Sensitivity of resident killer whale population dynamics to Chinook salmon abundance

Prepared by:

L. Antonio Vélez-Espino[1,£], John K.B. Ford[2], Charles K. Parken[1], Graeme Ellis[2], Eric Ward[3], Larrie LaVoy[4], Ken Balcomb[5], M. Bradley Hanson[3], Dawn P. Noren[3], Tom Cooney[4], Rishi Sharma[6,7]

(1) Salmon and Freshwater Ecosystems Division, Fisheries and Oceans Canada; (2) Marine Mammal Division, Fisheries and Oceans Canada; (3) Conservation Biology Division, Northwest Fisheries Science Center (NOAA); (4) Salmon Management Division, Northwest Region (NOAA); (5) Center for Whale Research, WA; (6) Columbia River Inter-Tribal Fish Commission; (7) Current: Indian Ocean Tuna Commission.

£ Pacific Biological Station
3190 Hammond Bay Road
Nanaimo, BC V9T 6N7
(250) 756-7119
Antonio.Velez-Espino@dfo-mpo.gc.ca

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EXECUTIVE SUMMARY

Two distinct populations of resident killer whales (*Orcinus orca*) in the northeastern Pacific Ocean have been listed in Canada and the U.S. as of conservation concern. The Southern Resident Killer Whale (SRKW) population is currently listed as endangered in both countries. The Northern Resident Killer Whale (NRKW) population has been listed as threatened in Canada. The major threats recognized for these two populations are nutritional stress associated to prey abundance levels and availability, pollution and contaminants, and disturbances from vessels and sound. An important difference in the population dynamics of these two populations is that, in spite of their home range overlap and potential access to similar resources, SRKW has remained at a population size of less than 100 individuals for the last four decades with an average of 85 individuals in the last decade whereas NRKW's population size has been generally increasing for the last 4 decades with 268 individuals at the end of 2011.

The predominance of Chinook salmon (*Oncorhynchus tshawytscha*) in the summer diets of both killer whale populations has been evidenced by recent studies, and there is also indication that the frequency of occurrence of Chum salmon (*O. keta*) increases in both populations at the end of the summer, surpassing Chinook salmon frequency of occurrence by early fall. Other studies have identified correlations between indices of Chinook salmon abundance and killer whale survival and fecundity rates and hypothesized strong linkages between Chinook salmon abundance and the population dynamics of resident killer whales. Additional effort is now required to quantify these linkages and their influence on the population viability of these two populations.

This study uses demographic models and population viability analysis (PVA) of endangered SRKW and threatened NRKW that incorporate linkages between killer whale vital rates (i.e., sex- and stage-specific survival probability and fecundity rates) and Chinook salmon abundance to address some of the pressing questions that have recently engaged the efforts of scientists and managers interested in: (1) the factors limiting population growth of SRKW; (2) explanations for the marked differences in the observed population trajectories of SRKW and NRKW in spite of their large home range overlap; (3) the role of Chinook salmon on the population dynamics of both killer whale populations; and, (4) the potential benefits for killer whale population viability expected from reductions in Chinook fishing mortality and changes in Chinook fishery regimes. Significant linkages between Chinook abundance and killer whale population viability were based not only on statistical significance but also on their influence on observed and expected population growth rates as quantified by retrospective and prospective perturbation analyses. In addition, we have provided a hypothesis framework designed to assist in the interpretation of results as they pertain to linkages between killer whale demographic rates and Chinook stock aggregates exhibiting different degrees of evidence based on diet-composition

studies. Moreover, the relevance of Chum salmon as a covariate of killer whale vital rates was also included in the study given the importance this species seems to have in both killer whale populations diet during the summer-fall transition.

Our results showed that, based on their demographic rates during the last killer whale generation (25 y), expected population growth is 0.91% annual decline ($\lambda_{stochastic}$ = 0.9909; 95% CI: 0.9719-1.0081) for SRKW and 1.58% annual increase ($\lambda_{stochastic}$ = 1.0158; 95% CI: 1.0027-1.0285) for NRKW. If the observed range of variation and covariation in its vital rates remain the same and mean vital rate values remain unchanged (i.e., status quo conditions), SRKW's extinction risk in 100 years is projected to be approximately 50%. In demographic terms, SRKW's lower expected population growth is mainly due to this population's lower production and survival of viable calves. In addition, greater variation in vital rates and a strong influence of demographic stochasticity on future population dynamics, both associated to a small population size, contribute to the lower population viability in SRKW. Based on the information used and produced in this study, we found no evidence that differences in demographic rates between killer whale populations are due to differential levels of access to common Chinook resources, to declines in Chinook abundance, or to increases in fishing mortality rates of relevant stocks. Although indices of Chinook abundance used in this investigation do not necessarily represent the Chinook salmon available for killer whales, they represent the best available information to address these questions.

Numerous interactions between Chinook abundance aggregates and killer whale vital rates were found. Although we found no evidence that current levels of Chinook abundance are limiting SRKW's population growth, the numerous significant relationships between Chinook abundance and the vital rates of both SRKW and NRKW are deemed as resulting from predator-prey dynamics. However, other factors (genetic, environmental and/or anthropogenic) must be at play limiting SRKW's population growth and possibly masking and confounding the detection of stronger interactions between killer whale vital rates and Chinook abundance. Moreover, the influence of cumulative effects of Chinook abundance levels on killer whale vital rates was also evident in this study. Thus, it seems important to develop alternative methods to quantify these effects while enabling pragmatic monitoring and tracking of benefits to killer whales generated by potential management actions.

Perturbation analyses showed there is a low sensitivity of killer whale population growth rates to changes in the Chinook abundance of multiple stock aggregates. Hence, the exploration of fishing scenarios focused on either the maximization of Chinook abundance or the maximization of vital rates for SRKW, depending upon which one occurred first. Given the clearly positive population growth in NRKW, population responses focused on either halting population growth or maximizing fishing mortality, depending upon which

one occurred first. The selection of scenarios for SRKW was justified by the implicit need to recover this population in terms of population size and population growth. The selection of scenarios for NRKW did not respond to a management objective *per se* but to our research objective of evaluating this population's response to changes in Chinook fishing mortality while gaining insights into the potential effects of large increases in harvest rates.

Although interactions were weak on both statistical and demographic grounds, some had support for causation given the weight-of-evidence regarding the importance of specific Chinook stocks in the killer whale diet. Chiefly, Fraser River (Fraser Early and Fraser Late) and Puget Sound Chinook emerged as important covariates of demographic rates of both killer whale populations. The size of Chinook terminal runs from the Fraser River and Puget Sound stock aggregates exhibited a low interaction with SRKW's fecundity. Nevertheless, PVA results showed that these low interaction levels could still produce slightly positive population growth rates approximately 50% of the time under extreme reductions to fishing mortality such as those resulting from the closure of ocean fisheries targeting these stocks. In the case of NRKW, it was the ocean abundance of the Fraser Early and Puget Sound aggregates that interacted with this population's fecundity and juvenile survival, respectively, and showed some potential to influence its expected population growth. In spite of the importance of Fraser River and Puget Sound Chinook salmon stocks to influence the population dynamics of both killer whale populations, it may not be pragmatic to precisely manage mixed-stock fisheries around few stocks. Furthermore, if new studies confirm the prevalent and critical importance (as resulting from killer whale's limitation to switch to other prey during winter and spring or when Chinook density is low) of Chinook salmon in the killer whale's year-round diet, pragmatic management could consider adjustments to coastwide Chinook ocean abundance. This combination of stock aggregate and abundance type was among the Chinook covariates with the largest influence on population growth rates of both killer whale populations.

Our analyses showed some support for Chum salmon as a covariate for killer whale vital rates and unlike relevant Chinook salmon aggregates, the declining trend in Chum salmon terminal run from the Northern/Central BC aggregate could be affecting prey availability for NRKW. These results point to the need for additional efforts to quantify the importance of Chum salmon on killer whale diet, and to identify the contributions of different Chum salmon stocks to killer whale diet during the fall and year-round.

Future research efforts are needed to identify the causes of depressed production and survival of viable calves in SRKW. Similarly, the continuance of studies of killer whale diet composition in fall, winter, and spring is deemed as essential to substantiate relevant interactions uncovered under some of the hypotheses in this study. This information is critical to move away from potentially spurious correlations and it is required to support causation.

The modelling components of most analyses conducted and described in this report have been compiled into a single programming platform using R software and provided in Appendix 8 to facilitate additional explorations of fishing scenarios and to enable future revision and development of the themes making up the present study.

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1. INTRODUCTION

Two distinct populations of resident killer whales (*Orcinus orca*) in the northeastern Pacific Ocean have been listed in Canada and the U.S. as of conservation concern. The Southern Resident Killer Whale (SRKW) population is currently listed as endangered under the U.S. Endangered Species Act mainly due to its small population size and vulnerability to demographic stochasticity and catastrophic events such as oil spills (NMFS 2008). In Canada, SRKW is listed as endangered due to its small and declining population size while the Northern Resident Killer Whale (NRKW) population is listed as threatened due to its small population size under the Species At Risk Act (COSEWIC 2008). The major threats identified for these two populations are nutritional stress associated with prey abundance levels and availability, pollution and contaminants, and disturbances from vessels and sound (COSEWIC 2008, NMFS 2008). An important difference in the population dynamics of these two populations is that, in spite of their home range overlap and potential access to similar resources (see Ford 2006), SRKW has remained at a population size of less than 100 individuals for the last four decades with an average of 85 individuals in the last decade whereas NRKW population size has been generally increasing for the last four decades with 268 individuals at the end of 2011. Average population growth rates of 2.3 percent per year for 14 years for downlisting and 28 years for delisting, respectively, were specified as recovery goals in the U.S. recovery plan for SRKW (NMFS 2008). In Canada, specific viability criteria are not provided in the recovery strategy and the recovery goals for these two killer whale populations (RKW; hereafter used to refer to both SRKW and NRKW) are to ensure their long-term viability (DFO 2008).

The availability of Chinook salmon (*Oncorhynchus tshawytscha*) has been identified as a potential limiting factor to the population dynamics of both SRKW and NRKW (COSEWIC 2008, Ford et al. 2010a, 2010b) and recent studies indicate the majority of the Chinook salmon stocks eaten by these two killer whale populations in their summer ranges and critical habitats originate mainly from the Fraser River and Puget Sound in the case of SRKW (Hanson et al. 2010) and Fraser River in the case of NRKW

(Ford and Ellis 2006, Ford et al. 2010a). Chinook stocks from Northern British Columbia (BC), Central BC, West Coast Vancouver Island (WCVI), Upper Georgia Strait, Puget Sound, and Upper Columbia River have also being identified as important in the summer diet of NRKW (Ford and Ellis 2006, Ford et al. 2010a). These studies also indicate that the frequency of occurrence of Chum salmon (*O. keta*) increases in both populations at the end of the summer and surpasses Chinook salmon frequency of occurrence by early fall (Ford and Ellis 2006, Ford et al. 2010a). Chum salmon in NRKW's diet originate mainly from Fraser, east coast Vancouver Island, and Southern British Columbia coast stocks (Ford and Ellis 2006, Ford et al. 2010a) whereas Puget Sound Chum salmon is believed to be the prevalent Chum salmon source in SRKW's fall diet (B. Hanson, pers. comm.). Recent studies have recognized correlations between indices of Chinook salmon abundance and RKW survival rates (Ford et al. 2010b) and fecundity (Ward et al. 2009) and hypothesized strong linkages between Chinook salmon abundance and RKW population dynamics. Additional effort is now required to quantify these potential linkages and their influence on RKW population viability.

This study uses demographic models of endangered SRKW and threatened NRKW that incorporate linkages between RKW vital rates rates (i.e., stage- and sex-specific survival probabilities and fecundity rates) and prey levels, specifically including Chinook salmon abundance. These models are used to address the following objectives: (i) to quantify the differences in demographic rates between SRKW and NRKW; (ii) to determine the relative influence of RKW's vital rates on observed and expected population growth; (iii) to assess the sensitivity of RKW's population dynamics to Chinook abundance; and, (iv) to quantify the necessary changes in Chinook fishing mortality required to attain recovery targets or to maximize benefits to population growth. In addition, and as a logical extension of this modeling framework, population viability analysis (PVA) is conducted to assess SRKW and NRKW extinction risk and probabilities of falling below abundance thresholds as well as recovery probabilities given alternative levels of Chinook abundance resulting from selected fishing scenarios.

2. METHODS

2.1 An overview of the approach

Extensive work has been conducted compiling and structuring life history data for SRKW and NRKW (Bigg et al. 1990, Olesiuk et al. 1990, Olesiuk et al. 2005, NWFSC 2008, The Center for Whale Research 2012), identifying prey in general (Ford et al. 1998, Ford and Ellis 2006) and Chinook salmon stocks in particular eaten by RKW (Ford et al. 2010a, Hanson et al. 2010), and posing hypotheses on the role Chinook salmon availability plays at limiting RKW's vital rates and population dynamics (Ford et al. 2010b, Ward et al.

2009). This investigation builds on these previous efforts by conducting perturbation analyses of RKW stochastic matrix models constructed with up-to-date RKW demographic data representing SRKW and NRKW population dynamics in detail while facilitating the incorporation of vital rates as random variables in some cases and as a function of stock-specific (or stock aggregates) Chinook abundance in others and test hypotheses regarding RKW-Chinook salmon interactions. Chinook stocks from northern California to southeast Alaska were included in the analysis of interactions.

Rarely is one line of evidence sufficient to demonstrate causation, and assembling information from various sources is useful to determine the weight-of-evidence (Burkhardt-Holm and Scheurer 2007). Box 1 details two hypotheses for each RKW population, where hypotheses 1a for SRKW and 1b for NRKW correspond to RKW-Chinook salmon interactions supported by additional evidence in the form of diet-composition studies. Statistical significance in these interactions will provide stronger weight-of-evidence for causation than the remaining hypotheses 2a (SRKW) and 2b (NRKW). Statistical significance of the latter hypotheses would provide weaker weight-of-evidence for causation because they rest on the assumption that Chinook salmon remains a determinant diet component year-round in the RKW's diet and outside their critical (summer) habitats.

The probability of RKW encountering and preying on specific Chinook stocks would directly depend on the size of the stock or stock aggregate (i.e., the larger the stock the greater the probability of encounter), its ocean (pre-terminal) distribution, and its terminal run timing and distribution. Hence, the selection of stocks encompassed in hypotheses 2a and 2b were based on three criteria: stock size, and both temporal and spatial overlap with RKW. The final selection of stocks and stock aggregates to be considered under each hypothesis was determined via expert opinion, based on those criteria, in a 2-day workshop at the Pacific Biological Station, Nanaimo BC, on November 14-15, 2012.

Box 1. Hypotheses addressed in this investigation regarding RKW-Chinook salmon interactions.

- Hypothesis 1a (based on current evidence):
  there is a strong link between SRKW population growth and the terminal run size[1] of Fraser Early, Fraser Late, and Puget Sound Chinook stocks[2]

- Hypothesis 1b (based on current evidence):
  there is a strong link between NRKW population growth and the terminal run size[1] of Northern BC, Central BC, WCVI, Upper Georgia Strait, and Lower Georgia Strait Chinook salmon stocks as well as the ocean (pre-terminal) abundance of Fraser Early, Puget Sound, and Upper Columbia Chinook stocks[2]

- Hypothesis 2a (assuming Chinook salmon remains an important diet component year-round and outside identified critical habitats):
  there is a strong link between SRKW population growth and the terminal run size of large stocks such as Sacramento Fall, Klamath Fall, Columbia Upriver Brights, Columbia Spring/Summer/Fall, Oregon Coastal, WCVI, or coastwide (excluding Northern BC, Central BC, and Southeast Alaska[3]), as well as the ocean (pre-terminal) abundance of ocean-type[4] stocks with large contributions to ocean fisheries such as WCVI, Columbia Upriver Brights, Fraser Late, Oregon Coastal, Puget Sound, or coastwide (excluding Southeast Alaska[5])

- Hypothesis 2b (assuming Chinook salmon remains an important diet component year-round and outside identified critical habitats):
  there is a strong link between NRKW population growth and the terminal run size of Fraser Early and Puget Sound[6], and large stocks such as Columbia Upriver Brights, Columbia Spring/Summer/Fall, Fraser Late, Oregon Coastal, or coastwide (excluding Sacramento Fall, Klamath Fall[7] but including Southeast Alaska[8]), as well as the ocean (pre-terminal) abundance of ocean-type [3] stocks with large contributions to ocean fisheries such as WCVI, Fraser Late, Oregon Coastal, or coastwide (excluding Southeast Alaska[5])

  1 The terminal run includes terminal catch, which occurs after fish are available for killer whales, and therefore represents the Chinook available for RKW in their summer ranges.

  2 Based on diet composition studies

  3 Out of the known preferred geographic range of SRKW

  4 Ocean-type Chinook stocks spend most of their ocean life in coastal waters and are therefore within known RKW geographic range

  5 South East Alaska Chinook salmon stocks exhibit a stream-type life history and perform extensive offshore oceanic migrations, and it is unlikely they are available for RKW. These stocks contribute on average less than 1% to the Chinook salmon available for PST ocean (pre-terminal) fisheries

  6 Although Fraser Early is not among the larger stocks, NRKW encounters with both Puget Sound and Fraser Early terminal runs could be greater than determined by current observations

  7 Out of the known preferred geographic range of NRKW

  8 Within the known geographic range of NRKW

Figure 1 depicts the flow of data and analytical steps towards the execution of demographic perturbation analyses (Caswell 2000). Prospective evaluations (Brault and Caswell 1993, Fujiwara and Caswell 2001, Vélez-Espino and Koops 2009a) were conducted to quantify the relative effects in SRKW and NRKW population dynamics associated with interactions between RKW vital rates and the abundance of Chinook salmon stocks in an hypothesis-driven framework (see Box 1). A retrospective evaluation (i.e., life table response experiments (LTRE; Cooch et al. 2001, Bruna and Oli 2005) was conducted to identify those demographic factors underpinning the observed variation in RKW abundance and population growth. Perturbation analyses, when combined with recovery goals and fishing scenarios, were used to quantify the sensitivity of SRKW and NRKW population growth and viability to changes in Chinook abundance.

Perturbation analyses are based on the analysis of asymptotic dynamics and stable stage distributions (SSD), and many risk assessments of endangered species ignore the importance of transient dynamics caused by deviations from the SSD (Wiedenmann et al. 2009). Transient dynamics of long-lived, slow reproducing species (e.g., killer whales) are more responsive to population state than short-lived, fast reproducing species (Koons et al. 2005). This could be important for RKW since population growth rates derived from SSD can be a biased estimate of short-term population growth rate when population structure is unstable. For these reasons we studied transient dynamics in SRKW and NRKW to inform the minimum length of time horizons recommended for PVAs.

