, in a manner that will support all life-history stages and provide for connectivity among the various life stages. In this sense, habitat is not just another one of the “H’s”—salmon populations do not need hydroelectric dams, hatcheries, or harvest to be viable but they do need good habitat. Habitat conservation, restoration, and protection are essential components of salmon recovery.

While the TRT has focused thus far on criteria related to salmonid growth and abundance, we have begun to conceptually frame some issues related to freshwater and estuarine habitat criteria. This work is in the preliminary stage, but has resulted in general habitat criteria and a preliminary list of habitat attributes to be considered (Table 7.1). These criteria largely serve as placeholders until more specific criteria can be developed. TRT members have explored some specific habitat criteria involving temperature tolerances for salmonids (Appendix L). These temperature criteria were developed as a first example of what specific habitat criteria might look like. Temperature was selected for this first example not because it was identified as the most important factor, but because is likely to be one of the important factors and data availability made it a tractable place to start. Additional questions about temporal and spatial scale still have to be answered.

The habitat criteria were derived from well-established principles about the relationship between salmon and the habitats on which they depend. First, habitats have a limited carrying capacity, which depends on habitat quality. In order to recover populations, there must be adequate amounts of freshwater and estuarine habitat of sufficient quality to support viable populations identified for recovery. Salmon require different types of habitat at different life-history stages (Table 7.1), therefore the habitats on which these populations depend must also have a spatial distribution sufficient to maintain viable populations identified for recovery. Second, salmon have evolved under natural disturbance regimes. These disturbance regimes have resulted in diversity, over time and space, of habitat types and conditions. Therefore, the diversity of habitats for recovered populations should resemble historical conditions given expected natural disturbance regimes (e.g., wildfire, flood, volcanic eruptions, etc.). Historical

Table 7.1 Examples of habitat attributes and life-history stages for which each attribute is particularly critical.

Habitat Attribute	Return to Spawn	Egg Incubation	Juvenile Rearing	Out- migration	Ocean Transition
Stream flow	X	X	X	X	X
Water temperature	X	X	X	X	X
Sediment		X			X
Dissolved oxygen		X			X
Chemical contaminants	X	X	X	X	X
Nutrients		X	X	X	
Physical barriers (fish passage)	X		X	X	
Percent pools			X		
Large woody debris			X		
Substrate	X	X			
Off-channel refugia			X	X	
Interactions with exotics	X		X	X	X
Streambank stability		X	X	X	
Trophic dynamics	X		X	X	X
Floodplain connectivity			X	X	X
Tidal flat connectivity				X	X
Channel width:depth ratio	X	X	X		
Road density		X			
Landscape disturbance history					
Riparian condition	X	X	X	X	

conditions represent the only known template for a viable population, and the closer the habitat resembles the historical diversity, the greater the confidence in its viability. Third, large-scale processes have a driving influence on both habitat conditions and salmonid population performance. At smaller scales, habitat quality varies naturally. Therefore habitats must be maintained and restored to ensure a trend toward an appropriate range of conditions for salmonid viability. At a large scale, freshwater and estuarine habitat conditions should be maintained in a nondeteriorating state.

Relationship of Habitat to Other Criteria

Since habitat is a key driver of fish population performance, we expect some overlap between criteria describing habitat and the other criteria (i.e., growth and abundance, JOM, diversity, and spatial structure). However, as described in the introduction to this document, each criterion contributes distinct information about population risk. The greatest potential overlap is between spatial structure and habitat criteria. An alternative conceptual structure for criteria development would place spatial structure, habitat quality, and habitat dynamics as components of the habitat criteria. The TRT elected to retain spatial structure as a separate attribute because

evaluating the spatial structure of a population involves examining the distribution and dispersal behavior of the fish themselves. This is a different exercise than examining the distribution and quality of available habitats. Evaluating habitat spatial structure and quality allows for the incorporation of sublethal effects of reduced habitat quality and of a gradation in habitat quality beyond the presence or absence of fish. The high level of correlation between the habitat and spatial structure criteria should be considered as the criteria are integrated into an overall assessment of population viability.

Critical Uncertainties

In developing habitat criteria, several assumptions must be acknowledged. First, distribution of historical populations is assumed to be reasonably accurate. Second, the habitats in which historical populations resided are assumed to have been spatially arranged and of sufficient productive capacity to provide demographically independent VSPs. Third, the ideal arrangement and spatial distribution of habitats for a given viable population is unknown and likely fluctuates over time. Fourth, our understanding of fish-habitat relationships, while improving over the last several decades, is incomplete, making it difficult to accurately predict productive capacities for specific watersheds. Fifth, our understanding of natural disturbance regimes and the roles they play in the ecological succession of aquatic habitats for salmon is imperfect. Incorporating these concepts into “recovered salmon landscapes” in a manner that connects headwater areas to mainstem rivers to estuarine habitats must rely heavily on analyses generated from historical habitat reconstructions and simulations of natural disturbance regimes tempered with the existing, but limited, empirical data and professional judgment.