Future population dynamics, including probability of recovery and extinction risk, ideally require demographic models because they are the only framework that can integrate the vital rates that determine expected change in population size (Caswell 2001). The second research component, population viability analysis (PVA), was based on demographic simulations with linkages to changing levels of Chinook salmon abundance defined by specific fishing scenarios. Figure 2 shows how input data for relevant fishing scenarios is combined with the results of the analysis of transient dynamics and the incorporation of demographic and environmental stochasticity, to run PVAs allowing the exploration of the influence of Chinook abundance on RKW extinction probabilities. In addition, this framework was also used to evaluate probabilities of recovery for SRKW on the basis of their identified U.S. recovery goal of an average growth of 2.3 percent per year for 14 years for downlisting and 28 years for delisting (NMFS 2008).
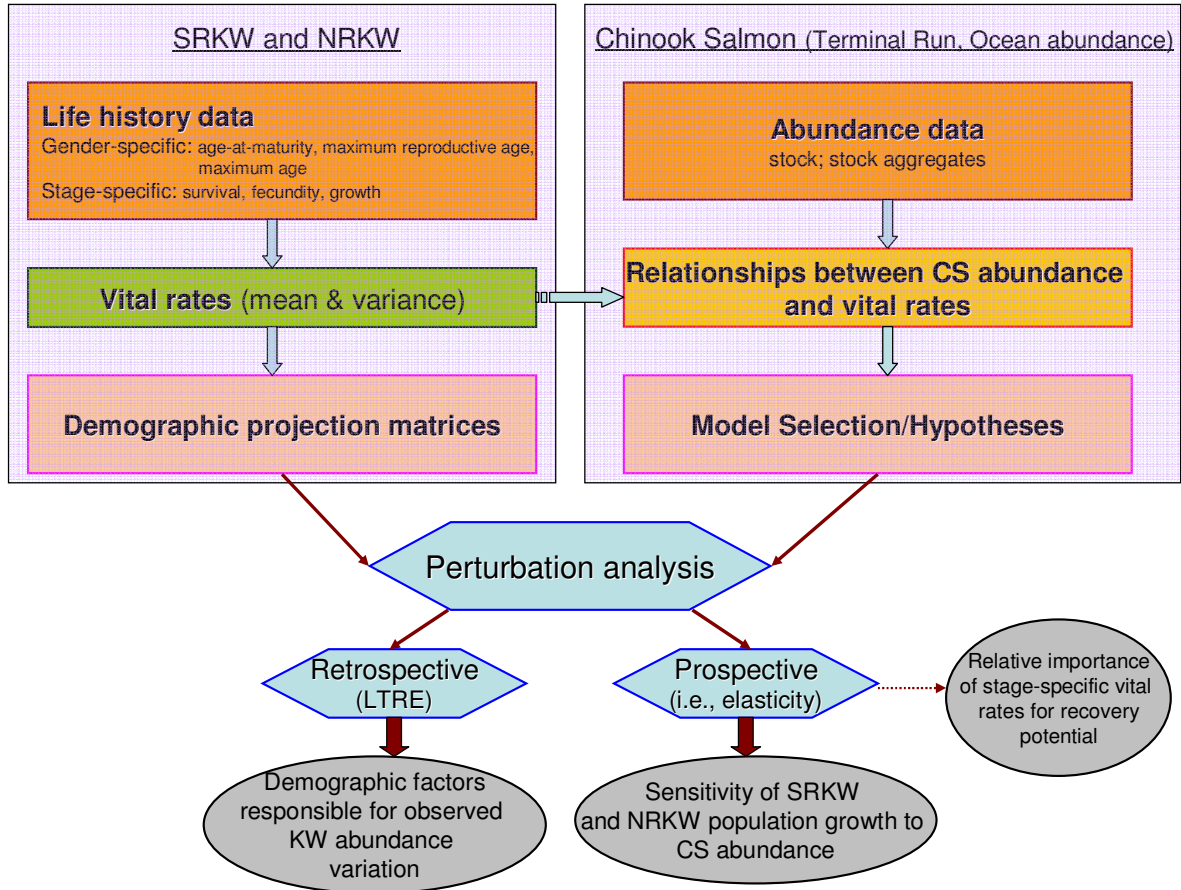
Figure 1. Flow diagram showing data components and major analytical steps towards the execution of retrospective and prospective demographic analyses, including the sensitivity of SRKW and NRKW viability to the abundance of Chinook salmon (CS) stocks within the hypothesis framework in Box 1.
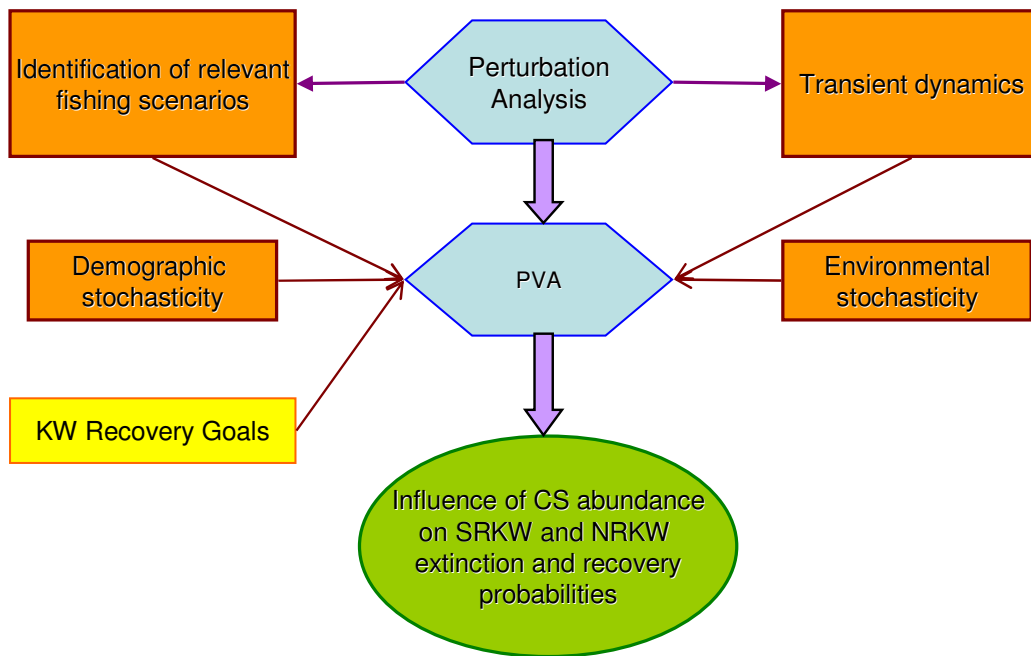
Figure 2. Flow diagram showing the elements of the PVA for SRKW and NRKW, including the role of prospective perturbation analysis, to assess the relationship between extinction and recovery probabilities and Chinook salmon (CS) abundance.

2.2 Killer whale matrix population modeling

Matrix models constitute a demographic approach to the quantitative analysis of population responses to perturbations that has proven to be robust to many parameter uncertainties (de Kroon et al. 2000, Heppell 2007). These models have also proved to be valuable and efficient tools to address relevant management questions related to conservation and recovery of aquatic populations (Getz and Haight 1989, Vélez-Espino and Koops 2009b), mammals in general (Heppell et al. 2000, Oli and Dobson 2003) and cetaceans in particular (e.g., Brault and Caswell 1993, Caswell et al. 1998; Fujiwara and Caswell 2001). The life cycle of SRKW and NRKW was represented by two separate stage-structured matrix models because these two populations are demographically isolated with no interchange of individuals between them (Bigg et al. 1990). There is no evidence of NRKW males fathering SRKW offspring, or viceversa, therefore reinforcing the demographically isolated nature of these two populations (Ford et al. 2011). SRKW and NRKW populations are also

acoustically, genetically, and culturally distinct (Ford et al. 1998, Ford et al. 2000, Barrett-Lennard and Ellis 2001, Ford et al. 2011).

The life cycles of these two populations were modeled as two-sex stage-structure models with seven life stages: (1) calves (individuals in the first year of life); (2) juveniles (past one year but no mature [ages 1-9]; mostly undetermined sex); (3) young reproductive females (ages 10-30); (4) old reproductive females (ages 31-50); (5) post-reproductive females (51 year old and older); (6) young mature males (ages 10-21); and, (7) old mature males (22 year old and older). Note that, for practical reasons, some figures and tables use "Female 1", "Female 2", and "Female 3" to refer to model stages 3, 4 and 5, and "Male 1" and "Male 2" to refer to model stages 6 and 7. Although most matrix models portray only female demography, significant differences in life history traits between female and male killer whales (Olesiuk et al. 1990, Olesiuk et al. 2005) would be better represented by two-sex models. Age intervals are similar to those in Krahn et al. (2004), but we decided to split the reproductive females stage into two stages (young and old) to account for differences in reproductive potential associated to reproductive senescence (Ward et al. 2010) and, based on current data, updated the age at maturity (10) and maximum reproductive age (50) of females. Similarly, mature males were split into two stages because there is evidence for a clear increase in male reproductive success with age (Ford et al. 2011). The latter study found no evidence for male reproductive senescence.

The life cycle and its corresponding population matrix are shown in Figure 3 and Figure 4, where P_i is the probability of surviving and remaining in stage i, G_i is the probability of surviving and moving to the next stage, and F_i is the fertility rate of stage i. In Figure 4, $P_1 = 0$, because the length of the calf stage is equal to the projection interval (1 year). The term F_2 for reproductive output of juveniles represents those individuals that mature and reproduce during the projection interval (Crouse et al. 1987, Brault and Caswell 1993). A stage-structured model requires defining three lower-level parameters, namely vital rates: σ_i as the annual survival probability of an individual in stage i, γ_i as the probability of moving from stage i to stage j given σ_i, and μ_i as the mean offspring production by females in stage i (hereafter referred also as "fecundity" to differentiate from the "fertility" matrix element F_i). Then, the matrix elements P_i and G_i are defined as σ_i (1-γ_i) and $\sigma_i \gamma_i$, respectively, where the term γ_i is the reciprocal of the stage duration. Only G_2 included an additional parameter to represent the proportions of juveniles transitioning into young reproductive females (φ_f) or young mature males (φ_m) as $G_{2f} = \sigma_2 \gamma_2 \varphi_f$ and $G_{2m} = \sigma_2 \gamma_2 \varphi_m$. These proportions were computed from the total number of 10-year old males or females during the study period (1987-2011); age-10 is the first age class within the young-reproductive-female and young-mature-male stages. Since births occur year-round, a birth-flow matrix variant (Caswell 2001) was used, with $F_i = \sigma_1^{0.5} \left((1+P_i) \mu_i + G_i \mu_{i+1} \right) / 2$ and $G_1 = \sigma_1^{0.5}$, where $\sigma_1^{0.5}$ is the probability of a viable calf individual surviving the first half of the

first age interval, at which time it will be counted in $t+1$. We did not base these computations on newborn individuals because not all killer whale births are observed, which means that pregnancy rates and birth rates are expected to be higher than the recruitment of viable calves (see Olesiuk et al. 1990). Thus, viable calves are defined as those individuals that survived to at least 0.5 years of age. For convenience, we refer to this stage simply as calves in most of the remaining sections.

Since most births seem to occur between fall and spring (Bigg et al. 1990, Olesiuk 1990) and most encounters (RKW sightings) occur during the summer months (Ford 2006), individuals encountered in the summer are assumed to be censused at the midpoint between birthdays. Thus, January 1st was used to determine stage affiliations in a given year and as the beginning of the projection interval. Vital rates were computed following a horizontal life table approach where the fate of particular cohorts was followed through time as it aged, thus eliminating the bias introduced by violations to the stationarity assumption embedded in vertical life tables (Wunsch et al. 2002). Vital rates σ_i and μ_i were therefore computed as:

$$\sigma_{i,t} = \frac{n_{i,t+1}}{n_{i,t}} \tag{1}$$

and

$$\mu_{i,t} = \frac{\text{\# viable calves by females in stage } i \text{ at year } t}{\text{\# females in stage } i \text{ at year } t} \tag{2}$$

Notice that although neonate mortality is unknown, it is absorbed into the fecundity rate in Equation 2 (see also Olesiuk et al. 1990).
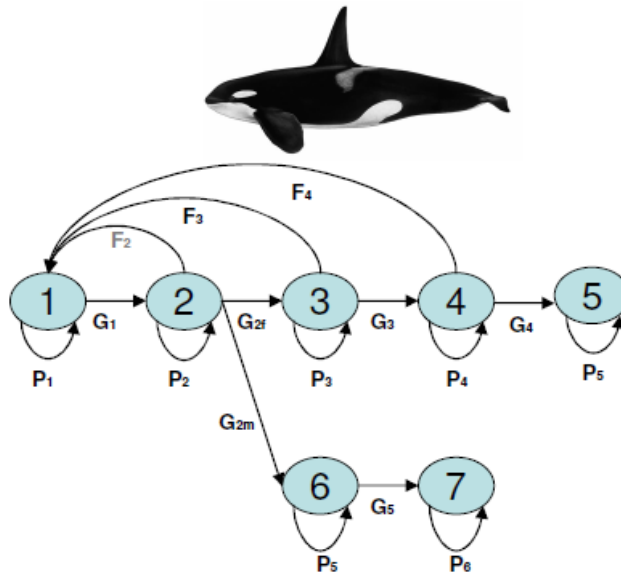
Figure 3. Stage-structured life cycle of resident killer whales with seven life stages: (1) calves; (2) juveniles; (3) young reproductive females; (4) old reproductive females; (5) post-reproductive females; (6) young mature males; and (7) old mature males. F_i represent fertility; G_i represent stage transition probabilities, with female and male juvenile-to-adult transitions indicated as G_{2f} and G_{2m}, respectively; and, P_i represent the probability of surviving and remaining in stage i.

$$M = \begin{pmatrix} 0 & F_2 & F_3 & F_4 & 0 & 0 & 0 \\ G_1 & P_2 & 0 & 0 & 0 & 0 & 0 \\ 0 & G_{2f} & P_3 & 0 & 0 & 0 & 0 \\ 0 & 0 & G_3 & P_4 & 0 & 0 & 0 \\ 0 & 0 & 0 & G_4 & P_5 & 0 & 0 \\ 0 & G_{2m} & 0 & 0 & 0 & P_6 & 0 \\ 0 & 0 & 0 & 0 & 0 & G_5 & P_7 \end{pmatrix}$$

Figure 4. Stage-structured projection matrix corresponding to the resident killer whale life cycle in Figure 3. Upper left sub-matrix describes the production of juveniles and mature females by females, the lower left sub-matrix the production of mature males by females, the lower right sub-matrix the production of mature males by males, and the upper right sub-matrix the production of females by males.

Alternative killer whale matrix population models were used for some aspects of this investigation and included a model with gender identification at birth and a truncated female-only model that excluded post-reproductive females (Appendix 1).

2.3 Data sources

2.3.1 Killer whale demographic data

Demographic data for resident killer whale were obtained from long-term registries maintained by the Cetacean Research Program, Pacific Biological Station, CDFO (for NRKW), and the Center for Whale Research, Friday Harbor, WA (for SRKW). These registries are based on annual population surveys using photo-identification of individual whales from natural markings. Surveys have occurred annually without interruption since 1973 for NRKW and 1974 for SRKW. Each year, all observed animals in the populations are photo-identified to establish the status of individuals (e.g., reproductive state) and to document new births and deaths. Since these field studies began, 734 whales have been documented, 350 of which were alive in 2010. Of these, about 85% were born since the study began. These precise demographic data have been used successfully in the past to develop detailed population dynamics models and related analyses (Olesiuk et al. 1990, 2005, Ford et al. 2005, 2010, Ward et al. 2009, 2010).

Although encounter data go back to the early 1970's, thisstudy focuses on demographic data derived from a horizontal life table encompassing the last 25 years (1987-2011), which represents approximately one generation time in both populations (Olesiuk et al. 1990, Olesiuk et al. 2005). This step was considered important not only to remove from the analyses the effect on stage structures caused by the large live-capture fisheries in the 1960's and 1970's but also to include mostly census data generated by direct observations rather than reconstructed life table data as for the early years of RKW demographic studies. Life history and demographic data for the earlier years of the full time series were thoroughly reconstructed to fill age information gaps (see Olesiuk et al. 1990). The procedures for reconstruction relied on numerous assumptions such as (i) female age at first birth remained constant, (ii) genealogical trees by Bigg et al. (1990) were accurate, (iii) calving intervals remained constant, (iv) survival rates remained constant. For a count-based model some of these assumptions may have a small weight but they matter for demographic modelling. The quality of demographic and life history data improved with the years of study to the point that today both populations are censused with high standards. The first criterion influencing our time-period selection was to base our analyses on the best data possible (the data set with the least uncertainty). Another factor contributing to the quality and attributes of the demographic data for the earlier years of the full time series is that it begins right after the end of the killer whale live-capture fishery,

which for resident killer whales lasted from 1962 to 1973 (Bigg 1975, Olesiuk et al. 1990). This fishery was heavily biased towards juveniles and young males and impacted more heavily the SRKW. Consequently, this fishery affected not only population size but also the structure of the population (Appendix 2). The purging of this perturbation on population structure can take several years. Thus, a second criterion in our decision was to base our analyses on years with RKW population structures more representative of current conditions while trying to minimize the effect of the live-capture fishery on demographic rates. This is crucial for population projections since the population structure observed in the first years of the time series of encounter data is radically different from that of the present (Appendix 2). Lastly, generation time is relatively stable in long-lived, late maturing populations. We estimated a generation time of ~25 years in both SRKW and NRKW, similar to those estimated by Olesiuk et al. (1990, 2005) and Caswell (2001), and decided to use a time series long enough to represent at least one generation. Given these three criteria, we based our analyses on the last 25 years of the time series (1987-2011), equivalent to one RKW generation time. This period includes high quality data with ~75% of the RKW individuals alive in 2011 born during the selected 1987-2011 period.

In addition, one limitation with using early times series for the analysis of interactions between RKW and Chinook salmon is the uncertainty of the pre-terminal exploitation rates for Chinook salmon, since fewer stocks were represented by coded wire tags compared to the recent period (PSC 2011a). In the 1970s, coded wire tags (CWT) were being explored as a new technique for Chinook salmon assessments in BC and by 1980, three of the 11 Canadian stock groups had CWT-based estimates of pre-terminal fishing rates. However, during the next decade the CWT program flourished in BC and by 1991, 10 of the 11 stock groups had CWT-based estimates of pre-terminal fishing rates.

2.3.2 RKW life table uncertainties

For animals of uncertain year of death, amortized partial values were used. For instance, an animal with probable death over a span of two years was counted as 0.5 for the first year and 0.0 for the second year. There were few age 10-14 NRKW individuals of unknown sex between 1996 and 2011. The sex ratio of NRKW's known-sex individuals of age 10-14 for this period was used to assign sex for annual counts.

2.3.3 Chinook salmon abundance (terminal run and ocean abundance)

Two sources of Chinook salmon abundance data were used: (1) time series of vulnerable cohort abundance reported by the Pacific Salmon Commission's Chinook Technical Committee (CTC) model were used as ocean abundance metrics for subsequent analyses

(these cohort abundances vulnerable to ocean fisheries are the stock components of AABM[1] fishery indices); and, (2) terminal run reconstruction indices (age-3 and older fish) derived from time series assembled by R. Kope and C. Parken (Appendix 3) were used as terminal run metrics for subsequent analyses. Indices of terminal run were based on direct run reconstruction using coded wire tag recoveries for stocks from Canada, spring-runs in the Upper Columbia River, and stocks originating south of Cape Blanco, and using the CTC model estimates for others (PSC 2011a).

For the exploration of fishing scenarios where changes in terminal run size occur as a result of changes in ocean (i.e., pre-terminal) harvest rates, terminal run equivalents (*TRE*) were used to account for the fact that only a portion of the fish not caught in ocean fisheries in a given year is expected to become part of the terminal run according to their maturation rates (*MR*), which are time-variant and stock specific. Using up-to-date catch and *MR* data by age (*a*) from CTC exploitation rate analyses (data required to generate *TRE*s for Sacramento Fall and Klamath Fall were obtained from PFMC 2012), *TRE* for an indicator stock by calendar year (*y*) were computed as:

$$TRE_{indicator,y} = \sum_{PreTerm\ Fishery} \sum_{a=3}^{6} Catch_{a,y} * MR_{a,y}$$

(3)

*TRE*s were then used to compute both proportional increases in terminal run size in the absence of pre-terminal fishing and the terminal run scalars resulting from a specified change in ocean harvest rates in CTC exploitation rate indicator stocks. These scalars were then used to calculate changes in terminal run of a stock of interest following procedures detailed in Appendix 4. This data was then used for the exploration of fishing scenarios (Section 2.7).

2.3.4 Other covariates

In addition to Chinook salmon abundance, there are several other covariates that might contribute to fluctuations in RKW population dynamics, namely, non-Chinook prey, environmental indices, and intrinsic population effects such as density dependence. Trying to minimize covariate confounding effects and focusing on covariates that could be influenced by management actions, it was decided to include Chum salmon abundance as an additional covariate. While Chinook salmon represent the majority of RKW diet in

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[1] Aggregate Abundance-Based Management (AABM) fisheries encompass all mixed-stock ocean fisheries under the Pacific Salmon Treaty and include southeast Alaska sport, net, and troll (SEAK), northern British Columbia troll and Queen Charlotte Islands sport (NBC), and west coast Vancouver Island troll and outside sport (WCVI).

summer months (Ford et al. 2010a, Hanson et al. 2010), less is known about the seasonal importance of other fish species in non-summer months. Recently, Chum salmon runs have been recognized as an important component of the fall diet (Ford et al. 2010a, Hanson et al. 2010). Terminal run reconstructions of BC Chum salmon for years 1980-2010 compiled by CDFO (David Peacock, Prince Rupert BC; Pieter Van Will, Port Hardy BC) were stratified as Northern/Central BC (areas 1-13) and Southern BC (areas 14-29, including Fraser River). While Northern/Central BC Chum included both summer and fall run types, Southern BC Chum included only fall run type; summer Chum comprise only a small portion of the aggregated Southern BC terminal run. Chum terminal run data from Washington for years 2000-2009, compiled by the PSC Chum Technical Committee (PSC 1987 to 2011b), was stratified as Washington Fall (by far the largest component) and Washington Summer/Fall/Winter.

2.4 Functional relationships between RKW vital rates and Chinook salmon abundance

Associations between RKW vital rates (fecundity and survival) and Chinook abundance were evaluated in light of the four hypotheses in Box 1. Beta regressions (Cribari-Neto and Zeileis 2010) with abundance lags 0 and 1 were used to examine relationships with survival rates whereas abundance lags 0, 1, and 2 were used to examine relationships with fecundity. Beta regressions incorporate features such as heteroscedasticity or skewness which are commonly observed in data taking values in the standard unit interval, such as rates or proportions. The rationale for the use of lag-1 models for survival is that the effects of nutritional stress can be capitalized on mortalities the next year after food shortage occurred. The study of Ford et al. (2005) revealed that mortality deviations were most highly correlated to changes in Chinook abundance after a lag of one year. Following the same rationale, lag-2 models were used for fecundity to account for malnutrition or starvation effects on pregnancy as well. Pregnancy lasts about a year in RKW. In addition, and in order to account for cumulative effects of Chinook abundance on RKW vital rates, a 5-year running average (Chinook abundance from t-4 to t) was also used for regression analyses.