Future Development of Specific Habitat Criteria

The habitat criteria need to be developed into more specific “measurable and objective criteria” to evaluate extinction risk. Two general approaches could be taken for future development of habitat criteria. One approach is to develop standards for specific habitat attributes, then evaluate all habitats relative to those standards. An example of this approach is the maximum temperature criteria developed in Appendix L. An alternative approach does not rely on the initial development of uniform standards; instead it focuses on watershed analyses to identify a distribution of target conditions appropriate for a particular time and place. The distribution of target conditions would be determined by examining historical and current watershed processes and correlating them with the requirements of fish populations. Both approaches might ultimately result in similar criteria. That is, the standards approach might result in the development of condition-dependent standards that can be tailored to a specific time and place, while the watershed analysis approach might result in the identification of generally required habitat conditions that could be developed into a set of standards for specific locations. We are not providing a full discussion of the strengths and weaknesses of the two approaches in this document, but both have merit and the TRT has been divided on which approach to pursue. In addition, the TRT has not identified the best methods for incorporating nearshore conditions

into the habitat criteria, but the members do agree that further work is needed on nearshore habitat requirements and criteria.

Habitat Risk Characterization

Because they are so numerous and complex, the environmental factors known to affect salmonids cannot be readily comprehended, inventoried, and evaluated. To facilitate the characterization of habitat and its ability to support VSPs, we rely on a subset of key habitat components or processes, measured at appropriate times and places, as indicators of habitat quality. These key habitat indicators, when individually and collectively monitored and evaluated, provide useful information of the current status and trend of environmental conditions. Based on measurements of indicators and our understanding or observation of their effects on fish, we can make some judgment as to the overall quality of habitat present at a particular location and time. Moreover, if we are able to reliably forecast future changes in habitat conditions based on current trends, we can also predict their probable impact on salmonid populations.

Indicators of important habitat components and processes have been compiled in the scientific literature, and are routinely used by fisheries scientists to quantitatively describe habitat conditions. Table 7.1 lists a subset of habitat indicators derived substantially from the Matrix of Pathways and Indicators developed by NMFS as part of its “Checklist for Documenting Environmental Baseline and Effects of Proposed Action(s) on Relevant Indicators” (NMFS 1996). A more extensive list of habitat indicators, including known or presumed effects on the survival of different life stages of salmonids, are used to parameterize the Ecosystem Diagnosis and Treatment model (Mobernd Biometrics 1996).

One or more specific parameters and evaluation protocols can be identified for each indicator. For example, streamflow at a specific location can be statistically described by reference to several hydrologic parameters that characterize the magnitude, frequency, timing, duration, and rate of change in discharge for the period of record.

The actual parameters measured for each indicator are referred to as indicator variables. The biological response of individual fish to different levels of indicator variables or, alternatively, the quantitative relationship between a given habitat component or process and the associated fish population, can be deduced or postulated based on empirical data or expert judgment. These types of relationships vary with species, life stage, and interactions with other variables.

There is ample evidence that fish respond in predictable ways to changing habitat conditions. In particular, we know that certain conditions are associated with and presumably are responsible for different levels of fish performance. Habitat conditions are acceptable—that is, capable of supporting viable populations of salmonids—if they fall within the normal range of variability for undisturbed systems.

For each indicator variable, there is a threshold below which conditions are considered unacceptable or impaired. This impairment threshold is a value or range of values that are specific to the species, life stage, and area (i.e., habitat type, watershed, ecosystem) in question. In areas where values fall below identified impairment thresholds for one or more key indicator variables, the habitat is considered impaired.

The indicators, indicator variables, and impairment thresholds (e.g., “properly functioning [habitat] conditions”) recommended by NMFS (1996, 1999), Spence et al. (1996), and other sources reported in the literature are a useful starting point for assessing habitat within areas utilized by salmonid populations in freshwater, estuarine, and marine ecosystems. The timing, distribution, and specific ecological requirements of the population and life stage in question will need to be determined at appropriate spatial scales. The relationship between habitat and fish performance, and the range of values associated with impaired and nonimpaired habitat, as measured by ecologically relevant indicator variables, will need to be determined through best available science applied to local conditions.

Separate lists of key habitat features can be compiled for freshwater, mainstem, estuarine, and marine areas occupied by the population over its life cycle. If necessary, more refined lists of indicators and indicator variables can be compiled for different life stages and applied to subareas within these larger ecosystems.

Once appropriate evaluation metrics and standards have been defined, the habitat within a particular ecosystem (e.g., freshwater, main stem, etc.) can be qualitatively evaluated with respect to its overall effect on population performance. Both existing and future habitat conditions may be predicted. Those responsible for the assessment will need to devise a rational approach to measuring or estimating, weighting, and integrating the values obtained for different indicator variables and indicators. Careful consideration will need to be given to the selection of indicator variables, the spatial and temporal scales at which they are measured and expressed, and their synthesis and integration across appropriate scales of time and space, as defined by the population.