Likelihood based model selection tools (AIC; Burnham and Anderson 2002) were used for model selection between simple beta-regression models with Chinook salmon abundance as only predictor and multiple beta-regression models including both Chinook and Chum salmon abundance as predictors. Beta-regression models were fit to the data and a stepwise approach was used to identify the best subsets of predictors (combinations of abundance type and time lags for both Chinook and Chum). The existence of marginal increases in Chinook regression coefficients was used as a second criterion for model selection. Thus, a multiple beta regression with Chinook and Chum as independent

variables was considered superior to a simple beta regression with Chinook only when two criteria were met: (i) a lower AIC value, and (2) a marginal increase in its Chinook regression coefficient. This model-selection process was structured by hypothesis (Box 1) and vital rate. In addition, variance inflation factors (VIFs) were calculated to quantify collinearity levels (Hair et al. 2006) in the multiple beta-regression models. Multiple beta-regression models were discarded when VIF values were greater than 5, indicating collinearity problems with the predictors in a given model.

2.5 Perturbation analysis

Demographic perturbation analysis asks how population statistics respond to changes in the vital rates that determine matrix entries (Caswell 2001). Important population performance statistics derived from this analysis are the asymptotic population growth (λ), the stable stage distribution (SSD), and the reproductive values (RV). The term λ is represented by the largest eigenvalue of a projection matrix. Notice that λ represents the expected population growth rate (assuming vital rates means and variances are going to remain stable in the long term) and not the observed or realized population growth, which is the rate of change computed from counts of total population size. A population is projected to be at equilibrium when $\lambda = 1.0$, declining when $\lambda < 1.0$, and growing when $\lambda > 1.0$. The SSD is represented by the right eigenvector (**w**) of a projection matrix, which indicates the proportion of the population in each stage once enough time has passed to dampen fluctuations due to initial conditions, while RV is described by the left eigenvector (**v**) of individuals in each stage (de Kroon et al., 1986). Perturbation analysis is used in two distinct ways. Prospective analyses (sensitivity and elasticity) explore the functional dependence of λ on the vital rates. They predict the changes in λ that would result from any specified change in the vital rates and are independent of previous patterns of variability of the vital rates. Retrospective analyses (e.g., life table response experiments LTRE) express observed variation in λ as a function of observed covariation in the vital rates. Those results are specific to the observed pattern of variation. Sensitivity and elasticity analysis can be used to identify potential management targets because changes in vital rates with high sensitivity or elasticity will produce large changes in λ (Vélez-Espino et al. 2006). Retrospective analyses cannot identify potential management targets because they compare the contributions of past changes in vital rates, not the effects of future changes (Caswell 2000). However, past fluctuations in vital rates or their covariates (e.g., Chinook abundance) could inform management actions if these fluctuations can be predicted with low levels of uncertainty.

Demographic modelling of SRKW and NRKW was conducted to inform prospective and retrospective perturbation analyses, and make inferences about the demographic components of these two populations responsible for the observed differences

in population growth and stage structure as well as their relative dependence on stock-specific Chinook salmon abundance. Although life history and population dynamics of SRKW and NRKW have been studied in the past (Olesiuk et al. 1990, Brault and Caswell 1993, Krahn et al. 2002, 2004, Olesiuk et al. 2005), perturbation analyses within the context of Chinook salmon linkages are a novel contribution to our understanding of SRKW and NRKW population dynamics that could be used in the future to inform conservation and management decisions. Moreover, the identification of factors driving past and present population dynamics of SRKW and NRKW is expected to bring new light to explain observed SRKW's small population size and limited population growth.

2.5.1 Prospective

The influence of vital rates on the population growth rate is indicated by the partial derivatives of λ with respect to a_{kl}, the individual elements of the matrix. Elasticities (ε_{kl}) scale these derivatives to adjust for the magnitude of the vital rates (i.e. reproductive rates in some species can be several orders of magnitude larger than survival probabilities), and they are calculated as:

$$\varepsilon\left(a_{kl}\right) = \partial \log \lambda / \partial \log a_{kl} \qquad (4)$$

Elasticities of matrix elements are additive and sum to one. Multiplying the elasticities by λ produces a set of contributions which sum to λ, and the ε_{ij} themselves give the relative contribution of each transition to λ (de Kroon et al. 1986). Equation 1 calculates the elasticities of matrix elements, not vital rates (v_i), which usually contribute to more than one matrix element (see Section 2.2). Thus, the chain rule for differentiation was used as a first order computation of vital rate elasticities:

$$\varepsilon\left(v_i\right) = \frac{v_i}{\lambda} \frac{\partial \lambda}{\partial v_i} = \frac{v_i}{\lambda} \sum \frac{\partial \lambda}{\partial a_{kl}} \frac{\partial a_{kl}}{\partial v_i} \qquad (5)$$

These analytical solutions are robust for perturbations up to 30% and occasionally up to 50% (Caswell 2001). Nonlinearities, often exhibited between vital rates and λ (see Mills et al. 1999; de Kroon et al. 2000), reduce the accuracy of projections using elasticities for larger perturbations. Hence, we also conducted prospective perturbation analysis by directly perturbing the projection matrices (Ehrlén and van Groenendael 1998). Direct perturbations can involve an iterative process, altering the magnitude of the vital rate in question while keeping all other matrix elements unchanged.

2.5.2 Sensitivity of RKW population growth to Chinook salmon abundance

This component of the analysis is the core of the demographic analysis and deals with the linkage between Chinook salmon abundance and RKW population dynamics. Mean elasticities of interactions between individual vital rates and Chinook salmon abundance were computed through direct perturbations and the chain rule of differentiation (e.g., Nichols and Hines 2002):

$$\varepsilon\left(x_{Chinook \to v_i}\right) = \sum_i \frac{\partial \log \lambda}{\partial \log a_{kl}} \frac{\partial \log a_{kl}}{\partial v_i} \frac{\partial v_i}{\partial x_{Chinook}} \tag{6}$$

where $x_{Chinook}$ denotes Chinook abundance from specific stocks or stock aggregates, and $\varepsilon\left(x_{Chinook \to v_i}\right)$ denotes the proportional change in λ resulting from a small change in $x_{Chinook}$. Notice that the effects of $x_{Chinook}$ on more than one vital rate are additive.

Stochastic elasticities were generated through simulations with vital rates represented as random variables. Vital rate annual values from 1987 to 2011 were used to generate their mean and variances for each of the killer whale populations. Simulations generated 5000 random matrices with vital rates drawn from defined probability distributions. The beta distribution was used to simulate variation in stage-specific survival (σ_i). This distribution is appropriate for binary events (such as survival) and produces random variables confined to the interval 0 to 1. The lognormal distribution was used to simulate fecundity values (μ_i). This distribution produces only positive random variables bounded by zero and infinity. Population growth rates and vital rate elasticities were calculated for each of the 5000 matrices, and a parametric bootstrap was used to estimate mean stochastic elasticities and their 95% confidence intervals.

Deterministically, changes in SRKW and NRKW population growth rates (λ) associated to observed and/or projected stock-specific Chinook salmon abundance were determined on the basis of linkages with one or more vital rates. These computations used elasticities because the consequences of simultaneous perturbations affecting multiple rates can be promptly assessed by adding elasticities (Mills et al. 1999). The effect of single or multiple perturbations can be approximated using the formula of Caswell (2001):

$$\lambda_{new} = \lambda\left(1 + \sum \varepsilon(v_i) \cdot \delta(v_i)\right) \tag{7}$$

where λ_{new} is the population growth rate after exerted perturbations, $\delta(v_i)$ are the simulated perturbations (i.e., proportional changes in vital rates corresponding to observed and/or projected Chinook salmon abundance). This λ_{new} can be then compared to a recovery

population growth rate target. For instance, the U.S. recovery plan for SRKW recommends an average growth of 2.3 percent per year (i.e., $\lambda = 1.023$). If λ_{new} is smaller than the recovery target, then the calculations can be inverted to obtain the necessary increase in Chinook salmon abundance that achieves a target population growth rate:

$$\delta\left(x_{Chinook}\right) = \left(\frac{1}{\sum \varepsilon\left(x_{Chinook \rightarrow i}\right)}\right)\left(\frac{\lambda_{target} - \lambda_{new}}{\lambda_{new}}\right) \qquad (8)$$

However, $\delta\left(v_i\right)$ which depends on the ability to increase λ by improving individual vital rates, will depend not only on the elasticities of survival or fecundity rates but also on the capacity to improve each vital rate (Morris and Doak 2002). This consideration should be particularly important for RKW since annual survival has been greater than 80% in all life stages and both sexes in SRKW (Krahn et al. 2004) and greater than 90% in NRKW (Olesiuk et al. 2005), thus leaving little room for improvement. Consequently, we also calculated the maximum proportional change in λ due to maximization of vital rates ($\Delta\lambda_{max}/\lambda$) as:

$$\Delta\lambda_{max}/\lambda \approx \sum\left(\varepsilon\left(v_{i,max} - v_i\right)/v_i\right) \qquad (9)$$

where $v_{i,max}$ is the maximum value determined as feasible for that vital rate. Maximum vital rate values were estimated separately for each killer whale population from their observed values: 1.0 for survival and upper 95% CL for fecundity. Finally, if the population growth rate $\lambda + \Delta\lambda_{max}/\lambda$ is smaller than λ_{target}, this will indicate that an identified SRKW recovery goal is unfeasible and that it could be replaced by $\lambda + \Delta\lambda_{max}/\lambda$. If this was the case, equation 7 used the latter for computations of $\delta\left(v_i\right)$.

Stochastic versions of $\lambda_{new}, \delta\left(x_{Chinook}\right),$ and $\Delta\lambda_{max}/\lambda$ were computed through methods described in sections 2.6 and 2.7 to explore the sensitivity of RKW population viability to levels of Chinook abundance defined by hypothetical fishing scenarios.

2.5.3 Retrospective

The retrospective perturbation analysis was implemented separately for SRKW and NRKW to express the observed variation in λ as a function of variation in vital rates in both killer whale populations. The retrospective analysis relied on the random design methodology used for life table response experiments (LTRE) (Caswell 1989, Brault and Caswell 1993, Levin et al. 1996), which involves matrix construction breaking down the variance of λ

into the contributions from the variances in the vital rates. The study period was divided in six four-year periods and projection matrices were created from each one of them. The sensitivity matrices ($\mathbf{S}$) corresponding to individual matrices and the covariance matrix ($\mathbf{C}$) were used as entries for the calculation of the matrix of contributions $\mathbf{V}(\lambda)$. Sensitivity was calculated as $\partial \lambda / \partial a_{kl} = (v_k w_l) / \langle \mathbf{w}, \mathbf{v} \rangle$, where the denominator is the scalar product of the vectors. The variation in vital rates was summarized in a covariance matrix $\mathbf{C} = \boldsymbol{\varepsilon}$ [(x_i - X_i) ($x_i - X_i$)'], where $\boldsymbol{\varepsilon}$ is the elasticity matrix, x_i is the vital rate and X_i is the mean of x_i. The matrix of contributions $\mathbf{V}(\lambda)$ denotes the variance in λ produced by the variation in the vital rates. Because the contributions to $\mathbf{V}(\lambda)$ are made by pairs of matrix entries (Brault and Caswell 1993), it can be approximated as:

$$\mathbf{V}(\lambda) \approx \sum_{ij} \sum_{kl} \mathbf{S}_{ij} \mathbf{S}_{kl} \mathbf{C}(a_{ij} a_{kl}) \qquad (10)$$

where a_{ij} and a_{kl} represent the elements of each possible pair of matrices. The outcome columns in the $\mathbf{V}(\lambda)$ matrix are summed and scaled to 1 to obtain proportional contributions of vital rates to the variance of λ. Contributions to the variance in λ were also calculated in terms of vital rates by defining a vital rate vector $\mathbf{p}$ and computing the variance as:

$$V(\lambda) \approx \sum_{ij} \mathbf{C}(p_i, p_j) \frac{\partial \lambda}{\partial p_i} \frac{\partial \lambda}{\partial p_j} \qquad (11)$$

We also computed variance-standardized elasticities, following Zuidema and Franco (2001), as the product of vital rate elasticities and their temporal CV. This is an analogous metric to the contribution of vital rates to the variance in λ in equation 11 but it does not adjust for covariance between vital rates. These analyses were conducted with a population matrix sub-model (Figure 5) including only those stages with contributions to λ. This sub-model (4 x 4 matrix) was therefore a truncated female-only model that excluded post-reproductive females, with $G_2 = \sigma_2 \gamma_2$, and μ_i as the product of mean offspring production by females in stage i and the proportion of females (φ_f).

Figure 5. Stage-structured projection matrix for resident killer whales used for retrospective perturbation analysis: female-only matrix model (highlighted area), excluding stages not contributing to population growth (post-reproductive females and males).

2.5.4 Transient dynamics

Transient dynamics were analyzed for the unperturbed projection matrices to evaluate the necessary time to achieve the stable distribution and the asymptotic population growth (λ). This information is important to determine the minimum length of the time horizon used in PVAs (see next section). The parameter λ summarizes the long-term dynamics of the population assuming that environmental conditions are maintained indefinitely. Because this is unlikely to happen, it is useful to evaluate the short-term or transient dynamics that dictate the rate of convergence to the stable stage distribution, which is governed by the second largest eigenvalue (λ_2; Lefkovitch 1971). The subdominant eigenvalue λ_2 may be a real or complex number. If complex, it produces oscillations during convergence (Caswell 2001) that will be faster the larger λ is relative to λ_2. A measure of the rate of convergence to the stable structure is the damping ratio $\rho = \lambda / |\lambda_2|$, where the subdominant eigenvalue can have a complex structure $\lambda_2 = a + bi$, and $|\lambda_2| = (a^2 + b^2)^{1/2}$. When λ_2 is raised to powers representing projection intervals (t):

$$\lambda_2 = |\lambda_2|^t \, 2 \, cos \, \theta \, t \qquad (12)$$

where $\theta = tan^{-1}(b/a)$ is the angle (in radians) formed by λ_2 in the complex plane and the convergence takes place with an oscillation period of $2\pi/\theta$ (Keyfitz and Flieger 1971). Convergence to the SSD depends on how close ρ is to 1, and the damping time is defined as $\tau = ln(z)/ln(\rho)$ (Haridas and Tuljapurkar 2007), where z is the number of times the contribution of λ becomes as great as that of λ_2. Damping times at $z = 10$ were used to define minimum time horizons for projections of population size.

2.6 PVA

Projection matrices were used to compute stochastic population growth and run stochastic simulations of quasi-extinction risk and recovery probabilities under an independently and identically distributed (IID[2]) environment with the aid of MATLAB R2009a (The MathWorks, Inc.) and in a fully stochastic fashion using the population viability analysis software RAMAS$_{GIS}$ (Akcakaya 2002). The two types of simulations were designed to identify the importance of demographic stochasticity and environmental stochasticity vs. IID environments on quasi-extinction and recovery probabilities. For each of the RKW populations, six matrices constructed with vital rates representatives of four-year periods across the time period encompassed in this study were randomly drawn to generate 5000 realizations of population growth to project future population size and compute stochastic population growth and 95% confidence intervals. The fraction of realizations hitting population size thresholds during or before a given time horizon was used to generate a cumulative distribution function and estimate quasi-extinction and recovery probabilities. Input data for RAMAS simulations consisted of a projection matrix of mean values and a corresponding matrix of standard deviations for each modeled RKW population. Mean and standard deviation matrices were computed from the means and standard deviations of matrix elements from the six four-year matrices. Initial conditions in both simulations were represented by their stage composition in 2011, and projection matrices were constructed using vital rates with linkages to Chinook salmon abundance derived from the regression models (hypothesis-based for Chinook salmon and AIC-based for Chum and Chinook models) and used to evaluate the effect of this interaction on RKW population viability under selected fishing scenarios. Extinction risk was assessed for time horizons large enough for convergence to stable stage structures (i.e., damping times) as derived from the analysis of transient dynamics.

RAMAS computer simulations consisted of 5000 realizations of population size per time step from projection matrices with matrix-elements drawn from lognormal distributions parameterized by the mean and standard deviation matrices. The probability of falling below a population threshold (quasi-extinction probability in RAMAS) was computed as the proportion of realizations of population size at or before the specific time step determined by the analysis of transient dynamics that is reduced to 30 individuals for SRKW and 250 for NRKW. Thirty individuals for SRKW was considered small enough to enable inbreeding depression, Allee effects, and exacerbated demographic stochasticity

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[2] In probability theory and statistics, a sequence or other collection of random variables is independent and identically distributed (IID) if each random variable has the same probability distribution as the others and all are mutually independent. In the case of projection matrices, the IID concept entails the independence of individual period-specific matrices constructed with vital rates drawn from identical distributions in each case. Simulations based on projection matrices in an IID environment thus assume that past conditions apply in the future.

playing important roles on extinction dynamics (see Morris and Doak 2002). For NRKW, with a clearly positive population growth and 268 individuals in 2011, 250 individuals was identified as a useful threshold for exploration of fishing scenarios. We also computed interval extinction risks for both populations, which are defined as the probability that abundance will fall below a range of abundances at least once during the next 100 years. Probabilities of recovery in SRKW were computed using as population size targets 120 and 164 individuals as derived from an average growth of 2.3 percent per year for 14 years for downlisting and 28 years for delisting, respectively, specified in the recovery plan for this population (NMFS 2008). Lastly, expected minimum abundance was calculated for NRKW. The expected minimum abundance is the average (over all replications) of the minimum population abundance of the trajectory. This metric is an estimate of the smallest population size that is expected to occur within the simulated time period. The expected minimum abundance can be used as an index of propensity to decline, especially when the population variability and risks of decline are low (McCarthy and Thompson 2001), which presently is the case for NRKW's population dynamics.

Demographic stochasticity was modeled by sampling the number of survivors from a binomial distribution with parameters P_i and $N_i(t)$ as sample size and the number of calves from a Poisson distribution with mean $F_i \cdot N_i(t)$. Fecundity and survival rates were correlated within each modeled population to maintain their covariation structure and survival rates were constrained to values between 0 and 1, with the sum of all survival transitions from a given stage being ≤ 1 in any time step (see Akcakaya 2002). Density dependence at high population size was not explicit in the RAMAS simulations given the paucity of information on carrying capacities for both RKW populations and the short time frames used for risk assessment. Catastrophe probabilities, a simulation component explicit in RAMAS, were not included either because the objective is to identify the influence of various levels of Chinook salmon abundance on RKW population viability rather than evaluating the influence of other pervasive sources of environmental uncertainty. The relative effect of salmon abundance on population viability would be obscured and confounded by the large effects catastrophes can have on PVAs (Menges 1990, Lande 1993, Mangel and Tier 1994, Vélez-Espino and Koops 2012).

2.7 Fishing scenarios

The identification of Chinook salmon stocks or stock aggregates with the largest influence on RKW population dynamics was based prospectively on the value of elasticities of vital rate-Chinook salmon interactions and retrospectively on their contributions to the observed variation in population growth for 1987-2011. Since the abundance of specific Chinook salmon stocks can interact with more than one vital rate, their added elasticities were considered for selection. This selection process was also framed by the hypotheses

specified in Box 1. In the case of SRKW, for which population size increases are desirable, fishing scenarios were designed to maximize effects on vital rates or minimize fishing mortality and evaluate best-case scenarios for increases in population growth rate. As before, maximum vital rate values were estimated separately for each killer whale population from their observed values: 100% for survival and upper 95% CL for fecundity. The most extreme case of minimization of fishing mortality rates was that corresponding to fishery closures for selected stock aggregates and abundance type (i.e., ocean abundance or terminal run). The effects of maximization of vital rates or minimization of fishing mortality were quantified deterministically through direct perturbations following methods described in Section 2.5.2 and stochastically through simulations. For NRKW, we explored fishing scenarios that slow population growth or produce equilibrium (i.e., $\lambda = 1.0$) because this population currently has positive growth rates. A variant of equation 8 was used as a first approximation to identify equilibrium conditions:

$$\delta\left(x_{Chinook}\right) = \left(\frac{1}{\sum \varepsilon\left(x_{Chinook \to i}\right)}\right)\left(\frac{1-\lambda_{NRKW}}{\lambda_{NRKW}}\right) \qquad (13)$$

A limitation of equation 13 is that it applies the same proportional reduction $\delta\left(x_{Chinook}\right)$ in all vital rates and it is necessary to use an iterative solving process to identify a fishing scenario producing exactly $\lambda = 1.000$. Hence, the effects of extreme increases in fishing mortality were explored and their effects on NRKW vital rates (and ultimately population growth) were first approximated deterministically through direct perturbations and then estimated stochastically through simulations.