The result of the habitat assessment, which necessarily will rely heavily on expert opinion, will be a characterization of habitat within the occupied (or potentially occupied) geographic range of the population for the specified time period of interest. The assessment comprises two types of information: (1) a measure of the current status of the habitat within areas occupied by the population; and (2) a measure of the likely trend in habitat conditions, given anticipated natural and human-induced changes in the environment over the foreseeable future. By “future” we mean over a 20- to 100-year time span. Habitat within areas occupied by each population can be categorized into one of five levels as described in Table 7.2.

The recommended procedure for evaluating habitat considers the existing and probable future status of habitat measured at appropriate scales, relative to impairment thresholds specified for key environmental indicator variables. Probable future conditions can be predicted based on observable trends in habitat condition, as indexed by indicators of human population growth and distribution, land and water use, and other predictors of natural and human-caused environmental impact.

Table 7.2 Risk Characterization for habitat criteria.

Persistence Probability Category	Description
0	Habitat is incapable of supporting fish or is likely to be incapable of supporting fish in the foreseeable future.
1	Habitat exhibits a combination of current impairment and likely future conditions such that the population is at high risk of extinction.
2	Habitat exhibits a combination of current impairment and likely future condition such that the population has a moderate risk of extinction.
3	Habitat is nonimpaired and likely future conditions will support a viable salmon population.
4	Habitat conditions and likely future conditions support a population with an extinction risk lower than that defined by a viable salmon population. Habitat conditions consistent with this category are likely comparable to those that historically existed.

8. WITHIN-POPULATION SPATIAL STRUCTURE CRITERIA

WITHIN-POPULATION SPATIAL STRUCTURE CRITERIA GUIDELINES

1. The spatial structure of a population must support the population at the desired productivity, abundance, and diversity levels through short-term environmental perturbations, longer-term environmental oscillations, and natural patterns of disturbance regimes. The metrics and benchmarks for evaluating the adequacy of a population's spatial structure should specifically address:
 - a. Quantity: Spatial structure should be large enough to support growth and abundance, and diversity criteria.
 - b. Quality: Habitat underlying spatial structure should be within specified habitat quality limits for life-history activities (spawning, rearing, migration, or a combination) taking place within the patches.
 - c. Connectivity: Spatial structure should have permanent or appropriate seasonal connectivity to allow adequate migration between spawning, rearing, and migration patches.
 - d. Dynamics: The spatial structure should not deteriorate in its ability to support the population. The processes creating spatial structure are dynamic, so structure will be created and destroyed, but the rate of loss should not exceed the rate of creation over time.
 - e. Catastrophic Risk: The spatial structure should be geographically distributed in such a way as to minimize the probability of a significant portion of the structure being lost due to a single catastrophic event, either anthropogenic or natural.

Overview

The spatial distribution of a population is the distribution of fish and the processes that generate that distribution (McElhany et al. 2000). Spatial distribution is important because the viability of a population is closely linked to it in both the short and long term. Viability is linked to spatial structure in a variety of ways. Most simply, there must be sufficient high-quality habitat to support the population, and habitat areas must be connected so that fish can move from one area to the next as their life history requires. However, spatial structure affects viability in more subtle ways as well. We know from metapopulation theory that spatial structure can affect extinction risk in ways that would be undetectable from short-term observations of population growth and abundance (Hanski and Gilpin 1997, Tilman and Lehman 1997, Cooper and Mangel 1999). Some areas of high abundance may actually be production sinks, while other areas with less fish abundance may be responsible for most of the production (Pulliam 1988). Also, because of the demographic interplay between areas, the genetically effective size of a population may be

smaller than would be otherwise assumed (Whitlock and Barton 1997). Spatial structure is also linked to genetic diversity (see Section 6). Diversity in population structure promotes genetic diversity, which is a key component of long-term viability. Finally, the spatial structure of a population often determines its susceptibility to catastrophic risk. In general, the more dispersed the population, the less likely it is to be heavily impacted by a landslide, volcanic eruption, or other catastrophe. An extensive account of spatial structure and its role in salmonid population viability can be found in McElhany et al. (2000).

Spatial structure can be considered at any spatial scale. Spatial structure at the ESU level has already been covered in an earlier section. In this section we consider the spatial structure of individual demographically independent populations identified in the Lower Columbia and Willamette ESUs (Myers et al. 2002). The spatial structure of an individual population is characterized by the spatial distribution of its habitat, its dispersal patterns and dynamics, and the quality and quantity of its habitat. Complexity of spatial structure can be expected to vary according to species; life-history types; and the basin's hydrographic, physical, chemical, and biological processes. Thus, we would expect to see differences in spatial structure between chinook salmon and steelhead populations, between spring- and fall-run chinook populations, and possibly even between fall-run chinook populations in the coastal ecoregion and those in the Cascade Crest ecoregion.

Because spatial structure cannot exist without supporting habitat, there can be a natural tendency to consider the two as synonymous. However, certain aspects of spatial structure clearly are not habitat, and aspects of habitat are not spatial structure. Figure 8.1 presents a good conceptual framework for understanding how these two aspects of viability relate to each other, though opinions may vary about the relative sizes of the circles and the extent of overlap.

The area of overlap in Figure 8.1 reflects the extent to which spatial structure is determined by habitat distribution, quality, and quantity. The area of no overlap reflects the determination of spatial structure by genetic differentiation and population-specific dispersal patterns. The large amount of overlap with habitat means that a considerable amount of discussion about spatial structure will necessarily be a discussion of habitat. At times this may

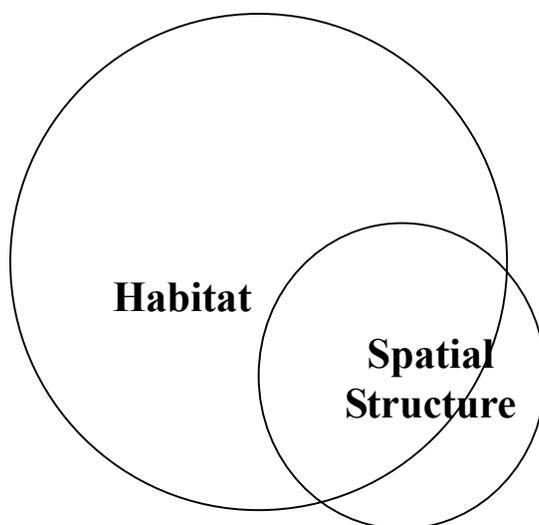


Figure 8.1 Venn diagram of relationship between habitat and spatial structure.

seem redundant. We have tried to limit this redundancy but feel a certain level of it is appropriate, even to the extent of having close correspondence between several of the spatial structure and habitat criteria guidelines.

In discussing the spatial structure criteria, it is useful to use the term patch (Levins 1969) to refer to an area of habitat. We define patch as an area of homogenous habitat that is consistently used during a particular life stage. Patches can be anywhere from a few meters to many kilometers in size. They may be continuous or discontinuous, and their boundaries may be determined by discontinuities in habitat features. However, utilization must also be considered. This can make clear identification of patches difficult. For example, consider a long stream reach that may appear to be good spawning habitat, but in which the fish spawn in only two very localized areas. The homogeneity of the reach may be a strong argument for considering it a single patch for spatial structure assessment purposes, but the utilization pattern would argue that this area consists of a group of occupied and unoccupied patches. However, in a year in which the number of returning adults is very high, spawners may utilize the entire reach, making it in effect a single patch. We classify patches according to their most obvious usage—spawning, rearing, or migration—but these distinctions are somewhat arbitrary. For example, spawning patches are also invariably early rearing patches, and because fish move through them on their way to other rearing areas, they are also to some extent migration patches.

Approaches Considered

Our initial goal was to develop a simple and consistent set of criteria, consistent with the five general recommendations of McElhany et al. (2000), that could be applied uniformly over all populations of all species without creating situations that seem either arbitrary or illogical. The simplest approach was to require a minimal level of dispersal, for example, requiring that spawning occur in at least two or three geographically distinct areas. Obvious variation among species made this approach seem illogical. For instance, Wind River summer steelhead now spawn and probably historically spawned in the headwaters of Panther Creek, Trout Creek, and the Wind River, whereas Coweeman River fall chinook salmon now spawn and probably historically spawned in a single long stretch of the main stem of the river. Thus, a simple dispersal rule makes sense for the steelhead, which exhibit a considerably branched (dendritic) spawner distribution, but not necessarily for the fall chinook salmon. As we examined a variety of existing and presumed historical spatial structures, it became clear that geological features also influenced spatial structure complexity. Some basins have the capacity to support a highly dendritic structure, while others did not. It became clear early on, as with the diversity criteria (Section 6) that the only logical, uniform approach was a set of general criteria flexible enough to allow for variation among populations and basins.

In the face of uncertainty, the general guideline on all viability issues is to use the historical situation as a template (McElhany et al. 2000). We considered this an appealing concept because our knowledge of habitat processes, and fish-habitat and dispersion dynamics, is too limited to specify appropriate spatial structures for individual basins. Presumably the historical spatial structure worked, so it should provide a good model. But there are problems with wholesale adoption of the historical spatial structure as a recovery template. First and most obvious, the historical spatial structure may not be well known and may even be unknown.