The procedure to translate changes in fishing mortality, portrayed by selected fishing scenarios, into PVA metrics entailed four steps. First, 1987-2011 (1985-2009 for 2-year lagged models) Chinook abundance time series were modified according to the characteristics of fishing scenarios. Second, new time series of target vital rates were generated using beta-regression models (Section 2.4). Third, new sets of modified projection matrices were created and mean and standard deviation matrices were constructed. Lastly, stochastic simulations were ran as described in Section 2.6. PVA metrics considered for the comparison of fishing scenarios were: (i) stochastic population growth; (ii) mean abundance τ years in the future, where τ is the damping time derived from the analysis of transient dynamics (section 2.5.4); (iii) probability of falling below a population threshold (30 individuals for SRKW and 250 for NRKW) in the future; (iv) extinction probability 100 years in the future; and, (v) probability of U.S. downlisting for SRKW and expected minimum abundance for NRKW.

3. RESULTS

3.1 RKW demography

In general, vital rate mean values were similar between SRKW and NRKW (Figure 6). Mean survival ranged from 0.785 (calf) to 0.985 (young reproductive female) in SRKW and from 0.883 (post-reproductive female) to 0.989 (young reproductive female) in NRKW. Mean fecundity was 0.116 and 0.069 in SRKW and 0.142 and 0.101 in NRKW for young reproductive females and old reproductive females, respectively. Nonetheless, calf survival and old-reproductive-female fecundity were significantly different (Nonparametric Kolmogorov-Smirnov test p < 0.05) between SRKW and NRKW. In addition, the overall proportion of juveniles transitioning into young reproductive females from 1987 to 2011 was higher in NRKW (0.55) than in SRKW (0.45). This larger proportion of females could partly explain NRKW's higher fecundity rates. Vital-rate coefficients of variation were greater for fecundity rates than for survival rates in both populations. Variation in vital rates was noticeably greater for all vital rates in SRKW than in NRKW, except for post-reproductive females (Figure 7). In spite of the similarity in the vital rate mean values of the two populations, there was generally low covariation for vital rate and abundance from 1987 to 2011 (Figure 8). The largest correlation coefficient was 0.46 for the survival of old mature males. Time series of vital rates and abundance for SRKW and NRKW are shown in Appendix 5.

Demographic matrices parameterized with vital rates representative of the last RKW generation (1987-2011) produced deterministic population growth rates projecting a 0.92% annual decline for SRKW and a 1.59% annual increase for NRKW. Similarly, stochastic population growth rates were 0.91% annual decline ($\lambda = 0.9909$; 95% CI: 0.9719-1.0081) for SRKW and 1.58% annual increase ($\lambda = 1.0158$; 95% CI: 1.0027-1.0285) for NRKW (Figure 9). The current stage distribution of NRKW was closer to the stable stage distribution than it was in SRKW (Figure 10) with a noticeably higher proportion of post-reproductive females in SRKW than in NRKW (6.8% vs. 3.7%) and a higher proportion of juveniles in NRKW than in SRKW (34.8% vs. 27.3%). This also means that if current conditions persist (i.e., mean vital rates do not change), NRKW stage distributions will experience little change in the future while greater changes are likely for SRKW. Moreover, the analysis of transient dynamics produced damping times of 35 years for SRKW and 25 years for NRKW. These are the time horizons it would take for the subdominant eigenvalue (λ_2) to become 10% of the dominant eigenvalue (λ) and identified as minimum for projections of population size derived from projection matrices.

The relative importance of individual vital rates on population growth rates (i.e., elasticities) was similar for both populations (Figure 11) and it was greatest for the survival of young reproductive females (0.55 for SRKW and 0.53 for NRKW) and lowest for the

fecundity of old reproductive females (0.009 for SRKW and 0.012 for NRKW). The elasticities of male survival and post-reproductive female are zero because these stages do not contribute directly to population growth. The elasticity of the sex ratio (represented by the proportion of females) was relatively small and comparable to that of calf survival (0.032 for SRKW and 0.044 for NRKW) in both populations. Although any change in the survival of young reproductive females is expected to have the greatest effect on population growth (as determined by its elasticity), the little room for improvement in this vital rate (and in survival rates in general) limits the proportional increase in population growth achieved after maximizing the survival of young reproductive females. Greater proportional increases in population growth are achieved after maximization of fecundity rates (Figure 12), particularly the fecundity of young reproductive females in SRKW. The maximization of the latter is projected to produce a 1.7% annual increase in SRKW, which is still less than the 2.3% U.S. downlisting recovery target. This also means that the feasibility of meeting such a recovery target will require substantial and simultaneous increases in several vital rates and most likely will include the fecundity of young reproductive females. The relationship between elasticity and expected changes to population growth can also be examined without the limitations to increase a given vital rate (as in the case for the already high survival rates) by analyzing the necessary change to halt population growth (i.e., $\lambda = 1.0$) in NRKW (Figure 13). Due to its largest elasticity, a small reduction (3.1%) in the survival of young reproductive females would be enough to halt NRKW's population growth. On the other extreme, even an extreme reduction in fecundity of old reproductive females to zero would not halt NRKW's population growth (Figure 13).

The retrospective perturbation analysis identified survival of young reproductive females (matrix element P3) as the largest contributor to the variance in observed population growth for SRKW, and the fertility of young reproductive females (matrix element F3) as the largest contributor for NRKW (Figure 14; upper panel). Similarly, at the vital-rate level, the young-reproductive-female annual survival was the largest contributor to the CV in observed population growth for SRKW whereas the fecundity of young reproductive females was the largest contributor for NRKW (Figure 14; lower panel). These results indicate that the survival of young reproductive females is not only the vital rate with the greatest potential to influence future population growth but also the vital rate with the greatest influence on the observed (1987-2011) variation in population growth for SRKW. For NRKW, the survival of young reproductive females was also the vital rate with the greatest potential to influence population growth. However, the fecundity of young reproductive females had the greatest influence on observed population growth. This latter vital rate, if maximized, also had the greatest potential to increase population growth in both populations (Figure 12).

3.2 Role of Chinook abundance on RKW population growth

3.2.1 Southern Resident Killer Whales

Twenty-five significant ($p < 0.05$) and positive (slope > 0.0) relationships between Chinook abundance and SRKW vital rates were identified (Table 1). Nine of these relationships represented interactions with Chinook salmon terminal run and 16 with ocean abundance. Four of the 25 interactions corresponded to hypothesis 1a (stronger causation weight-of-evidence) while 21 corresponded to hypothesis 2a (weaker causation weight-of-evidence). Twenty of the 25 interactions involved fecundity (15 for young reproductive females and 5 for old reproductive females) and 5 involved the survival of old reproductive females. Within hypothesis 1a, the strongest interaction (based on statistical significance alone) occurred between the fecundity of old reproductive females and the two-year lagged terminal run of Chinook salmon from Puget Sound stocks (Pseudo-R^2 = 0.164; p = 0.0076). Interactions with the individual stocks of the Fraser Early stock aggregate were not significant but there were significant interactions between the Fraser Early/Puget Sound aggregate and the fecundity of old reproductive females. The interaction between Fraser Late terminal run and the fecundity of young reproductive females was also significant. Since interactions with the survival of males or post-reproductive females have no direct effect on RKW population growth or viability, they were not selected for subsequent analyses regardless of their statistical significance. Within hypothesis 2a, four stock aggregates had linkages to more than one vital rate contributing to population growth: Columbia Spring/Summer terminal run showed significant relationships with the survival and fecundity of old reproductive females whereas the ocean abundance of the five stocks with the largest contributions to ocean abundance (WCVI, Columbia Upriver Brights, Fraser Late, Oregon Coastal, and Puget Sound)[3], coastwide ocean abundance (all stocks, excluding southeast Alaska [SEAK] stocks), and Oregon Coastal ocean abundance showed significant relationships with the survival of old reproductive females and the fecundity of young reproductive females. On statistical grounds alone, the strongest interaction between Chinook abundance and an individual vital rate was between lag-0 coastwide ocean abundance and the survival of old reproductive females (Pseudo-R^2 = 0.488; p = 0.0028).

The potential effect on population growth and viability of any uncovered interaction between Chinook abundance and killer whale vital rates would depend not only on the statistical significance (namely pseudo-R^2 and p-value) of the relationship but also on the slope of the regression and the elasticity of the vital rates involved. The slope of the regression determines the net change in a vital rate resulting from a change in Chinook abundance (as indicated by the far-right term in Equation 6). In general, interactions with

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[3] These stocks have the largest Chinook salmon contributions to ocean mixed-stock fisheries managed under the Pacific Salmon Treaty as estimated by the PSC Chinook Model (PSC 2011a).

greater regression coefficients and involving vital rates with larger elasticities are expected to have a greater effect on population growth. In terms of time lags our approach was to select the stock aggregate-time lag combination whose interaction with a given vital rate had the greatest elasticity (i.e., the greatest relative influence on population growth rate). Moreover, interactions with Chinook stock aggregates exhibiting linkages to more than one vital rate will have an additive effect (as shown in Equation 6). These effects can be inferred from the individual interaction elasticities because elasticities are partial derivatives and additive by definition.

Figure 15 shows the mean stochastic elasticities for all significant regressions in Table 1. Interactions occurred only with the fecundity of young and old reproductive females and the survival of old reproductive females. This figure shows how the majority and the stronger interaction elasticities involved the fecundity of young reproductive females in spite of this vital rate having an elasticity lower than the survival of old reproductive females (Figure 11). This happens because the regression slopes are greater for fecundity than for survival. Figure 16 shows a subset of interactions with the largest elasticities for both hypothesis 1a and 2a (see Appendix 6 for a glossary of stock aggregate definitions). The largest mean elasticity of interactions under hypothesis 1a was that of Puget Sound terminal run and the fecundity of old reproductive females ($\varepsilon = 0.025$), closely followed by the interaction between this vital rate and Fraser Early/Puget Sound terminal run. The largest additive mean elasticity within hypothesis 2a and without cumulative effects was that of the interaction between the five stocks with the largest contributions to ocean abundance (WCVI, Fraser Late, Puget Sound, Columbia Upriver Brights, and Oregon Coastal) and both the fecundity of young reproductive females and the survival of old reproductive females (additive $\varepsilon = 0.046$), followed by the interaction between these vital rates and coastwide ocean abundance (additive $\varepsilon = 0.038$). The largest mean elasticity involved cumulative effects (represented by 5-year abundance running average) of the interaction between the ocean abundance of the five large stocks (WCVI, Fraser Late, Puget Sound, Columbia Upriver Brights, and Oregon Coastal) and the fecundity of young reproductive females.

Retrospectively, the contribution to the variation in observed population growth was smaller for interactions under hypothesis 1a than interactions under hypothesis 2a (Figure 17). In this case, the interaction with Fraser Late terminal had a greater contribution (0.8%) than either Puget Sound or Fraser Early\Puget Sound terminal run. Similar to the results of the prospective perturbation analysis, the interaction with the ocean abundance of the five large stocks (WCVI, Fraser Late, Puget Sound, Columbia Upriver Brights, and Oregon Coastal) had the largest contribution (1.33%) to the variation in observed population growth, followed by the interaction with coastwide ocean abundance (1.05%). In spite of the low elasticities of the interactions with WCVI terminal run and WCVI ocean abundance (reason why they were not included in Figure 16) these interactions had relatively large

contributions to the variation in population growth (Figure 17). This was partly due to the greater variation in WCVI terminal run (CV = 0.47) and WCVI ocean abundance (CV = 0.59) relative to the variation in Oregon Coastal ocean abundance (CV = 0.38), included in Figure 16, during 1987-2011.

Based on the summaries provided by prospective and retrospective perturbation analyses, indices of Chinook abundance with the largest potential effects on SRKW population growth were selected for the exploration of fishing scenarios. The interactions with Puget Sound terminal run and Fraser Early/ Puget Sound terminal runs were selected to represent hypothesis 1a while the interactions with the ocean abundance of the five large stocks (WCVI, Columbia Upriver Brights, Fraser Late, Oregon Coastal, and Puget Sound) and coastwide ocean abundance (excluding SEAK) were selected to represent hypothesis 2a. In addition, the interaction involving cumulative effects of the ocean abundance of the five large stocks was included in the list of scenarios. The time series of abundance of these stock aggregates are shown in Figure 18.

3.2.2 Northern Resident Killer Whales

Many more significant relationships between Chinook abundance and vital rates were identified for NRKW than for SRKW. A total of 66 significant ($p < 0.05$) and positive (slope > 0.0) interactions are shown in Table2. Forty-two of these relationships represented interactions with Chinook salmon terminal run and 24 with ocean abundance. Seventeen of the 66 interactions corresponded to hypothesis 1b (stronger causation weight-of-evidence) while 49 corresponded to hypothesis 2b (weaker causation weight-of-evidence). In contrast to the interactions found for SRKW where the vast majority of interactions involved fecundity, significant relationships were found between Chinook abundance and all vital rates directly contributing to population growth for NRKW. Within hypothesis 1b, the strongest interaction (based on statistical significance alone) occurred between the survival of young reproductive females and the one-year lagged terminal run of Northern BC stocks (Pseudo-R^2 = 0.335; p = 0.0016), followed by the interaction between one-year lagged Puget Sound ocean abundance and juvenile survival (Pseudo-R^2 = 0.265; p = 0.0031). Within hypothesis 2b, the greatest interaction (based on statistical significance alone) occurred between Oregon Coastal ocean abundance and the survival of young reproductive females (Pseudo-R^2 = 0.514; p = 0.0003), followed by the interaction between one-year lagged coastwide ocean abundance (excluding SEAK stocks) and the survival of young reproductive females (Pseudo-R^2 = 0.359; p = 0.0008). Without consideration of cumulative effects (represented by 5-year abundance running average), Puget Sound terminal run and Fraser Early/Puget Sound terminal run were the only two stock aggregates showing interactions with more than one vital rate contributing to population growth: juvenile survival and fecundity of old reproductive females for Puget Sound, and fecundity

of young and old reproductive females for Fraser Early/Puget Sound. If cumulative effects are considered, the time series of 5-year running average abundances of as many as six stock aggregates had interactions with two vital rates (Table 2).

Moving from statistical significance to potential and observed effects on population growth requires perturbation analyses of those significant interactions between Chinook abundance and killer whale vital rates. Figure 19 shows the mean stochastic elasticities for all significant regressions in Table 2. Interactions occurred with all vital rates directly contributing to population growth. The majority and the stronger interaction elasticities for NRKW involved the fecundity of old reproductive females. Figure 20 shows a subset of interactions with the largest elasticities for both hypothesis 1b and 2b. The magnitudes of elasticities of interactions for NRKW within hypothesis 1b are comparable to those of hypothesis 2b and also comparable to those observed for SRKW. The greatest elasticities within hypothesis 1b were those of the interaction with Fraser Early ocean abundance with ($\varepsilon = 0.0465$) and without ($\varepsilon = 0.035$) cumulative effects, followed by Lower Georgia Strait Terminal Run terminal run ($\varepsilon = 0.015$) and Northern BC terminal run ($\varepsilon = 0.013$). Notice that although cumulative effects of Upper Georgia Strait terminal run had a statistical interaction that was stronger than the interaction with Lower Georgia Strait terminal run (see Table 2), the former had a smaller interaction elasticity (reason why is not in Figure 20) because interactions with survival had in general smaller regression coefficients and therefore smaller influence on population growth resulting from changes in Chinook abundance. The relative strength of interactions between NRKW's vital rates and bothh Upper and Lower Georgia Strait aggregates is consistent with the migration routes of these Chinook stock aggregates. While Upper Georgia Strait stocks are far north migrating and return to their terminal areas via Johnstone Strait, the Lower Georgia Strait stocks return via both Johnstone Strait and Juan de Fuca Strait (PSC 2011a). Regarding hypothesis 2b, the largest added elasticities corresponded to the interactions with Fraser Early/Puget Sound terminal run with ($\varepsilon = 0.042$) and without ($\varepsilon = 0.051$) cumulative effects, followed by that of coastwide ocean abundance ($\varepsilon = 0.010$) and Oregon Coastal ocean abundance ($\varepsilon = 0.007$).

Retrospectively, the contribution of the interactions to the variation in observed population growth were comparable between hypotheses 1b and 2b (Figure 21), except for the contribution of Fraser Early/Puget Sound terminal run whose contributions were at least twice as large as the remaining stock aggregates, including those interactions representing cumulative effects. In spite of the low elasticities of the interactions with WCVI terminal run and (reason why it was not included in Figure 20) this interaction had a relatively large contribution to the variation in population growth (Figure 21). This was partly due to the greater variation in WCVI terminal run (CV = 0.47) relative to the variation in Puget Sound ocean abundance (CV = 0.27), included in Figure 20, during 1987-2011.

Indices of Chinook abundance with the largest potential effects on NRKW population growth were selected for the exploration of fishing scenarios based on the summaries provided by prospective and retrospective perturbation analyses. The interactions with Fraser Early ocean abundance and Northern BC terminal run were selected to represent hypothesis 1b while interactions with Fraser Early/Puget Sound terminal run and coastwide ocean abundance (excluding SEAK stocks) were selected to represent hypothesis 2b. In addition, the interaction involving the largest cumulative effects, Fraser Early ocean abundance, was included in the list of scenarios. The time series of abundance of stock aggregates selected for hypothesis 1b are shown in Figure 22. The time series of stock aggregates for hypothesis 2b were included in Figure 18.

3.3 Chum salmon as a covariate of RKW population growth

Nine multiple beta-regression models with Chinook and Chum salmon as predictors and no collinearity (VIF << 5) had significant (p < 0.05) interactions with common vital rates structured by hypothesis (Table 3). The terminal runs of Chum salmon stock aggregates relevant in these models were Northern/Central BC and Washington Summer/Fall/Winter. Figure 23 depicts the time series of Chum salmon abundance for these stock aggregates. Four of these relationships represented interactions with SRKW vital rates whereas five occurred with NRKW vital rates. Interactions contributing to population growth involved the fecundity of young and old reproductive females for SRKW, and juvenile survival, the survival of young reproductive females, and the fecundity of old reproductive females for NRKW. Only four of the nine significant multiple regressions showed both a marginal increase in the Chinook regression coefficient and lower AIC relative to their corresponding simple regression models with Chinook as only predictor (Table 4). From these four multiple regressions, one represented hypothesis 1a, one hypothesis 2a, and two hypothesis 2b; there was no multiple regression representing hypothesis 1b, which is hypothesis supporting causation for NRKW.

For SRKW, the inclusion of Northern/Central BC Chum terminal run as a covariate in the interaction between Fraser Late Chinook terminal run and the fecundity of young reproductive females, under hypothesis 1a, increased the elasticity of the interaction by ~17%. However, the interaction between Puget Sound Chinook terminal run (no Chum as covariate) and the fecundity of old reproductive females still displayed the largest elasticity (Figure 24) and therefore the largest influence on population growth under hypothesis 1a. The inclusion of the same Chum stock aggregate, Northern/Central BC Chum terminal run, as a covariate in the interaction between the ocean abundance of the five large stocks (WCVI, Fraser Late, Puget Sound, Columbia Upriver Brights, and Oregon Coastal) and the fecundity of young reproductive females, under hypothesis 2a, produced the largest increase in the elasticity of the interaction (~61%). The elasticity of this latter interaction

was even greater than the largest elasticity for Chinook-only interactions (without cumulative effects) under hypothesis 2a (Figure 24). Appendix 7 shows a glossary of Chum salmon stock aggregate definitions.

For NRKW, the inclusion of Northern/Central BC Chum terminal run as a covariate in the interaction between Oregon Coastal Chinook ocean abundance and the survival of young reproductive females, under hypothesis 2b, increased the elasticity of the interaction by ~10%. Similarly, the inclusion of Washington Summer/Fall/Winter Chum terminal run as a covariate in the interaction between Fraser Early/Fraser Late/Puget Sound Chinook terminal run and the fecundity of old reproductive females, under hypothesis 2b, increased the elasticity of the interaction by ~10%. However, the interaction between Fraser Early/Puget Sound Chinook terminal run (no Chum as covariate) and the fecundity of young and old reproductive females still displayed the largest elasticity (Figure 25) and therefore the largest influence on population growth under hypothesis 2b.

Although there is statistical support for Chum terminal run as a covariate in Chinook-RKW vital rates interactions, the translation of these interactions into effects on population growth became important only for SRKW under hypothesis 2a. However, hypotheses 2a and 2b have a weaker weight-of-evidence for causation than hypotheses 1a and 1b, respectively. Subsequent analyses focused on Chinook-only interactions due to the relatively small increase in the elasticity of the interaction under hypothesis 1a and the lack of a significant Chum stock covariate under hypothesis 1b. In addition, Chinook-only interactions with substantially greater influence on population growth rates occurred for NRKW under hypothesis 2b.