Second, the spatial structure within natal watersheds of most populations within the Lower Columbia and Upper Willamette ESUs has been changed substantially by land use, channel modification, and hydroelectric development; and the downstream structure of all populations has been changed by development of the Columbia. Developing appropriate spatial structures to support viable populations in these ESUs in many cases is not a matter of repairing habitat here and there to restore the historical structure. Some of these basins may have changed so much that any workable spatial structure would be substantially different from the historical spatial structure. Finally, spatial structure is not an end unto itself. An appropriate spatial structure is an interaction between fish and habitat that supports the population in ways that allow it to be both abundant and resilient. An appropriate spatial structure is thus one that works, and that may or may not require it to be quite similar to the historical structure. Any recovery approach will almost certainly require restoration of parts of the historical spatial structure, but devoting ourselves too slavishly to the complete restoration of the historical structure could be an expensive, misguided effort. We concluded that developing a viable spatial structure should be informed by knowledge both of the historical spatial structure and of the spatial structures of relatively undisturbed conspecific populations in comparable settings. However, following this approach, the point of attempting to completely restore the historical spatial structure or mimic that of a reference population may not be necessary or wise. Functionality is the key.

Assuming that a historical or reference population spatial structure will be used to guide development of a viable spatial structure, we then considered simple utilization/dispersion criteria based on these templates. Possible criteria were that spawning (or other usage) should occur in all tributaries that historically supported spawning or in some fraction of those tributaries. Several problems arose, including defining what percentage of historical was sufficient, and how to take into account areas in which historical spawning areas seemed to be permanently lost. We also explored the idea of core areas, regions of very high utilization by one or more life stages. Again, there were several problems. Any rule that allowed some historical spots to be neglected ran the risk of having a core area neglected. Also, it wasn't clear that trying to force a former core area to become one once again always made sense. Spatial structure is dynamic, because the forces creating it are dynamic. For example, natural processes are constantly altering stream characteristics such as spawning substrate distribution and depth (Benda 1994, Reeves et al. 1995). In a properly functioning basin, natural processes will destroy habitat patches and create new ones. The relative importance of patches will be dynamic as well, with sources becoming sinks and vice versa. A healthy system will contain a diversity of patch quality and occupancy, as fish move from degrading patches into new high-quality ones. Core areas will come and go. The key to viability is insuring that the spatial structure processes create a dynamic structure that is always adequate to maintain the population. Trying to force a particular usage or dispersal pattern could easily be a misguided effort. Again, the goal is functionality.

In developing a viable spatial structure, existing structure needs to be considered. What structure there is should be conserved and used as a foundation in developing the recovery spatial structure. Special attention should be given to protecting existing core usage areas. Study of these areas and other currently used areas will be invaluable in understanding population-specific interactions of fish and habitat.

A key characteristic of spatial structure is connectivity. Adults must be able to get to the spawning grounds, fry must be able to get from spawning areas to rearing areas, and outmigrants must be able to go downstream to the Columbia River. Connectivity does not have to be

permanent, but needs to be seasonally adequate; that is, when fish need to move from one area to another, the areas need to be connected. In restoring connectivity, we should consider that existing connectivity may give us an erroneous picture of historical spatial structure. What may appear to be a connectivity problem for one species may limit the life-history diversity of another. Connectivity can be achieved by natural or artificial means. Natural connectivity is preferred over artificial means, such as trapping and hauling, for two reasons. First, human interventions into the natural life cycle of the fish may cause domestication, diminishing the ability of the population to sustain itself without that intervention. Second, assisted migration is inherently risky due the vagaries of funding and planning. However, we realize that achieving natural connectivity may be very difficult and perhaps not possible in the case of large dams, such as those on the Cowlitz, Lewis, and Willamette tributaries. Also, there may be occasions in many populations when assisted migration will avoid catastrophic losses.

Spatial structure is intimately associated with genetic differentiation. Spatial structure encompassing a diversity of habitats promotes genetic differentiation. Genetic differentiation in turn allows exploitation of new habitats and thus expands spatial structure. An appropriate spatial structure should therefore promote genetic differentiation, but how this translates to physical spatial structure is unclear. Clearly, quality habitat should be distributed in a way that encourages both natural patterns of fish dispersal and gene flow. However, maintaining the appropriate size and complexity of spatial structure is a difficult balancing act. In a healthy spatial structure, some patches may be so remote from others that homing fidelity will create some level of genetic differentiation, which is desirable. However, there may be a trade-off between distance and occupancy, with closer patches tending to be more occupied (Dunham and Reiman 1999). In addition, if patches are so distant as to be near those of other demographically independent populations, natural straying may blend populations. On the other hand, if the spatial structure is too restricted, occupancy may be assured but diversity and catastrophic risk may be increased. Although it was clear that too little or too much dispersal might have undesirable consequences, we were unable to distill these general ideas into criteria that would provide any real guidance.

A special case of genetic differentiation is the existence of subpopulations. In Myers et al. 2002, subpopulations are listed for many putative historical demographically independent populations, considering that there may have been some opportunity for genetic differentiation among major tributaries within a population's spatial area. In no case, however, was there actual evidence of subpopulations with any degree of genetic distinctness. So while it seems logical and desirable that historical subpopulation structure should be part of a viable spatial structure, we have virtually no guidance on what historical subpopulation structures were. Here is another case in which reference to other conspecific but less impacted populations in similar settings would be useful. Simple rules, such as insisting the population should inhabit all the major stream areas within its basins, simply do not consider the possible source-sink dynamics underlying what might have historically existed. An especially interesting case is putative historical demographically independent populations that span multiple basins draining independently into the Columbia, such as Elochoman fall chinook. The geographical range of this population includes both the Elochoman River and the Skamokawa Creek basins. In such cases, it makes sense to require some utilization of both basins, until it is shown that it is unlikely a single stock inhabited both.

A population's spatial structure should protect it from losses due to catastrophes (see Appendix K) or normal disturbance regimes. A single hundred-year flood, landslide, fire, or other catastrophic event should not be able to destroy a significant portion of the structure.

Avoiding risk from volcanoes will be difficult and perhaps impossible in basins near Mount St. Helens, Mount Rainier, and Mount Hood. There may also be some risk in the Willamette tributaries. A number of anthropogenic factors also need to be considered, with the most important being spills of toxicants. With so much of the drainages in the habitats of these ESUs close to railroads and sizable roads, spills of toxic chemicals can be a substantial risk. It is important to recognize that all populations in these ESUs use the Columbia River estuary for migration and possibly rearing, so catastrophic occurrences in the estuary can have far reaching impacts. Knowledge of catastrophic processes and recovery processes is critical to making correct decisions about this risk to structure (Dale et al. 1998). Normal disturbance regimes obviously need to be considered as well in terms of risk to spatial structure. Viewed in one sense, they are slow catastrophes. The normal disturbance regimes need to be understood sufficiently that recovery planners believe they will result in no net loss of structure.

Finally, we also considered the total geographical extent of a population's spatial structure: in physical terms, where it starts and ends. Technically, the spatial structure of any individual population in these ESUs includes the entire area occupied by the population during its life cycle. Thus spatial structure includes distribution and habitat from spawning and rearing areas in the natal basin, downstream into major migratory corridors (the Willamette and/or Columbia), and hundreds of miles into the ocean. We recognize that in practical terms the ability of local recovery planners to understand, influence, and monitor the spatial structure of a population diminishes drastically in the downstream direction to the point of extreme impracticality. It is therefore entirely understandable that most recovery planning with respect to spatial structure will be done at the watershed level. At the same time, however, the out-of-basin freshwater and nearshore areas need to be considered as critical areas for all populations. Thus, spatial structure criteria should include consideration of these geographical areas.

Strategies Selected

As explained and implied above, no single, simple rule for spatial structure will suffice for all populations of a given species or life-history type. Spatial structures that meet recovery criteria will be population-specific, reflecting the population's characteristics and the basin's processes. We offer general criteria addressing the concerns described above and leave it to the local recovery planning entities to develop objective measurable criteria that will adequately address the general concerns outlined above.

There seems a logical way for recovery planners to proceed with developing these objective and measurable, population-specific spatial structures. Both the current spatial structure and as much as possible of the historical structure for each population must be identified and mapped. If information on historical structure is lacking, then it can be inferred from historical habitat information and from relatively unimpacted conspecific populations in similar settings. As part of these analyses, highly productive (core) spawning, rearing, and migration patches must also be identified. Immediate steps should be taken to ensure the conservation of these areas, as they will almost certainly be the foundation of the viable spatial structure to be developed. For recovery purposes, a population's spatial structure should include all freshwater and nearshore areas it utilizes. This will require that recovery planners work collaboratively on these out-of-basin areas.

Locally developed, objective, measurable criteria for spatial structure need to address the following factors:

1. **Quantity.** A population's spatial structure must be large enough to support the growth and abundance levels required for viability. In other words, the habitat base and its utilization patterns must be adequate to support the population. A population's spatial structure should be considered to include all freshwater and nearshore areas it utilizes.
2. **Quality.** The habitat areas comprising the spatial structure must be of sufficient quality, demonstrated both by habitat attributes and utilization, for the life-history activities (spawning, rearing, migration, or a combination) taking place there. Habitat quality specifications have not yet been established for all criteria we consider critical, but an example of some types of habitat factors can be found in the Matrix of Pathways and Indicators (NMFS 1996). However, as described above, distribution of habitat types and variability in habitat factors should be the goal rather than a set of static minimums.
3. **Connectivity.** The spatial structure must have permanent or appropriate seasonal connectivity, demonstrated both physically and by utilization, that allows adequate migration between spawning, rearing, and migration patches. Normal weather fluctuations may result in occasional blockage or stranding of some individuals of particular life stages, but overall connectivity should be such that significant events are rare. Additionally, consideration should be given to establishing connectivity beyond the appropriate seasonal level, because connectivity may limit the expression of life-history diversity.
4. **Dynamics.** The spatial structure must not deteriorate in its ability to support the population over time. The processes creating spatial structure are dynamic, so it will change as habitat is created and destroyed, but the rate of patch destruction must not exceed the rate of patch creation. The spatial structure, evaluated in terms of habitat attributes and fish distribution, should remain relatively constant or grow in quality, size, and complexity over a long time frame. However, in the short term an immediate change from deteriorating to nondeteriorating habitat will be needed in most basins. Protection of existing core patches should be emphasized as well as restoration of other patches. Currently unoccupied but apparently suitable patches should also be maintained, because colonization may occur over a period of years.
5. **Catastrophic Risk.** The spatial structure should be geographically distributed in such a way as to minimize the probability of a significant portion of the habitat base or the population being lost due to catastrophic events, either anthropogenic or natural (Appendix K).