3.4 RKW population viability under selected fishing scenarios

Numerous scenarios could be explored to assess effects of changes to fishing mortality on SRKW population viability, but in light of the relatively small effects of Chinook salmon abundance on population growth (as determined from prospective and retrospective perturbation analyses), we focus on the exploration of fishing scenarios maximizing benefits to SRKW. Similar effects on population growth were identified for NRKW but given the clearly positive population growth rate of this population it is of interest to invert the focus of fishing scenarios. More specifically, interactions with the largest elasticities and contributions to population growth were selected to explore fishing scenarios with the potential to halt NRKW's population growth. Six scenarios were selected for each RKW population, including: a status-quo scenario (i.e., no Chinook interactions; scenarios 1 and 7) as reference, two scenarios relevant for hypothesis 1, two scenarios relevant for hypothesis 2, and one scenario to represent cumulative effects of Chinook abundance levels (i.e., 5-year running average). Scenarios 1-6 correspond to SRKW while scenarios 7-12

correspond to NRKW. The characteristics and targeted vital rates of these scenarios are shown in Table 5.

Scenarios 2 and 3 in this table are characterized by no ocean fishing on Puget Sound Chinook salmon stocks and no ocean fishing on Fraser Early and Puget Sound Chinook, respectively, thus maximizing terminal runs of these stock aggregates. In these two scenarios the elimination of fishing mortality increased SRKW target vital rates but did not maximize them. Scenarios 4 and 5 are characterized by the maximization of target SRKW vital rates, which occurred after a 51% reduction in the ocean harvest rates of the five large stocks (WCVI, Columbia Upriver Brights, Fraser Late, Oregon Coastal, and Puget Sound) and a 36% reduction in coastwide (excluding SEAK) ocean harvest rates, respectively. Scenario 6 represents cumulative effects of changes in Chinook abundance and is characterized by 55.5% reductions in the ocean harvest rates of the five large stocks; these reductions maximized SRKW's target vital rate. Scenario 8 reduces NRKW population growth via the maximization of ocean harvest rates of Fraser Early Chinook; this scenario, however, did not halt population growth. Scenario 9 effectively halts NRKW population growth through reductions in NBC Chinook terminal run via 187% increases in ocean harvest rates on this stock. Scenario 10 reduces the terminal run of Fraser Early/Puget Sound aggregate via doubling of ocean harvest rates in this stock; this increment, however, did not halt NRKW population growth but maximized ocean harvest rates of some of the indicator stocks considered for this stock aggregate (see Appendix 4 for details on indicator stocks). Scenario 11 halts NRKW population growth through 66% increases in coastwide (excluding SEAK) ocean harvest rates. Lastly, Scenario 12 represents cumulative effects of changes in Chinook abundance and is characterized by maximization of ocean harvest rates of Fraser Early Chinook; this scenario, however, did not halt NRKW population growth.

Given the large number of analyses and figures describing the PVA procedures for each scenario, we provide complete details of results for four of the 12 scenarios. Next, we describe the PVA results for the two reference scenarios (i.e., status quo) and the scenarios with the maximum effect on population growth and viability (without cumulative effect) for each of the RKW populations. Identical procedures were applied to the remaining scenarios and a complete summary of the viability metrics across all selected fishing scenarios is shown in Table 6, which will be further addressed in Section 3.4.5.

3.4.1 Scenario 1: SRKW status-quo conditions

Under status-quo conditions, SRKW's expected population size in an IID environment was 84 in 10 years, 78 in 20 years, 71 in 30 years, and 68 in 35 years (Figure 26), with 35 years as the damping time for SRKW. Only a small fraction of the realizations of population size exceeded the initial population size ($N = 88$) at 10 and 20 years but at 35 years all

realizations of population size were below 88 and some were as low as 55-60. In an IID environment, the probability of falling below 30 individuals remained effectively zero for about 80 years, after which the probability increased rapidly reaching 0.5 at about 130 years (Figure 27). Accordingly, there was a zero probability of reaching 120 individuals in 14 years (U.S. downlisting target). However, projections of population size under demographic stochasticity showed that the probability of falling below 30 individuals can be greater than zero before 80 years and as early as 55 years in the future (Figure 28), thus demonstrating the importance of incorporating demographic stochasticity in PVAs for a population with such small population size. The incorporation of both environmental and demographic stochasticity produced a probability trajectory where the probability of falling below 30 individuals is greater than zero at 10 years, 0.5 at 47 years and approximately 0.8 at 100 years (Figure 29). When the time horizon is fixed, rather than fixing the population threshold (as in Figure 29), the interval extinction risk showing the probability of falling below a range of population thresholds (Figure 30) indicated an extinction risk of 49% in 100 years and an expected minimum abundance of 15 individuals during this timeframe.

3.4.2 Scenario 4: SRKW with 51% reduction of ocean harvests rates on the five large Chinook stocks (WCVI, FL, PS, URB, and OC)

Under scenario 4, which produced the maximum benefits to SRKW population growth and viability, stochastic population growth indicated a 1.80% annual increase ($\lambda = 1.01803$). SRKW's expected population size in an IID environment was 107 in 10 years, 128 in 20 years, 152 in 30 years and 166 in 35 years (Figure 31). None of the realizations of population size were smaller than the initial population size (N = 88) at 20 years and some were as large as 200 at 30 years and 230 at 35 years. In an IID environment, the probability of falling below 30 individuals remained effectively zero for about seven years, after which the probability increased rapidly reaching 0.5 at about 16 years (Figure 32). These results also showed that the probability of reaching the U.S. downlisting recovery target (i.e., after 14 years) was about 0.33. In spite of the positive population growth, projections of population size under demographic stochasticity can still produce large differences in population trajectories (Figure 33). The incorporation of both environmental and demographic stochasticity produced a probability trajectory where the probability of falling below 30 individuals is greater than zero at 10 years and approximately 0.27 after 100 years (Figure 34). When the time horizon is fixed, rather than fixing the population threshold (as in Figure 34), the interval extinction risk showing the probability of falling below a range of population thresholds (Figure 35) indicated an extinction risk of 13% in 100 years and an expected minimum abundance of 55 individuals during this timeframe.

3.4.3 Scenario 7: NRKW status-quo conditions

Under status-quo conditions, NRKW's expected population size in an IID environment was 315 in 10 years, 370 in 20 years, 401 in 25 years, and 434 in 30 years (Figure 36) with 25 years as the damping time for NRKW. However, projections for more than 25 years in the future seem impractical without knowing the carrying capacity. No realizations of population size were smaller than the initial population size (N = 268) at 10 years, and at 25 years some realizations of population size were as high as 480 individuals. In an IID environment, the probability of falling below 250 individuals remained effectively zero even after 250 years (no figure shown). Projections of population size under demographic stochasticity showed steadily increasing trajectories and no trajectory falling below 250 individuals (Figure 37). The incorporation of both environmental and demographic stochasticity produced a rapidly increasing probability trajectory where the probability of falling below 250 individuals was 0.5 at 30 years, and asymptotically increasing to 0.52 after 100 years (Figure 38). This pattern is different to the example scenarios for SRKW mainly due to the clearly positive population growth exhibited by NRKW. When the time horizon is fixed, rather than fixing the population threshold (as in Figure 38), the interval extinction risk showing the probability of falling below a given population threshold (Figure 39) indicated an extinction risk of zero in 100 years and an expected minimum abundance of 238 individuals during this timeframe.

3.4.4 Scenario 11: NRKW with 66% increase of coastwide Chinook ocean harvest rates

Scenario 11 effectively halted NRKW's population growth with a mean stochastic population growth at equilibrium $\lambda = 1.000$. NRKW's expected population size in an IID environment was 285 in 10 years, 295 in 20 years, 299 in 25 years, and 301 in 30 years (Figure 40). Only a small fraction of the realizations of population size were lower than 250 individuals at 10 and 20 years and some were as high as 370 individuals after 25 years. In an IID environment, the probability of falling below 250 individuals increased steadily after 3 years and probabilities greater than 0.45 were achieved after 100 years (Figure 41). Projections of population size under demographic stochasticity showed approximately equal numbers of increasing and declining trajectories and few of the declining trajectories showed less than 240 individuals after 25 years (Figure 42). The incorporation of both environmental and demographic stochasticity produced a probability trajectory where the probability of falling below 250 individuals was 0.5 at about eight years and 0.84 after 100 years (Figure 43). When the time horizon is fixed, rather than fixing the population threshold (as in Figure 43), the interval extinction risk showing the probability of falling below a given population threshold (Figure 44) indicated an extinction risk of 1.7% in 100 years and an expected minimum abundance of 162 individuals during this timeframe.

The increase in population size even after reducing vital rates to produce equilibrium is the result of population momentum. Population momentum is due to the departure of population structure from the stable stage distribution and it is characterized by time lags between a change in the vital rates and the actual observed impact on the population (Keyfitz 1971, Koons et al. 2005). The inertial effect of population momentum, which applies to demographic simulations bringing population growth to equilibrium (i.e., $\lambda = 1$), has proved to be especially important in the population dynamics of long-lived vertebrates (Koons et al. 2006).

3.4.5 PVA summary

Regarding hypothesis 1a, the maximization of terminal runs via the cessation of ocean fishing on Puget Sound Chinook salmon stocks (Scenario 2) or via the cessation of ocean fishing on the Fraser Early/Puget Sound aggregate (Scenario 3) produced marginal increases in SRKW's population growth relative to status-quo conditions (Scenario 1). These increases were enough to create slightly positive population growth rates (+0.6%) and halved extinction probabilities in Scenario 2, but population growth remained slightly negative (-0.02%) in Scenario 3 (Table 6). These counterintuitive results showing greater increases to SRKW population growth rates and viability from the closing of ocean fisheries impacting Puget Sound stocks relative to the closing of those impacting both Fraser Early and Puget Sound stocks is simply a statistical artifice; the interaction with the fecundity of old reproductive females displayed greater regression coefficients and statistical significance for Puget Sound than for the Fraser Early/Puget Sound aggregate. Histograms of stochastic population growth produced by these two scenarios (Figure 45) show the large overlap between the frequency distributions and the 95% confidence intervals from these two scenarios. These conditions suggest that interpretations of these results require the consideration of other lines of evidence, such as that provided for diet-composition studies that indicate that Fraser Early Chinook makes up a much larger portion of SRKW's diet in the summer months than Puget Sound Chinook (Hanson et al. 2010). Thus, PVA analyses for Scenario 3 are ecologically more robust than those for Scenario 2.

All scenarios selected to represent hypothesis 2a (scenarios 4, 5, and 6) produced positive population growth rates and substantially reduced extinction probabilities. This includes Scenario 6, which was selected to represent the effect of cumulative effects of Chinook abundance levels. This scenario, however, did not produce the largest increase in SRKW population growth and viability in spite of the scenario's effects being based on the same stock aggregate as Scenario 4 (i.e., five large stocks WCVI/FL/PS/URB/OC). As described in Section 3.4.2, Scenario 4 maximized effects without cumulative effects and through the maximization of both the fecundity of young reproductive females and the survival of old reproductive females whereas Scenario 6 maximized only the fecundity of

young reproductive females. Since this latter interactions pertain to hypothesis 2a (weak causation weight-of-evidence), any inference is subject to the assumption that the Chinook ocean abundances of these five large stocks remain crucial in SRKW' diet year-round.

Regarding hypothesis 1b, pre-terminal harvesting of all Fraser Early Chinook (Scenario 8) was not enough to halt NRKW"s population growth rate (+0.14%) but it produced extinction probabilities slightly greater than zero, and substantially reduced expected minimum abundance relative to status-quo conditions (Scenario 7). An equivalent scenario, but including cumulative effects of Chinook abundance levels for this stock (Scenario 12), also failed to halt population growth. However, reductions in the terminal run of NBC Chinook resulting from almost a tripling of the ocean harvest rates on this stock (Scenario 9), effectively halted population growth. This large increase in ocean harvest rates was possible due to the low terminal-run-equivalent harvest rates (average of 19% in the last three decades) on NBC's indicator stock (see Section 2.3.3 and corresponding appendices).

Regarding hypothesis 2b, reductions in the terminal run of the Fraser Early/Puget Sound aggregate resulting from doubling ocean harvest rates on this aggregate (Scenario 10) did not halt population growth. Larger increases in ocean harvest rates were not possible since some of the indicator stocks for this aggregate reached 100% at this level. Decreasing the survival of young reproductive females via 66% increases of coastwide ocean harvest rates (Scenario 11) effectively halted population growth. Although the probability of falling below 250 individuals reached 0.84 and the expected minimum abundance felled to 162 individuals, the risk of extinction in 100 years remained less than 2%. Nevertheless, any inference from scenarios 10 or 11 is subject to the assumption that the Chinook terminal run of the Fraser Early/Puget Sound aggregate or Chinook coastwide ocean abundance are critical in NRKW diet during the summer the former and year-round the latter.

From the results of the demographic analyses in Section 3.1 it is evident that survival of young reproductive females has by far the largest relative influence in the population growth rates of SRKW and NRKW. But since the average survival of young reproductive females is high in both populations (0.985 for SRKW and 0.989 for NRKW), there is little room to increase population growth by improving this vital rate. Conversely, large reductions in population growth can be exerted from reductions to this vital rate. That is why the fishing scenarios involving interactions with the survival of young reproductive females had a greater potential to halt NRKW's population growth than scenarios involving other vital rates (Table 6). Much greater is the room for improvement of fecundity rates (Figure 6), which explains fecundity's potential to produce greater proportional increases in population growth (Figure 12) and the greater potential of fishing scenarios involving fecundity to improve SRKW's population growth and viability (Table 6).

4. DISCUSSION

This study has addressed some of the pressing questions that have recently engaged the efforts of scientists and managers interested in: (1) the factors limiting population growth of SRKW; (2) explanations for the marked differences between the observed population trajectories of SRKW and NRKW in spite of their large home range overlap; (3) the role of Chinook salmon (in light of the vast evidence about the importance of the species in the summer diets of both killer whale populations) on the population dynamics of RKW; and, (4) the potential benefits for RKW population viability expected from reductions in Chinook fishing mortality and changes in Chinook fishery regimes. A purely demographic study of questions 1 and 2 was possible thanks to the high standards and temporal coverage of census data collected for these two populations. Linking RKW's demographic attributes to variations in the levels of Chinook abundance (question 3) necessarily required the simplification of ecological linkages and therefore overlooking many other factors (environmental and anthropogenic) potentially influencing RKW population dynamics. However, we acknowledge that model complexity is not directly proportional to model efficacy (Burnham and Anderson 2002). Addressing questions 3 and 4 was also possible due to the existence of indices of Chinook abundance representative of their pre-terminal and terminal phases for stocks originating in streams and rivers ranging from California to southeast Alaska. Although these indices do not necessarily represent the Chinook salmon available for killer whales, they represent the best available information to address these questions. Within these limitations, the exploration of how different fishing scenarios could influence RKW population viability (question 4) focused on the maximization of effects due to the relatively low sensitivity of RKW population growth rates to changes in Chinook fishing mortality uncovererd by some of our analyses. In addition, we have provided a hypothesis framework designed to assist with the interpretation of results as they pertain to linkages between RKW demographic rates and Chinook stock aggregates exhibiting different degrees of evidence based on from diet-composition studies.

Subsequently, we discuss the results of this investigation in light of these fundamental questions, including the relevance of Chum salmon as a covariate, and we also provide some perspective on the conditions involved in the evaluation of complex management scenarios and faced by pragmatic management. Since our exploration of fishing scenarios was necessarily limited to a small number of hypothetical situations, we have compiled all the analytical tools used in this investigation into a single programming platform using R software (R Development Core Team 2011) to facilitate future explorations and enable future revision and development of the themes making up the present study. Lastly, we provide some recommendations regarding future research and the need for caution to base management decisions on the outcome of the population viability analyses conducted herein.

4.1 Demographic differences between SRKW and NRKW

There are four main demographic factors that explain SRKW's lower demographic performance and viability relative to NRKW. In terms of vital rates, calf survival and the fecundity of old reproductive females during 1987-2011 have been on average significantly lower in SRKW than in NRKW (Figure 46). Calf survival rate in SRKW was effectively zero in 1988 and as low as 0.33 in 1999, 2006 and 2008, whereas the lowest calf survival in NRKW was 0.66 in 2000. In addition, there was no calf production in SRKW for the 1996-1997 annual interval. Differences were not as apparent for the fecundity of old reproductive females, but it was generally higher for NRKW and there was a 5-year period, from 1997 to 2001, when SRKW's fecundity of old reproductive females was zero. A noticeable exception happened in 2005 when SRKW fecundity reached 0.31 in 2005, compared to only 0.13 in NRKW (Figure 46). If the net value of differences in vital rates between the two killer whale populations is added annually in a sequential fashion, it becomes evident that the cumulative difference in calf survival stands out as the most important feature in favour of NRKW (Figure 47(top)). The only vital rate where the cumulative differences stand out in favour of SRKW is the survival of post-reproductive females (Figure 47(bottom)). However, this vital rate does not contribute directly to population growth rate and therefore does not increase directly the demographic performance of SRKW relative to that of NRKW. Nonetheless, the presence of post-reproductive females seems to substantially increase the survival probabilities of their sons older than 30 (Foster et al. 2012).

A third factor contributing to the lower growth rate of SRKW relative to NRKW is SRKW's lower proportion of juveniles transitioning into young reproductive females. Although the departures from a balanced sex ratio are small in both populations, they are significantly positive for NRKW (+5%) and negative (-5%) for SRKW, for a total difference of 10% in this vital rate in favour of NRKW. The proportion of females, φ_f, not only contributes to the stage-transition probabilities but also to fecundity rates (see Section 2.2). Sex ratio has a significant effect on a population's ability to increase from low numbers, and this ability is enhanced when females predominate and is depressed when males dominate (Caughley 1994). One of the advantages of our two-sex model is that the relative influence of the proportion of reproductive females on population growth can be quantified using elasticity analysis. Given our results, the proportion of females had elasticity values similar to those of calf survival (see Figure 11), and therefore these two demographic rates are expected to have similar influence on population growth rates.

Lastly, a fourth demographic factor explaining the lower population viability of the SRKW population is its greater vital rate variances. Temporal variation in vital rates was noticeably greater in SRKW than in NRKW, except for the survival of post-reproductive females (Figure 7). The demographic viability of a population will be mainly determined

by its capacity to increase from low numbers and its ability to buffer both density-dependent and environmentally-driven variability in its vital rates (Vélez-Espino and Koops 2012). Density-driven vital rate temporal variability can be linked to SRKW's small population size. There is evidence that inter-annual variability in survival in some vertebrate taxa increases at low abundance in an inverse density-dependent fashion and that this relationship has important consequences for recovery and population persistence (Minto et al., 2008). Thus this greater variability in vital rates could be associated with demographic stochasticity, which is the temporal variation in population growth driven by chance variation in the actual fates of different individuals within a year. Its magnitude is inversely related to population size, it can create substantial variability at low population sizes, and it can also translate into greater extinction risk (Morris and Doak 2002). Our analyses clearly demonstrated that demographic stochasticity is already an important factor in SRKW (e.g., Figure 28), with a strong negative influence on projections of population size.

The foregoing discussion identified those demographic factors deemed responsible for the lower performance of SRKW relative to that of NRKW. However, the factors underpinning differences in vital rates have not been identified and they could be genetic, environmental and/or anthropogenic. Among the genetic factors, inbreeding depression can occur. However, Ford et al. (2011) found no evidence of offspring produced by close relatives but found instead evidence of inbreeding avoidance in SRKW, which has been also observed in other killer whale populations (e.g., Barrett-Lennard 2000). It is therefore possible that inbreeding avoidance in a small population such as SRKW can be a deterrent for reproductive opportunities and ultimately a limiting factor for pregnancy and fecundity rates. In addition to prey availability, which is the focus of this investigation, environmental/anthropogenic factors that have been associated with the poor status of SRKW include exposure to pollutants (particularly PCBs and PBDEs; Krahn et al. 2007) and disturbance from boat traffic (Lusseau et al. 2009, Williams et al. 2009). Unlike NRKW, SRKW resides in a more urbanized environment and therefore they are more exposed to boat disturbance and environmental contaminants (Krahn et al. 2002).

Understanding the direct or indirect influence of oceanographic variables on RKW demographic rates remains a pressing challenge. Ward et al. (2009) found some evidence for sea surface temperature as an important covariate of fecundity when Chinook abundance affects annual fecundity rates. Interestingly, ocean conditions characterized by sea surface temperature following the timing of outmigration of smolts from freshwater to marine areas seem to have a significant effect on Chinook salmon survival (Sharma et al. 2012). Exploratory analyses have also provided statistical support for spring wind stress anomaly (a proxy for upwelling) in the northeast Pacific as an environmental covariate of RKW's vital rates and population abundance (Vélez-Espino et al. unpublished). Upwelling patterns are directly related to primary production (Bakun 1996) and therefore cumulative

or time-lagged patterns have the potential to directly influence Pacific salmon survival (Logerwell et al. 2003, Lawson et al. 2004) and consequently affect killer whale vital rates.