Risk Characterization

The approach the TRT has taken to integrating information from all population attributes requires that populations be characterized on a 0–4 scale for all attributes. Because spatial structure is so difficult to quantify, developing a scoring system for it is difficult, and a final

scoring system has not yet been developed. We offer here a tentative scoring system that is based on three general principles.

1. The scoring system needs to consider all five spatial structure subcriteria.
2. The five subcriteria differ in temporal scope. Clearly, quantity, quality and connectivity are criteria of more immediate importance than dynamics and catastrophic risk. It is also likely that more will be known about these three subcriteria than the other two.
3. The appropriateness of the spatial structure is tied to the population size that recovery planners specify. It doesn't make sense to give a very small but stable spatial structure a high rating. The possible downside to this third consideration is that it will invariably make the spatial structure score correlated with the abundance score. However, this also makes it logical: a large population cannot exist without the spatial structure to support it.

Score	Spatial Structure
0	Spatial structure is inadequate in quantity, quality, and connectivity to support a population at all.
1	Spatial structure is adequate in quantity, quality, and connectivity to support a population far below viable size.
2	Spatial structure is adequate in quantity, quality, and connectivity to support a population of moderate but less than viable size.
3	Spatial structure is adequate in quantity, quality, and connectivity to support population of viable size, but subcriteria for dynamics and/or catastrophic risk are not met.
4	Spatial structure is adequate in quantity, quality, connectivity, dynamics, and catastrophic risk to support viable population.

This scoring system is an initial attempt, and we expect to refine it considerably, especially with respect to quantitative levels. One factor that must be considered in the scoring system is the amount of information we have on the subcriteria, and thus our confidence that the subcriteria are being met. Some discounting of scores for suboptimal information quality seems appropriate, but how to do this without additional refinement of monitoring ideas is unclear at this time (see below).

Critical Uncertainties

The viability criteria guidelines above involve numerous critical uncertainties, some of which are resolvable and some of which are not. In most cases, resolving uncertainties will require a substantial investment of time and/or resources. In this section we describe some of the major uncertainties associated with spatial structure.

Perhaps the most important uncertainty relates to our reliance on historical conditions as a recovery template. Our overall method for dealing with uncertainty in developing viability criteria, such as the diversity and ESU-wide criteria, is to attempt a restoration of normative conditions, which in this case means a return as much as possible to historical processes and spatial structure. The assumption here is that historical conditions are a reasonable template for viability on a temporal scale of 100 years or more. This assumption may be reasonable, but we often lack the data or information to describe or understand historical conditions. We simply don't know how quickly populations were created or destroyed in the past. Our observations go back about a century, and most of the old records are of commercial catch, not size and distribution of individual populations.

Our understanding of the historical processes generating habitat is also limited. We have a reasonable understanding of large-scale geological and hydrological processes in these ESUs, but there is little smaller-scale or basin-specific information. For example, although we stress the importance of recognizing the dynamics of spatial structure, we have little understanding of the rate of patch cycling generally or specifically for the basins in these ESUs. It is known, however, that patches can be stable for 15 years or more (Bilby et al. 1999). An additional complication is the disruption of historical processes by land use and impoundments, as well as our limited knowledge of how quickly natural processes can be restored after disruption. By emphasizing restoration of the natural processes that create and destroy habitats, we can avoid some of the uncertainties inherent in an engineering approach (see Beechie et al. 2002).

There is little basin-specific information on historical spatial structure. What information there is (e.g., accounts in Myers et al. 2002) focuses on known or potential spawning areas. So, although we stress the importance of historical structure as a template, we expect that in most basins this will be largely conjecture. Perhaps the best that can be done in many cases is to model potential historical patches, based on the basin's geology and presumed hydrography. In many cases, there will also be gaps in information about current spatial structure and habitat conditions, simply a consequence of too many stream miles to survey for the available number of biologists. There are undoubtedly many stream reaches of these ESUs that have not been walked by management agency biologists in years. As already mentioned, knowledge of the spatial structure of relatively unimpacted conspecific populations in similar settings may be of some use in developing insights about viable spatial structures for particular populations.

Considerable debate surrounds our ability to precisely link habitat quantity and quality with fish production. Nevertheless, a number of studies have compared fish production to habitat characterizations at various levels of scale and sophistication to modelled population-size expectations. An example of a reasonably fine-scaled approach is the ecosystem diagnosis and treatment (EDT) method (Lichatowich et al. 1995, Mobrand et al. 1997), in which habitat is rated at a number of parameters to provide reach-by-reach values for equilibrium productivity and capacity. EDT (called HPVA in this document) estimates for productivity and capacity for a number of populations in the Lower Columbia and Upper Willamette ESUs are presented in Appendix J. Another approach is the work of Holsinger (2002) determining the chinook capacity of the Stillaguamish River: habitat spawner capacity is determined by typing physical habitat, then multiplying the quantities of typed habitat by the spawner densities observed for that habitat type in the basin. How precise these and other approaches are for predicting production is unknown.

Dispersal patterns and gene flow are critical factors in determining population structure, yet our understanding of natural gene-flow rates is poor. It is clear that homing to the natal

stream is determined by both genetic and environmental components (Quinn et al. 1991), but estimates of stray rates are highly variable, even within a given species (Quinn 1993). Most of the information on stray rates comes from recovery of coded-wire tags from hatchery releases, which raises questions about imprinting and stock origins. In addition, what constitutes a stray in terms of distance from the expected return site may vary from study to study.

The above discussion is just an overview of information gaps regarding the viability criteria. Each uncertainty encompasses several subsidiary uncertainties, each one a sizable area of study in itself. Clearly we need to know far more than we do now about spatial structure and fish-habitat relationships to be able to say with confidence that a given spatial structure will properly support a population over a sustained period of time. Understanding will come only from additional studies, especially of populations where historical processes still prevail, and from long-term monitoring. An adequate monitoring plan will include determining fish numbers and distributions at all life stages and measuring a large suite of habitat parameters. Monitoring spatial structure does not necessarily need to be continuous, but it does need to span extremes of variation in fish numbers and climatic conditions for changes in patch quality and occupancy to be evident. The duration of intensive monitoring should also be long enough to achieve an understanding of patch colonization, especially when evaluating restored or constructed patches. Wherever possible, monitoring should be linked to tests of specific hypotheses about population dynamics or fish-habitat relationships.

Monitoring and Evaluation

Monitoring spatial structure is conceptually simple within a given time stratum. There are two basic elements:

1. distribution and quantities of fish by life stage,
2. measurements of key habitat parameters in the areas where fish are present or desired to be present.

The information gathered in multiple time strata then must be compared to determine trends in either utilization or habitat quality. The same information will be used qualitatively to determine how natural forces shape spatial structure and to evaluate whether the structure is holding its own against change. Trend information will be especially important in evaluating the speed and magnitude of changes in utilization and habitat quality in response to habitat improvements.

Although it seems clear that a good monitoring program for spatial structure will utilize both distribution and habitat information, relying too much on one type can be misleading. There are dangers in relying too heavily on just distribution and abundance or on just habitat quality and quantity. As already mentioned, the complexity of metapopulation dynamics can make distribution misleading. Heavily occupied areas that are actually sinks may be incorrectly regarded as highly productive patches; conversely, some vacant areas may actually be high-quality source patches that are not occupied because of the population's dispersal dynamics. Similarly, our knowledge of fish production-habitat relationships is too sparse to rely solely on a habitat approach. Especially problematic is a situation in which fish may be abundant but the habitat imposes sublethal effects that may impair the population's productivity. For example, low

levels of particular classes of pesticides may impair salmon's olfactory sensitivity, potentially interfering with homing and antipredator behavior (Scholz et al. 2000).

Although simple in concept, monitoring habitat aspects of spatial structure seems extremely open-ended in terms of what variables should be monitored, with what precision, at how many places, and how often. These are difficult questions, which need to be addressed in a specific monitoring document, but some basic guidance is appropriate here. The simple answer is that monitoring has to be done in such a way to make recovery biologists confident that the criteria they set are met. What variables should be monitored will be determined largely by the habitat challenges in a given basin. Temperature will probably be a major concern everywhere. But perhaps sedimentation will be important in some areas and not others. The same goes for flow, turbidity, and a host of other variables. Precision requirements depend, of course, on how small an effect needs to be detectable, and in some cases detectability may determine which variables are chosen. We expect that habitat quality and fish distribution monitoring will be done in index areas. Perhaps several panels of such areas can be set up in a basin, with one panel done each year. A critical question, of course, is whether this type monitoring should be done for every population. It certainly should for every population that has to meet abundance criteria, but not necessarily for others. It is probably not necessary to monitor every year. However, it seems logical that monitoring be done most intensively at the outset of the recovery effort, then less frequently as we gain understanding of the dynamics of the spatial structure. Monitoring aimed at spatial structure is obviously closely related to monitoring for juvenile outmigrants and for diversity, and taking advantage of these commonalities can decrease costs.

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