Direct links between anthropogenic factors such as pollution and boat disturbance and RKW survival or fecundity are difficult to measure. However, there is an anthropogenic factor with direct and quantifiable links to RKW vital rates. The live captures for the aquaria trade caused a large reduction in population size and disruption of stage structure of both RKW populations, particularly SRKW. Olesiuk et al. (1990) estimated that 93% of the killer whales cropped between 1962 and 1977 were residents and that 76% of these were taken from SRKW. In addition, this fishery was heavily biased towards juveniles and young males and produced major alterations in stage structure (see Appendix 2). Although the influence of this perturbation on population structure seems to have diminished by the early 1990's, some of the early years in our study period would have been influenced by this anthropogenic factor. Low calving rates in SRKW during the years after cropping ended could be partly explained by a reduction in the number of mature males below a critical number for optimal productivity (Olesiuk et al. 1990). Currently, population proportions of mature males are similar for these two populations at 22.7% (38.6% reproductive females) in SRKW and 21.1% (36.7% reproductive females) in NRKW.

An important question arises regarding the significant differences in calf survival and the fecundity of old reproductive females between SRKW and NRKW. Can these differences be explained by the levels of Chinook abundance available for each population? Only one significant interaction with calf survival was found, involving the cumulative effect of Fraser Late Chinook ocean abundance and this vital rate in NRKW. Conversely, numerous stock aggregates interacted with the fecundity of old reproductive females in both killer whale populations, with Fraser Early ocean abundance and Fraser Early/Puget Sound terminal run showing the largest potential effects on NRKW's population growth and Fraser Early/Puget Sound terminal run on SRKW. As shown in Figure 18 and 22, there are no signs of declining trends for the abundances of these stock aggregates nor there is evidence of ocean fishery impacts increasing in these stocks relative to their terminal runs (Figure 48). On the contrary, the relative magnitude of fishery impacts has declined in recent years for these stock aggregates as well as coastwide (Figure 48). Given this information, it is unlikely that differences in vital rates between NRKW and SRKW can be explained as the result of different interaction levels with common Chinook aggregates, the result of declining trends in Chinook abundance from relevant stocks, or to excessive levels of fishing mortality. The possibility of territoriality taking place between SRKW and NRKW and suppressing feeding rates of SRKW on common Chinook salmon resources based on NRKW's higher abundance cannot be discounted. However, there is no evidence of territoriality in resident killer whales (Ford et al. 2000) or cetaceans in general (Mann et al. 2000).

4.2 Sensitivity of RKW population growth to Chinook and Chum salmon abundance

4.2.1 Chinook salmon

Although numerous interactions between Chinook abundance from specific stock aggregates and RKW's survival and fecundity rates were found statistically significant, those involving fecundity rates were more common and showed greater influence on the population growth rates of these populations (as indicated by their elasticities). Most of the interactions for SRKW involved the fecundity of young reproductive females whereas for NRKW involved the fecundity of old reproductive females, followed by the survival of young reproductive females and juvenile survival. The sensitivity of RKW's population growth rates to changes in Chinook abundance was small even for the interactions with the largest elasticities. The maximum expected change in population growth (based on mean stochastic elasticities), whether individual, additive or cumulative, resulting from a $\delta\%$ change in the Chinook abundance of a given stock aggregate, never exceeded $0.048 \cdot \delta$ in SRKW or $0.046 \cdot \delta$ in NRKW. Based on the 95% upper confidence limits of stochastic elasticities, maximum expected changes in RKW's population growth rates are unlikely to be greater than $0.1 \cdot \delta$. These relatively small effects led us to focus on fishing scenarios characterized by the maximization of effects.

In terms of hypotheses regarding RKW-Chinook salmon interactions, our analyses showed support for both, those hypotheses in which causation is supported given the weight-of-evidence and those that require key assumptions. Interestingly, Fraser Early Chinook emerged as an important stock aggregate under the first group of hypotheses for the two killer whale populations, with Fraser Early terminal run being important for SRKW and Fraser Early ocean abundance for NRKW. Similarly, Puget Sound terminal run seemed important for SRKW and Puget Sound ocean abundance for NRKW under the hypotheses supporting causation. In addition, slightly behind the importance of Fraser Early and Puget Sound stocks aggregates, Fraser Late terminal run was also important for SRKW under the causation hypothesis. Regarding the second type of hypotheses, those that require the assumption that Chinook from specific stock aggregates remain important in the killer whale diet year-round and/or outside identified critical habitats (see Ford 2006), stock aggregates common to the two killer whale populations were also identified. Coastwide Chinook ocean abundance (excluding southeast Alaska) and Oregon Coastal ocean abundance were among the common stock aggregates with the largest potential influence on population growth rates of SRKW and NRKW. The five large stocks (WCVI, Fraser Late, Puget Sound, Columbia Upriver Brights, and Oregon Coastal) emerged as important for SRKW but not for NRKW, for which Fraser Early/Puget Sound terminal run had the largest influence. The sampling of feeding events by NRKW (Ford and Ellis 2006) indicates that Fraser Early Chinook returning to their terminal areas are intercepted in the summer months by NRKW in Johnstone Strait and are mostly comprised by South

Thompson Chinook. South Thompson Chinook is a summer-run stock that represents the most abundant component of the Fraser Early complex and about 20% of the Chinook stocks returning to rivers around the Salish Sea, and it has a high relative importance in the diet of resident killer whales in both Johnstone Strait and Juan de Fuca Strait (Parken et al. 2011). Although Puget Sound Chinook is also intercepted by NRKW in Johnstone Strait during the summer, Puget Sound Chinook are frequently intercepted in Juan de Fuca Strait. Passive acoustic monitoring revealed that NRKW use the southern parts of their range more frequently than previously thought, and highlighted the importance of the southern entrance to the Salish Sea as a killer whale hotspot (Riera 2012). These observations indicate that NRKW's summer range can be larger and including the critical area identified for SRKW (Ford 2006) and suggest that the large influence of Fraser Early/Puget Sound terminal run on NRKW's population growth may not be spurious.

Our results also supported the importance of cumulative effects of Chinook abundance levels on the population growth rates of both killer whale populations, thus highlighting the importance of considering the levels of nutritional stress or population response to Chinook abundance levels beyond discrete annual intervals. For SRKW, the largest cumulative effect was that involving the levels of ocean abundance of the five large stocks (WCVI, Fraser Late, Puget Sound, Columbia Upriver Brights, and Oregon Coastal) on the fecundity of young reproductive females (Figure 16) whereas for NRKW, the largest cumulative effect was that involving the levels of Fraser Early ocean abundance and the fecundity of old reproductive females (Figure 20). It is also interesting that some significant relationships between specific stock aggregates and RKW vital rates were detected only for cumulative effects. Examples of these were Columbia UpRiver Brights ocean abundance and survival of SRKW's old reproductive females (Table 1), Upper Georgia Strait terminal run or Fraser Late ocean abundance and NRKW's survival of young reproductive females (Table 2). In fact, 26 of the 66 significant regressions for NRKW corresponded to interactions under cumulative effects. Only five of the 25 significant regressions for SRKW involved cumulative effects. There could be however some pragmatic limitations implementing management actions directed to produce changes in a cumulative index of Chinook abundance that encompasses a 5-year period (see Section 4.3.4 for additional discussion).

4.2.2 Chum salmon

Among the various Chun stock aggregates included in the analyses, Northern/Central BC and Washington Summer/Fall/Winter were the only ones identified as relevant covariates in significant Chinook-vital rate relationships. Chum salmon from the Northern/Central BC terminal run increased the Chinook effects for both SRKW and NRKW while increasing the overall fit of the regression models. These are important results that point to the need

for additional efforts to quantify the importance of Chum salmon on RKW's diet and to identify the contributions of different Chinook and Chum salmon stocks to RKW's diet during the fall and year-round.

Two aspects of Chum salmon as a covariate deserve further discussion. First, the inclusion of Northern/Central BC Chum terminal run substantially increased (~61%) the relative influence of ocean abundance of the five large stocks (WCVI, Fraser Late, Puget Sound, Columbia Upriver Brights, and Oregon Coastal) on SRKW's population growth rate (Table 4). However, this Chum stock aggregate includes terminal runs of Chum salmon ranging from the border to southeast Alaska to the south end of Johnstone Strait, including Haida Gwaii, and therefore overlaps only slightly with the distribution range exhibited by SRKW (see Ford 2006). Nevertheless, unlike the ocean abundance of the five large Chinook stocks, the aggregated terminal runs of Northern/Central BC Chum show a declining abundance trend (Figure 23) and therefore could be affecting prey availability for RKW, particularly for NRKW.

Second, the inclusion of Washington Summer/Fall/Winter Chum terminal run increased the relative influence of the Fraser Early/Puget Sound/Fraser Late Chinook terminal run on NRKW's population growth by approximately 10% (Table 4). This result reiterates the potential importance of salmon (Chinook and Chum) stocks bound to the Fraser and Puget Sound terminal areas for NRKW's fecundity and population performance. As discussed in the previous section, Fraser Early/Puget Sound terminal run exhibited the largest relative influence on NRKW's population growth under the weak hypothesis 2b (see Figure 20).

In spite of these aspects of Chum salmon as a covariate deserving attention, and although there is statistical support for Chum terminal run as a covariate in Chinook-RKW vital rates interactions, only the inclusion of Northern/Central BC Chum terminal run as a covariate in the interaction between the terminal run of Fraser Late Chinook and SRKW's fecundity of young females was framed by an hypothesis with support for causation (hypothesis 1a). In fact, the inclusion of Chum salmon as a covariate increased the relative influence of this interaction on SRKW's population growth by approximately 17% (Table 4). However, although Fraser Late Chinook terminal run had a larger contribution to the variation in observed population growth than either Puget Sound or Fraser Early Chinook terminal run (Figure 17), the interaction between Northern/Central BC Chum terminal run and SRKW's vital rates may be spurious.

4.3 Sensitivity of RKW population viability to Chinook fishing mortality

4.3.1 The purpose of PVAs

It has been a common occurrence that the results of PVAs are misinterpreted and seen as forecasting exercises. PVAs use stochastic models with fluctuating population size and varying demographic parameters to project population size and the probability of population persistence (or recovery or extinction) for a defined period under specific conditions (Marmontel et al. 1996). It is easy to overlook the last three words of this definition. It is not the purpose of a PVA to make predictions of future population state since there will always be unforeseen sources of uncertainty. PVAs are projections, conditional on a population model, enabling the exploration of population responses to perturbations assuming that the population is governed by specific processes operating in defined ways. And assuming these processes apply to the future, a PVA generates risks of extinction or projections of population size. Thus, PVA forms the basis for explorations of a given system (e.g., RKW-Chinook interactions) and allows projections of population response to management perturbations where knowing exactly and precisely a population's long-term growth rate or abundance is of lesser importance than obtaining a simpler, qualitative assessment of whether the population will tend to grow or decline (Morris and Doak 2002). Yet, PVA remains one of the most powerful analytical tools to prioritize conservation and management actions and facilitate decision making (Ralls et al. 2002). PVA provides a robust assessment of the relative efficacy of two or more management strategies and allows explorations of relative differences between simulation scenarios.

The foregoing paragraph sets the stage for an appropriate interpretation of the PVA results in this investigation. Now it is clear that the aim of the PVAs herein is not to provide perfect forecasts but to allow comparisons of scenarios under a number of assumptions such like "the relative importance of Chinook salmon abundance and other (unknown) factors have on vital rates will remain the same in the future" or "the observed range of variation and covariation in RKW's vital rates will remain the same (e.g., under an IID environment)". Within the context of fundamental question 4 regarding RKW population response to changes in Chinook fishing mortality, attention should be placed on the relative differences in population projections under the different selected scenarios rather than expecting absolute measures of population size and viability. Some of the factors not included in our PVA that have the potential to increase extinction probabilities and reduce projected population sizes could include indices of climate change, catastrophes, and loss of fitness due to genetic stochasticity (Lande 2002). Other factors that not only reflect the complexity of trophic interactions but also may yield less optimistic less optimistic population projections include the interactions between Chinook salmon and growing populations of other salmon eaters such as harbour seals and sea lions (e.g., Preikshot and Perry 2012). Factors moving the balance on the optimistic side, such as

the inclusion in our PVA of declining trends in ocean harvest rates, could have been incorporated for illustration purposes only. However, there is no reason to assume Chinook ocean harvest rates are going to continue declining given current management regimes under the Pacific Salmon Treaty and given the currently low ocean harvest rates (~20% coastwide). The PVA conducted herein therefore should be considered as a work in progress, but also considering that as model complexity increases by including additional processes, the increased difficulty of obtaining precise parameter estimates might quickly come to outweigh any perceived advantage of enhanced biological realism (Ludwig and Walters 1985, Burnham and Anderson 2002).

4.3.2 RKW population response to changes in Chinook fishing mortality

Due to the low sensitivity of RKW's population growth rates to changes in the Chinook abundance of multiple stock aggregates, including a coastwide aggregate and stock aggregates with little or no support for causation, our exploration of fishing scenarios focused on either the maximization of Chinook abundance or the maximization of vital rates for SRKW, whatever occurred first. Given the clearly positive population growth in NRKW, population responses focused on either halting population growth or maximizing fishing mortality, whatever occurred first. The selection of scenarios for SRKW stems from the implicit need to recovery for this population in terms of population size and population growth. The selection of scenarios for NRKW did not respond to a management objective *per se* but to our research objective of evaluating this population's response to changes in Chinook fishing mortality and gaining insights into the potential effects of large increases in harvest rates.

Among the hypotheses we explored, the one involving SRKW and Chinook stocks evoking greater weight-of-evidence for causation (i.e., hypothesis 1a) is without doubt the most important in terms of scientific evidence guiding management decisions. SRKW's small population size and low probabilities of positive population growth under status quo conditions (see Figure 9) is in greater need than NRKW of management actions directed to increase this population's viability. In addition, interactions under hypothesis 1a involve Chinook stocks that are overwhelmingly prevalent in the summer diets of SRKW (Hanson et al. 2012), thus supporting for causation. The fishing scenarios selected to represent hypothesis 1a essentially imply zero fishing mortality in pre-terminal areas (i.e., closing of ocean fisheries) for Fraser Early and Puget Sound Chinook stocks (Table 5). Scenario 3, which was more consistent with the contribution of Fraser Early to SRKW's summer diet (see Section 3.4.5), basically produces a central tendency to equilibrium ($\lambda \approx 1.0$; Figure 45). This slight increase in stochastic population growth rate represents however an improvement to status quo conditions, which produce a population growth that is expected to be slightly negative more than 70% of the time (Figure 9).

Much greater increases in SRKW's population growth are produced by scenarios framed by the weak hypothesis 2a (Table 6). These scenarios produce similar and strongly positive annual population growth rates (~1.8%) that are below the U.S. recovery target of 2.3%. But in spite of the great potential these scenarios hold to produce substantial positive improvement to status quo conditions, these scenarios do not represent interactions that have the support of other sources of evidence (such as diet-composition studies) and require the assumption that Chinook stock aggregates involved in those interactions are as important in the diet of SRKW year-round as Fraser Early and Puget Sound are in the summer or Fraser Late in the summer-fall transition. The two relevant stock aggregates for this hypothesis are not independent since the ocean abundance of the five large stocks (WCVI, Fraser Late, Puget Sound, Columbia Upriver Brights, and Oregon Coastal) is nested within the coastwide aggregate. The corresponding reductions in ocean harvest rates required to maximize the same vital rates (Table 5) are consistent with this nesting condition, with 51% reductions for the five large stocks and 36% for the coastwide aggregate.

The main benefits of exploring fishing scenarios halting NRKW's population growth or maximizing ocean harvest rates have been demonstrating that the population dynamics of NRKW are as sensitive as those of SRKW to changes in Chinook abundance and fishing mortality and showing that there are feasible levels of fishing mortality that can exert large reductions in population growth and even halt the positive trend NRKW have exhibited for the last decades. The fact that a 66% increase in coastwide ocean harvest rates has the potential to halt population growth (Table 5) also means that larger increases in harvest rates could actually exert declining condition; that is, if key assumptions of weak hypothesis 2b are validated.

Although presently causation cannot be invoked for the weak hypotheses 2a and 2b, and therefore scientific advice for management decisions cannot be provided on this basis, the results of the PVAs involving these hypotheses have generated a host of new hypotheses that go from the importance of Chinook ocean abundance from the Fraser Late aggregate or Oregon Coastal aggregate on the year-round diet of SRKW to the significance of the Chinook terminal run of the Fraser Early/Puget Sound aggregate on NRKW's summer diet to the relevance of cumulative effects of Chinook abundance levels on RKW's vital rates. The main drawbacks of these so called weak hypotheses occur on statistical and ecological grounds. On statistical grounds, it is possible that some of the interactions are spurious (Tables 1 and 2) and not necessarily representative of predator-prey dynamics. On ecological grounds, there is the possibility of RKW switching to non-salmon prey in months when feeding events have been poorly sampled (late fall, winter, and early spring). Several decades of RKW studies show however that these populations are not generalist predators and raise the possibility that their hunting specialization and prey selectivity can constrain their ability to switch prey in response to scarcity of their preferred prey or to the

relative abundances of other prey (Ford and Ellis 2006, Ford et al. 2010a, Hanson et al. 2010, Williams et al. 2011). Data from the limited number of predation events sampled during winter and spring seems to confirm this prey specialization and selectivity and suggest a prevalence of Chinook salmon in the year-round diet of RKW (Ford 2012).

4.3.3 Complex fishing scenarios

The responses of RKW population dynamics to changes in fishing mortality explored in this investigation have been based on fishing scenarios isolating the interactions between individual Chinook stock aggregates and one or more vital rates (e.g., the interaction between coastwide ocean abundance and SRKW's fecundity of young reproductive females and the survival of old reproductive females). Nonetheless, there is the potential to explore fishing scenarios of increasing complexity involving more than one Chinook stock aggregate. The motivation behind these complex scenarios can be for instance to produce a population response that improves SRKW's population viability relative to the responses produced by individual stock aggregates. However, five conditions have to be met in order to proceed with this kind of analysis. First, the two or more stock aggregates involved cannot be nested because their abundances would not be independent (e.g., there cannot be a complex scenario involving the coastwide aggregate because it encompasses all other stock aggregates). Second, the interactions must occur with different vital rates because the interactions of one vital rate with several stock aggregates are not independent, otherwise huge and unrealistic population responses could be produced by adding the individual effects of all interactions with a given vital rate. Third, a complex scenario cannot combine interactions representative of different hypotheses because they do not have the same weight-of-evidence. Fourth, cumulative and non-cumulative effects cannot be combined in a complex scenario because they represent different time intervals. Lastly, complex scenarios cannot combine stock aggregates involving different abundance types (e.g., terminal run or ocean abundance) because they represent different abundance units (see Section 2.3.3).

Complex scenarios were not investigated because they were not anticipated in the first stages of this project, because only a few cases can be currently identified (as expected from the number of conditions that have to be met), and because they are computationally demanding. We can still produce approximations of RKW's population responses based on the elasticity values of interactions involved in a given complex scenario. This is possible because elasticities are additive and because there are defined relationships between the elasticities of interactions and all PVA metrics resulting from a specified proportional change in Chinook abundance (i.e., PVA metrics and elasticities of interactions are strongly correlated for a given perturbation; see also Caswell 2001).

Perhaps, the identification of complex scenarios makes more sense for the causation hypotheses than for the weak hypotheses. The additional complexity may not be warranted when key assumptions still need to be addressed for the weak hypotheses. There is only one complex scenario for SRKW that meets all of the abovementioned criteria under hypothesis 1a (Table 1). This scenario involves two interactions: Fraser Late terminal run and the fecundity of young reproductive females, and Puget Sound terminal and the fecundity of old reproductive females. Their added elasticity ($\varepsilon = 0.043$) indicates that SRKW's population responses resulting from a small $\delta\%$ change in the Chinook abundance of these stock aggregates are expected to be about twice as large as those of the interaction between Fraser Early/Puget Sound terminal run and the fecundity of old reproductive females ($\varepsilon = 0.022$).

For NRKW, there are few combinations of stock aggregates that meet all of the abovementioned criteria under hypothesis 1b (Table 2), some of which involve terminal run and some involving ocean abundance. The complex scenario with the greatest added elasticities for terminal run includes two interactions: Northern BC and the survival of young reproductive females, and Lower Georgia Strait and the fecundity of old reproductive females. Their added elasticity ($\varepsilon = 0.028$) indicates that NRKW's population responses resulting from a small $\delta\%$ change in the Chinook abundance of these stock aggregates are expected to be about twice as large as those of the interaction between Northern BC terminal run and the survival of old reproductive females ($\varepsilon = 0.013$). In terms of ocean abundance, the complex scenario with the greatest added elasticity includes also two interactions: Fraser Early and the fecundity of old reproductive females, and Puget Sound and juvenile survival. Their added elasticity ($\varepsilon = 0.045$) is almost as high as that of the interaction involving Fraser Early ocean abundance under cumulative effects (see Figure 20).

Notice that relationships between elasticity and PVA metrics are not necessarily linear (Vélez-Espino and Araujo, unpublished). Greater departures from linearity can be expected from greater magnitudes of $\delta\%$ (see Mills et al. 1999, de Kroon et al. 2000, Vélez-Espino 2005). Hence, the main limitation of inferring RKW's population responses to complex scenarios from the added elasticities is that proportional changes in Chinook abundance ($\delta\%$) necessary to produce tangible changes in population growth and viability are rather large (due to the low sensitivity of RKW's population growth to changes in Chinook abundance). The magnitude of those changes in our selected scenarios are as large as those resulting from the closing of fisheries for SRKW's recovery objective or increasing harvest rates more than 100% for NRKW's equilibrium objective (see Table 5). Thus, assuming linearity between elasticities and PVA metrics poses a critical difficulty to the use of this information quantify large perturbations and potentially guide management decisions. The full development of direct perturbations and computer simulations is

therefore deemed as necessary for the exploration of large changes in Chinook abundance derived from complex scenarios (see Section 4.3.5).

4.3.4 Pragmatic management

Some analytical components of this investigation have focused on the sensitivity of RKW population viability to Chinook fishing mortality transpiring from interactions between Chinook stock aggregates and RKW's vital rates. The nature of these interactions has been defined by their weight-of-evidence and the probabilities of RKW encountering and preying on specific Chinook stocks (Box 1). However, there is a large leap between the identification of relevant interactions - and the characteristics of selected fishing scenarios - and the feasibility or practicality of directing management actions towards those Chinook stock aggregates identified as relevant. We are referring to the difficulty of exerting harvest rate adjustments to specific Chinook stock aggregates in mixed-stock fisheries. Given the highly migratory nature of Chinook salmon, ocean fisheries harvest Chinook from stocks originating in streams and rivers far away from the area where fisheries are taking place and inescapably intercept Chinook salmon from different jurisdictions (Shepard and Argue 2005). These mixed-stock fisheries are regulated by the Pacific Salmon Treaty and their catch composition is monitored and reported annually by the CTC (PSC 2011a). Although genetic data have been used to gain insight into population-specific migration timing (e.g., Parken et al. 2008) and in-season management of Chinook salmon (e.g., Winther and Beacham 2009), the current Chinook management framework under the PST has not fully incorporated genetic data to assist management strategies for mixed-stock Chinook fisheries.

It is therefore important to notice that management actions implemented to increase SRKW's population viability under current Chinook fishery regimes and targeting harvest rate changes for a specific stock aggregate are going to inexorably affect other stocks. Pragmatic management actions could be conservative and embrace this situation, make additional use of in-season genetic data or alternatively implement management actions directed to the coastwide aggregate. Assuming weak hypotheses are validated by future studies, the ocean abundance of the coastwide aggregate (excluding southeast Alaska) is one of the stock aggregates with the largest potential influence on SRKW's population growth and it was also identified as important for NRKW. Scenario 5 (Table 5) showed that if causation is assumed, a 36% reduction in coastwide harvest rates is expected to maximize SRKW's vital rates involved in the interaction and produce a clearly positive population growth rate.

Our analysis of interactions showed support for the importance of cumulative effects of Chinook abundance levels on RKW's vital rates and ultimately on RKW's

population growth and viability. Large, long-lived species (e.g., RKW) are expected to suffer less severe fluctuations in population size than smaller short-lived organisms (Pimm 1991) mainly due to their greater compensatory reserves (e.g., Vélez-Espino and Koops 2012) and their capacity to offset density-dependent variations in mortality (Rose et al. 2001) and population growth (Pianka 1970, Reznick et al. 2002). It is therefore biologically plausible that changes in RKW's vital rates associated to levels of food availability and nutritional stress become more tangible for indices of Chinook abundance representing time intervals encompassing several years. Multiyear cumulative effects are expected to have a greater potential than annual effects to subdue compensatory reserves and offset buffer mechanisms in RKW. The problem with management strategies based on 5-year cumulative effects on vital rates is that annual effects and RKW stage transition probabilities can be confounded and monitoring the impact of these strategies on RKW's population dynamics can be no longer tractable. It seems more pragmatic to base management decisions on non-cumulative basis understanding that continuous, uninterrupted implementation of a given strategy will eventually translate into cumulative effects.

4.3.5 An R tool for exploration of fishing scenarios

The present investigation was originally envisioned as phase-1 of a two-phase project contingent on second-phase funding from a CDFO-PSC Collaborative Agreement. The main goals of phase-1 were (1) the development of information to understand the role Chinook abundance and fishing mortality have on RKW population dynamics, and (2) the production of code in R software (R Development Core Team 2011) for the exploration of Chinook fishing scenarios on killer whale population viability. The modelling components of most analyses conducted and detailed in this report have been compiled into a single R-code available in Appendix 8. And as specified in the Collaborative Agreement, the R-code provided also produces the input files required for the Monte Carlo simulations in RAMAS that produce some of the viability metrics explored herein. The second phase was identified as an opportunity to refine analyses through additional efforts such as the incorporation of other covariates, automatic linking of the R-code with RAMAS, and most importantly the development of a user-friendly stand-alone application (R-Gui) allowing users to conduct real-time evaluations of scenarios of interest (including complex scenarios) and alternative biological hypotheses regarding RKW demography and linkages between prey abundance and RKW population parameters and viability.

4.4 Conclusions

- Based on their demographic rates during the last killer whale generation (25 y), expected population growth is 0.91% annual decline ($\lambda_{stochastic}$ = 0.9909; 95% CI: 0.9719-1.0081) for SRKW and 1.58% annual increase ($\lambda_{stochastic}$ = 1.0158; 95% CI: 1.0027-1.0285) for NRKW. The PVA results indicate that if the observed range of variation and covariation in its vital rates persists and mean vital rate values remain unchanged (i.e., status quo conditions), SRKW's extinction risk in 100 years is ~50%.

- In demographic terms, SRKW's lower expected population growth is mainly due to this population's lower production and survival of viable calves. In addition, greater variation in vital rates and a strong influence of demographic stochasticity on future population dynamics, both associated to a small population size, contribute to SRKW's lower population viability.

- Based on the information used and produced in this study, we found no evidence that differences in demographic rates between killer whale populations are due to differential levels of access to common Chinook resources, to declines in Chinook abundance, or to increases in fishing mortality of relevant stocks.

- Numerous interactions between Chinook abundance aggregates and RKW vital rates were found. Although we found no evidence that current levels of Chinook abundance are limiting SRKW's population growth, the numerous significant relationships between Chinook abundance and the vital rates of both SRKW and NRKW are deemed as indication of clear predator-prey dynamics. However, other factors (genetic, environmental and/or anthropogenic) must be limiting SRKW's population growth and possibly masking and confounding the detection of stronger interactions between killer whale vital rates and Chinook abundance.

- Although interactions were weak on both statistical and demographic grounds, some lent support for causation given the weight-of-evidence regarding the importance of specific Chinook stocks in RKW's diet. Chiefly, Fraser River and Puget Sound Chinook emerged as important stock aggregates under hypotheses supporting causation for the two killer whale populations. Fraser Early terminal run was important for SRKW and Fraser Early ocean abundance for NRKW. Similarly, Puget Sound terminal run seemed important for SRKW while Puget Sound ocean abundance for NRKW. In addition, slightly behind the importance of Fraser Early and Puget Sound stocks aggregates, Fraser Late terminal run was also important for SRKW under an hypothesis supporting causation. The size of Chinook terminal runs from the Fraser River and Puget Sound stock aggregates exhibited a low

interaction with SRKW's fecundity. Nevertheless, PVA results showed that these low interaction levels could still produce slightly positive population growth rates approximately 50% of the time under extreme reductions to fishing mortality such as those resulting from the closure of ocean fisheries targeting these stocks. In the case of NRKW, it was the ocean abundance of the Fraser Early aggregate that interacted with this population's fecundity and showed some potential to influence its expected population growth.

- Although the importance of Fraser River and Puget Sound Chinook salmon stocks to influence RKW's population dynamics is supported by this study, it remains a challenge exerting adjustments to ocean harvest rates of specific Chinook stock aggregates in mixed-stock fisheries. If new studies confirm the prevalent and critical importance (as resulting from RKW's limitation to switch to other prey during winter and spring or when Chinook density is low) of Chinook salmon in killer whale's year-round diet, pragmatic management could consider adjustments to coastwide Chinook ocean abundance. This combination of stock aggregate and abundance type was among the Chinook covariates with the largest influence on population growth rates of both killer whale populations.

- Our analyses showed some support for Chum salmon as a covariate for RKW vital rates and unlike relevant Chinook salmon aggregates, the declining trend in Chum salmon terminal run from the Northern/Central BC aggregate could be affecting prey availability for NRKW.

4.5 Recommendations

- Future research efforts are needed to identify the causes of depressed production and survival of viable calves in SRKW.

- The continuance of studies of killer whale diet composition in fall, winter, and spring is deemed as essential to substantiate relevant interactions uncovered under the weak hypotheses. This information is critical to move away from potentially spurious correlations and it is required to support causation.

- The influence of cumulative effects of Chinook abundance levels on RKW's vital rates was evident in this study. It seems important to develop alternative methods to quantify these effects while enabling the monitoring and tracking of benefits to RKW exerted by potential management actions.

- The U.S. downlisting recovery target of 2.3% annual growth rate for 14 years for SRKW seems biologically unfeasible. A pragmatic population growth-based recovery target for SRKW should not exceed the expected population growth for NRKW of 1.0158 (1.58% annual increase).

- Although this investigation stands alone as a research contribution, a second phase as envisioned in the original project proposal to the PSC Southern Boundary Restoration and Enhancement Fund, could address not only technical aspects such as automatic links between the R-code and other relevant software such as RAMAS and the development of a user-friendly R-interface but also the investigation of additional hypotheses generated by this study regarding linkages between Chinook (and Chum) salmon stocks and RKW's population viability. Other aspects deserving attention could include additional consideration to potentially important environmental covariates as well as cumulative effects of prey abundance levels and the exploration of complex management scenarios.

5. ACKNOWLEDGEMENTS

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TABLES

Table 1. Summary of positive significant interactions (beta-regression models with p < 0.05) between SRKW vital rates directly contributing to population growth and Chinook abundance. Interactions are grouped by abundance type, time lag (5YA: 5-year running average), and hypothesis.

Vital Rate	Stock or stock aggregate	Abundance Type	Lag	Pseudo-R2	P-value	Hypothesis
Fecundity (Female 2)	Fraser Early + Puget Sound	Terminal Run	1	0.086	0.0259	1a
Fecundity (Female 2)	Fraser Early + Puget Sound	Terminal Run	2	0.075	0.0275	1a
Fecundity (Female 1)	Fraser Late	Terminal Run	2	0.073	0.0327	1a
Fecundity (Female 2)	Puget Sound	Terminal Run	2	0.164	0.0076	1a
Survival (Female 2)	Columbia Spring/Summer	Terminal run	1	0.319	0.0130	2a
Fecundity (Female 2)	Columbia Spring/Summer	Terminal run	1	0.140	0.0110	2a
Fecundity (Female 2)	Columbia Spring/Summer	Terminal run	5YA	0.179	0.0300	2a
Fecundity (Female 1)	West Coast Vancouver Island	Terminal run	1	0.086	0.0177	2a
Fecundity (Female 1)	West Coast Vancouver Island	Terminal run	2	0.097	0.0220	2a
Survival (Female 2)	WCVI+URB+FL+OC+PS	Ocean Abundance	0	0.446	0.0027	2a
Fecundity (Female 1)	WCVI+URB+FL+OC+PS	Ocean Abundance	1	0.154	0.0059	2a
Fecundity (Female 1)	WCVI+URB+FL+OC+PS	Ocean Abundance	2	0.155	0.0029	2a
Fecundity (Female 1)	WCVI+URB+FL+OC+PS	Ocean Abundance	5YA	0.084	0.0114	2a
Survival (Female 2)	Coastwide (excluding SEAK)	Ocean Abundance	0	0.488	0.0028	2a
Fecundity (Female 1)	Coastwide (excluding SEAK)	Ocean Abundance	2	0.119	0.0194	2a
Fecundity (Female 1)	Coastwide (excluding SEAK)	Ocean Abundance	5YA	0.060	0.0365	2a
Fecundity (Female 1)	Fraser Late	Ocean Abundance	1	0.092	0.0246	2a
Fecundity (Female 1)	Fraser Late	Ocean Abundance	2	0.117	0.0156	2a
Fecundity (Female 1)	Fraser Late	Ocean Abundance	5YA	0.116	0.0196	2a
Survival (Female 2)	Oregon Coastal	Ocean Abundance	0	0.353	0.0322	2a
Fecundity (Female 1)	Oregon Coastal	Ocean Abundance	1	0.082	0.0349	2a
Fecundity (Female 1)	Oregon Coastal	Ocean Abundance	2	0.055	0.0395	2a
Fecundity (Female 1)	West Coast Vancouver Island	Ocean Abundance	1	0.098	0.0162	2a
Fecundity (Female 1)	West Coast Vancouver Island	Ocean Abundance	2	0.100	0.0105	2a
Survival (Female 2)	Columbia UpRiver Brights	Ocean Abundance	5YA	0.262	0.0415	2a

WCVI: West Coast Vancouver Island; **URB:** Colombia UpRiver Brights; **FL:** Fraser Late; **OC:** Oregon Coastal; **PS:** Puget Sound

Table 2. Summary of positive significant interactions (beta-regression models with p < 0.05) between NRKW vital rates directly contributing to population growth and Chinook abundance. Interactions are grouped by abundance type, time lag (5YA: 5-year running average), and hypothesis.

Vital Rate	Stock or stock aggregate	Abundance Type	Lag	Pseudo-R2	P-value	Hypothesis
Survival (Female 1)	Northern British Columbia (Areas 1-5)	Terminal Run	1	0.335	0.0016	1b
Survival (Female 1)	Upper Georgia Strait	Terminal Run	5YA	0.225	0.0028	1b
Fecundity (Female 2)	Lower Georgia Strait	Terminal Run	2	0.096	0.0072	1b
Fecundity (Female 2)	Lower Georgia Strait	Terminal Run	5YA	0.109	0.0062	1b
Survival (Female 1)	West Coast Vancouver Island	Terminal Run	0	0.156	0.0205	1b
Fecundity (Female 2)	Fraser Early	Ocean Abundance	5YA	0.142	0.0020	1b
Survival (Juvenile)	Fraser Early+Puget Sound+Columbia UpRiver Brights	Ocean Abundance	0	0.248	0.0138	1b
Survival (Juvenile)	Fraser Early+Puget Sound+Columbia UpRiver Brights	Ocean Abundance	1	0.177	0.0400	1b
Survival (Juvenile)	Fraser Early+Puget Sound+Columbia UpRiver Brights	Ocean Abundance	5YA	0.179	0.0137	1b
Fecundity (Female 2)	Fraser Early	Ocean Abundance	0	0.096	0.0164	1b
Fecundity (Female 2)	Fraser Early	Ocean Abundance	1	0.108	0.0053	1b
Fecundity (Female 2)	Fraser Early	Ocean Abundance	2	0.078	0.0064	1b
Survival (Juvenile)	Puget Sound	Ocean Abundance	0	0.176	0.0165	1b
Survival (Juvenile)	Puget Sound	Ocean Abundance	1	0.265	0.0031	1b
Survival (Juvenile)	Puget Sound	Ocean Abundance	5YA	0.197	0.0214	1b
Survival (Juvenile)	Columbia UpRiver Brights	Ocean Abundance	0	0.215	0.0390	1b
Survival (Juvenile)	Columbia UpRiver Brights	Ocean Abundance	5YA	0.139	0.0238	1b
Fecundity (Female 2)	Fraser Early+Puget Sound+Fraser Late	Terminal Run	0	0.136	0.0068	2b
Fecundity (Female 2)	Fraser Early+Puget Sound+Fraser Late	Terminal Run	1	0.097	0.0012	2b
Survival (Female 2)	Fraser Early+Puget Sound+Fraser Late	Terminal Run	5YA	0.177	0.0434	2b
Fecundity (Female 2)	Fraser Early+Puget Sound+Fraser Late	Terminal Run	5YA	0.081	0.0095	2b
Survival (Female 2)	FE+PS+FL+COLf+COLs+OC	Terminal Run	5YA	0.109	0.0452	2b
Fecundity (Female 1)	FE+PS+FL+COLf+COLs+OC	Terminal Run	5YA	0.146	0.0325	2b
Fecundity (Female 1)	Coastwide (excluding Sacramento Fall and Klamath Fall)	Terminal Run	5YA	0.143	0.0318	2b
Survival (Juvenile)	Columbia Fall (UpRiver Brights+ Tule)	Terminal Run	0	0.234	0.0173	2b
Survival (Juvenile)	Columbia Fall (UpRiver Brights+ Tule)	Terminal Run	5YA	0.113	0.0265	2b
Fecundity (Female 1)	Columbia Fall (UpRiver Brights+ Tule)	Terminal Run	5YA	0.156	0.0329	2b
Survival (Female 2)	Columbia Spring/Summer	Terminal Run	1	0.176	0.0328	2b
Survival (Female 2)	Columbia Spring/Summer	Terminal Run	5YA	0.142	0.0099	2b
Fecundity (Female 2)	Columbia Spring/Summer	Terminal Run	5YA	0.041	0.0346	2b
Fecundity (Female 2)	Fraser Early (Spring and Summer)	Terminal Run	0	0.098	0.0166	2b
Fecundity (Female 2)	Fraser Early (Spring and Summer)	Terminal Run	1	0.085	0.0091	2b
Fecundity (Female 2)	Fraser Early (Spring and Summer)	Terminal Run	2	0.091	0.0045	2b
Fecundity (Female 2)	Fraser Early (Spring and Summer)	Terminal Run	5YA	0.148	0.0015	2b
Survival (Female 1)	Fraser Early (Spring)	Terminal Run	0	0.245	0.0022	2b
Fecundity (Female 2)	Fraser Early (Summer)	Terminal Run	0	0.117	0.0118	2b
Survival (Female 2)	Fraser Early (Summer)	Terminal Run	1	0.191	0.0495	2b
Fecundity (Female 2)	Fraser Early (Summer)	Terminal Run	1	0.097	0.0102	2b
Fecundity (Female 2)	Fraser Early (Summer)	Terminal Run	2	0.096	0.0036	2b
Fecundity (Female 2)	Fraser Early (Summer)	Terminal Run	5YA	0.131	0.0026	2b
Fecundity (Female 2)	Fraser Early + Puget Sound	Terminal Run	0	0.131	0.0138	2b
Fecundity (Female 2)	Fraser Early + Puget Sound	Terminal Run	1	0.129	0.0028	2b
Fecundity (Female 1)	Fraser Early + Puget Sound	Terminal Run	2	0.146	0.0364	2b
Fecundity (Female 2)	Fraser Early + Puget Sound	Terminal Run	2	0.076	0.0068	2b
Survival (Female 2)	Fraser Early + Puget Sound	Terminal Run	5YA	0.182	0.0313	2b
Fecundity (Female 2)	Fraser Early + Puget Sound	Terminal Run	5YA	0.095	0.0053	2b
Survival (Juvenile)	Puget Sound (Summer and Fall)	Terminal Run	0	0.143	0.0215	2b
Survival (Juvenile)	Puget Sound (Summer and Fall)	Terminal Run	1	0.266	0.0043	2b
Fecundity (Female 2)	Puget Sound (Summer and Fall)	Terminal Run	1	0.086	0.0337	2b
Survival (Juvenile)	Puget Sound (Summer and Fall)	Terminal Run	5YA	0.226	0.0075	2b
Survival (Female 2)	Puget Sound (Summer and Fall)	Terminal Run	5YA	0.122	0.0362	2b
Survival (Female 1)	Oregon Coastal	Terminal Run	0	0.334	0.0092	2b
Survival (Female 1)	Oregon Coastal	Terminal Run	1	0.190	0.0220	2b
Survival (Female 1)	Oregon Coastal	Terminal Run	5YA	0.101	0.0181	2b
Survival (Female 1)	WCVI+FL+OC	Ocean Abundance	0	0.255	0.0068	2b
Survival (Female 1)	WCVI+FL+OC	Ocean Abundance	1	0.227	0.0060	2b
Survival (Female 1)	WCVI+FL+OC	Ocean Abundance	5YA	0.251	0.0076	2b
Survival (Female 1)	Coastwide (excluding SEAK)	Ocean Abundance	0	0.354	0.0145	2b
Survival (Female 1)	Coastwide (excluding SEAK)	Ocean Abundance	1	0.359	0.0008	2b
Survival (Female 1)	Coastwide (excluding SEAK)	Ocean Abundance	5YA	0.203	0.0024	2b
Survival (Female 1)	West Coast Vancouver Island	Ocean Abundance	0	0.138	0.0253	2b
Survival (Calf)	Fraser Late	Ocean Abundance	1	0.218	0.0168	2b
Survival (Female 1)	Fraser Late	Ocean Abundance	5YA	0.409	0.0013	2b
Survival (Female 1)	Oregon Coastal	Ocean Abundance	0	0.514	0.0003	2b
Survival (Female 1)	Oregon Coastal	Ocean Abundance	1	0.319	0.0020	2b
Survival (Female 1)	Oregon Coastal	Ocean Abundance	5YA	0.240	0.0056	2b

FE: Fraser Early**;** ; **PS:** Puget Sound; **FL:** Fraser Late; **COLf:** Columbia Fall; **COLs:** Columbia Spring/Summer; **OC:** Oregon Coastal; **WCVI:** West Coast Vancouver Island

Table 3. Comparison between simple beta-regression (SR) models with Chinook abundance (no cumulative effects) as the only predictor and multiple beta-regression (MR) models with Chinook and Chum abundance as predictors for common vital rates by hypothesis. Criteria for comparison are the regression coefficient for Chinook (β) and the AIC value. See Appendix 6 for Chinook stock definitions and Appendix 7 for Chum stock definitions.

Population	Chinook Stock	Chum Stock	Vital Rate	β (SR)	β (MR)	AIC_SR	AIC_MR	Hypothesis
SRKW	FL_TR_2	NBC_2	Female 1 Fecundity	6.15E-06	6.7E-06	-71.48	-72.22	1a
SRKW	PS_TR_2	WSH_Tot_1	Female 2 Fecundity	1.29E-05	6.7E-06	-183.36	-72.22	1a
SRKW	ALL2a_OA_2	NBC_2	Female 1 Fecundity	3.2E-06	4.73E-06	-77.77	-79.89	2a
SRKW	COLs_TR_1	WSH_Tot_1	Female 2 Fecundity	3.7E-06	1.86E-06	-183.45	-189.13	2a
NRKW	PS_OA_1	WSH_Tot_1	Juvenile Survival	1.72E-05	1.63E-05	-132.21	-129.52	1b
NRKW	NBC_TR_1	NBC_0	Female 1 Survival	2.86E-05	2.62E-05	-225.68	-226.64	1b
NRKW	PS_TR_1	WSH_Tot_1	Juvenile Survival	7.27E-06	6.78E-06	-131.63	-127.23	2b
NRKW	OC_OA_0	NBC_0	Female 1 Survival	1.50E-05	1.53E-05	-225.05	-231.43	2b
NRKW	ALL1a_TR_1	WSH_Tot_2	Female 2 Fecundity	4.49E-06	4.7E-06	-66.77	-70.25	2b

CHINOOK - FL: Fraser Late; **PS**: Puget Sound; **All2a**: WCVI, FL, PS, URB, and OC; **COLs**: Columbia spring/summer; **NBC**: Northern BC; **OC**: Oregon Coastal; **ALL1a**: FE, PS, and FL.

CHUM – NBC: Northern/Central BC; **WSH_Tot**: Washington Summer, Fall, Winter.

Table 4. Summary of regression models meeting selection criteria (greater regression coefficient for Chinook and lower AIC) for RKW vital rates and Chinook salmon abundance interactions (no cumulative effects) with Chum salmon terminal run as a covariate. The increase in the mean stochastic elasticity of the interaction owed to the incorporation of Chum abundance as a covariate is shown for each combination of common vital rate and hypothesis. See Appendix 6 for Chinook stock definitions and Appendix 7 for Chum stock definitions.

Population	VitalRate	Chinook Stock	Chum Stock	Pseudo-R2	P value	Mean Elasticity	Elasticity Increase	Hypothesis
SRKW	Female 1 Fecundity	FL_TR_2	NBC_2	0.114	0.0030	0.021	16.89%	1a
SRKW	Female 1 Fecundity	FL_TR_2	NA	0.073	0.0327	0.018		1a
SRKW	Female 1 Fecundity	ALL2a_OA_2	NBC_2	0.239	0.0025	0.064	61.44%	2a
SRKW	Female 1 Fecundity	ALL2a_OA_2	NA	0.155	0.0029	0.040		2a
NRKW	Female 1 Survival	OC_OA_0	NBC_0	0.520	0.0003	0.008	10.37%	2b
NRKW	Female 1 Survival	OC_OA_0	NA	0.514	0.0141	0.007		2b
NRKW	Female 2 Fecundity	ALL1a_TR_1	WSH_Tot_2	0.097	0.0012	0.033	9.52%	2b
NRKW	Female 2 Fecundity	ALL1a_TR_1	NA	0.092	0.0020	0.030		2b

CHINOOK - FL: Fraser Late; **All2a**: WCVI, FL, PS, URB, and **OCOC**: Oregon Coastal; **ALL1a**: FE, PS, and FL.

CHUM – NBC: Northern/Central BC; **WSH_Tot**: Washington Summer, Fall, Winter.

Table 5. Fishing scenarios selected for the assessment of the effects on RKW population viability. PVAs for SRKW focused on recovery objectives whereas PVAs for NRKW focused on producing equilibrium (i.e., $\lambda = 1.0$). Status quo scenarios were included as reference.

Population	Scenario	Hypothesis	Objective	Characteristics	Target Vital Rate(s)
SRKW	1	NA	Reference	Status quo	NA
SRKW	2	1a	Recovery	Maximization of PS Terminal Run: no ocean fishing on PS	Increasing the fecundity of old reproductive females
SRKW	3	1a	Recovery	Maximization of FE+PS Terminal Run: no ocean fishing on FE+PS	Increasing the fecundity of old reproductive females
SRKW	4	2a	Recovery	51% reduction in the ocean harvest rates of the five large stocks (WCVI, FL, PS, OC, and URB)	Maximizing the fecundity of young reproductive females and the survival of old reproductive females
SRKW	5	2a	Recovery	36% reduction in coastwide ocean harvest rates	Maximizing the fecundity of young reproductive females and the survival of old reproductive females
SRKW	6	2a (cumulative effects)	Recovery	55.5% reduction in the ocean harvest rates of the five large stocks (WCVI, FL, PS, OC, and URB)	Maximizing the fecundity of young reproductive females
NRKW	7	NA	Reference	Status quo	NA
NRKW	8	1b	Reduce population growth	Maximizing ocean harvest rates of Fraser Early Chinook	Reducing the fecundity of old reproductive females
NRKW	9	1b	Halt population growth	Reductions of NBC Terminal Run as a result of increasing NBC ocean harvest rates by 187%	Decreasing the survival of young reproductive females
NRKW	10	2b	Reduce population growth	Reductions of FE+PS Terminal Run as a result of doubling FE+PS ocean harvest rates	Decreasing the fecundity of young and old reproductive females
NRKW	11	2b	Halt population growth	66% increase of coastwide ocean harvest rates	Decreasing survival of young reproductive females
NRKW	12	1b (cumulative effects)	Reduce population growth	Maximizing ocean harvest rates of Fraser Early Chinook	Reducing the fecundity of old reproductive females

Table 6. Summary of PVA results for selected fishing scenarios characterized in Table 5. Viability metrics in the last column differ between SRKW and NRKW due to their differing trajectories and recovery targets. U.S. downlisting criteria have been specified for SRKW whereas there is no population-based recovery target for NRKW. The expected minimum abundance is used here as an index of the propensity to decline in NRKW.

Population	Scenario	Stochastic population growth	Mean abundance τ years in the future *	Extinction probability 100 years in the future	Probability of falling below 30 individuals in the next 100 years	Probability of downlisting (U.S.)
SRKW	1	0.99091	68	0.493	0.780	0.000
SRKW	2	1.00595	117	0.228	0.445	0.032
SRKW	3	0.99977	93	0.324	0.595	0.000
SRKW	4	1.01803	166	0.129	0.270	0.334
SRKW	5	1.01766	164	0.142	0.279	0.310
SRKW	6	1.01792	165	0.148	0.292	0.331
					Probability of falling below 250 individuals in the next 100 years	**Expected minimum abundance**
NRKW	7	1.01577	401	0.000	0.523	238
NRKW	8	1.00144	296	0.032	0.836	159
NRKW	9	1.00000	299	0.019	0.844	158
NRKW	10	1.00828	339	0.005	0.694	206
NRKW	11	1.00000	299	0.017	0.838	162
NRKW	12	1.00086	294	0.032	0.858	155

* Damping times (τ) were 35 years for SRKW and 25 years for NRKW

FIGURES
(3.1 RKW demography)
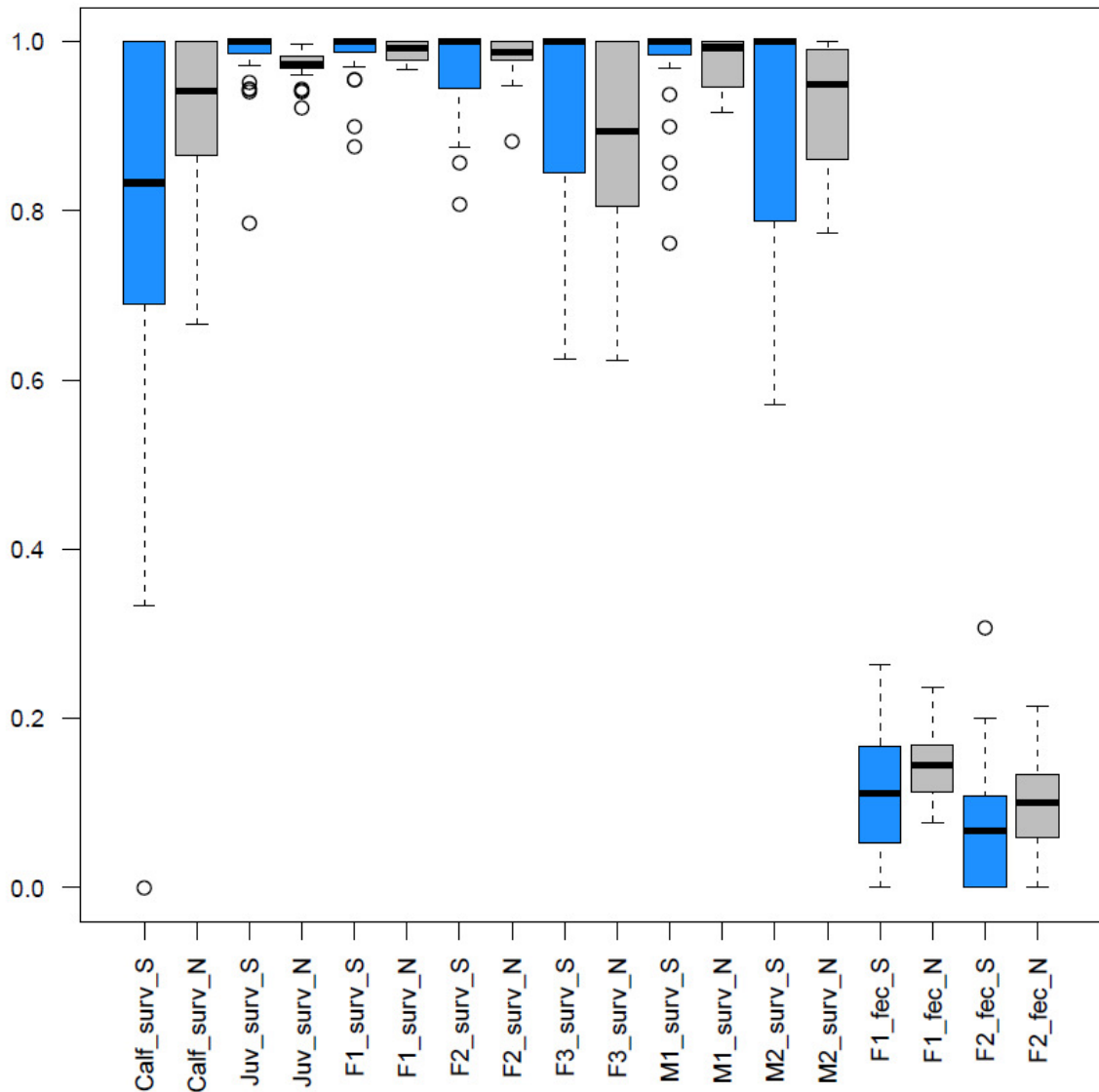
Figure 6. Box plot of vital rates for SRKW (blue) and NRKW (grey) corresponding to 1987-2011. Juv: Juvenile; F1: young reproductive female; F2: old reproductive female; F3: post-reproductive female; M1: young male; M2: old male.
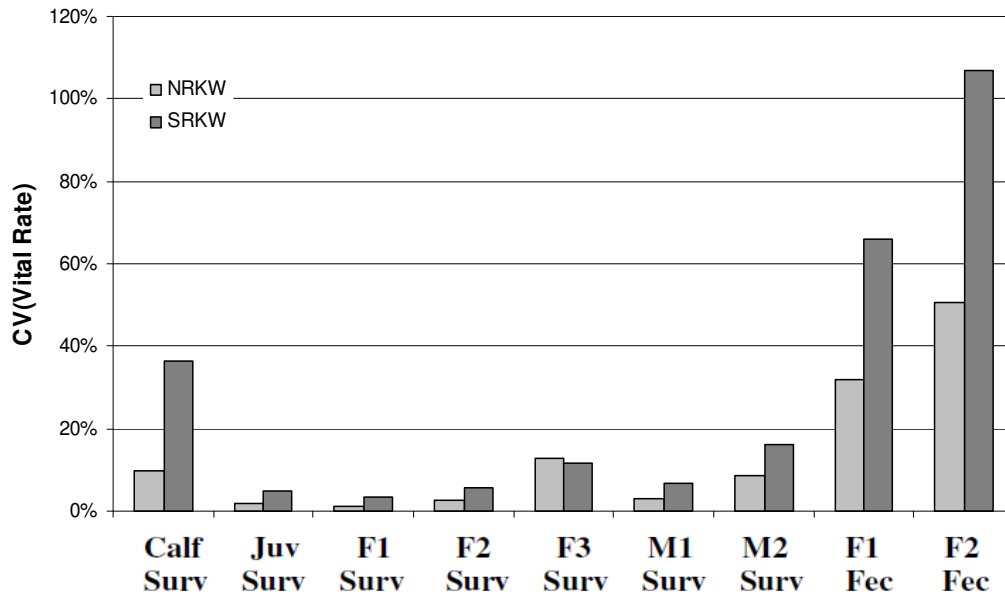
Figure 7. Coefficient of variation in vital rates of NRKW and SRKW corresponding to 1987-2011. F1: young reproductive female; F2: old reproductive female; F3: post-reproductive female; M1: young male; M2: old male.
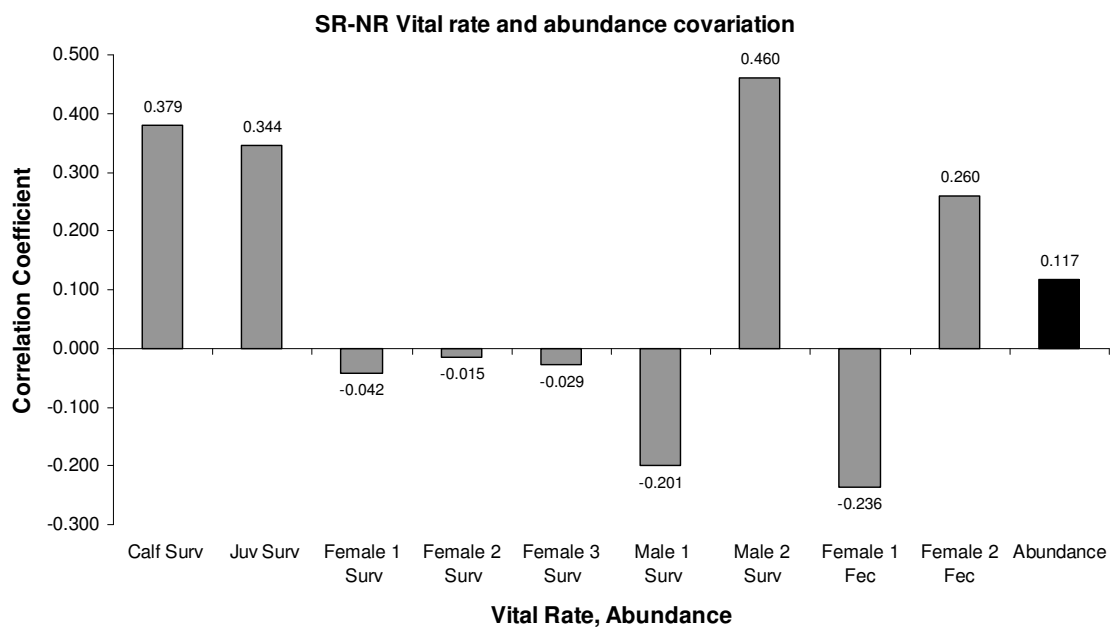
Figure 8. Vital-rate and abundance correlation coefficients between NRKW and SRKW for 1987-2011. Female 1: young reproductive female; Female 2: old reproductive female; Female 3: post-reproductive female; Male 1: young mature male; Male 2: old mature male.
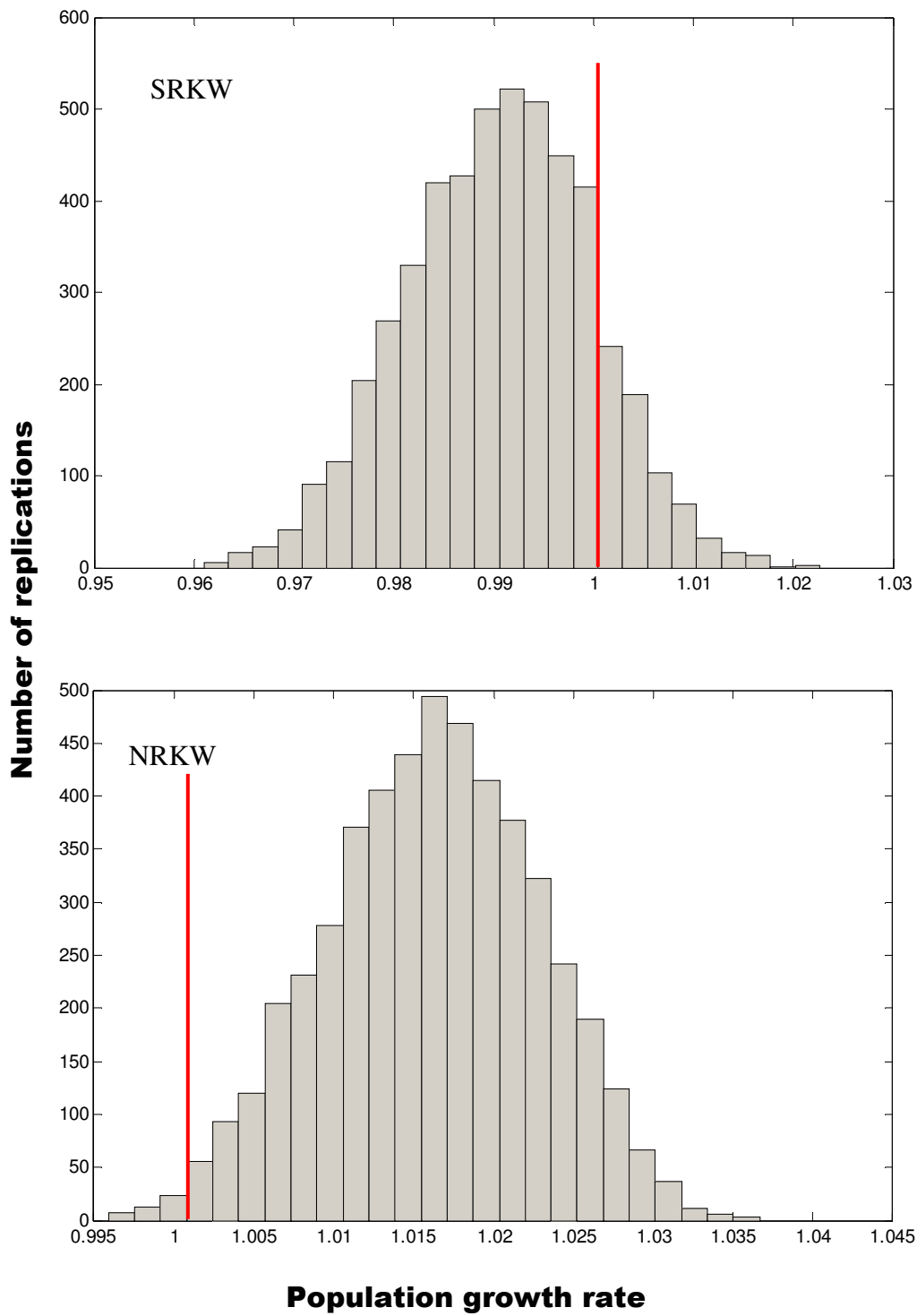
Figure 9. Frequency distribution of stochastic population growth computed through simulations (5000 replicates) for SRKW and NRKW.
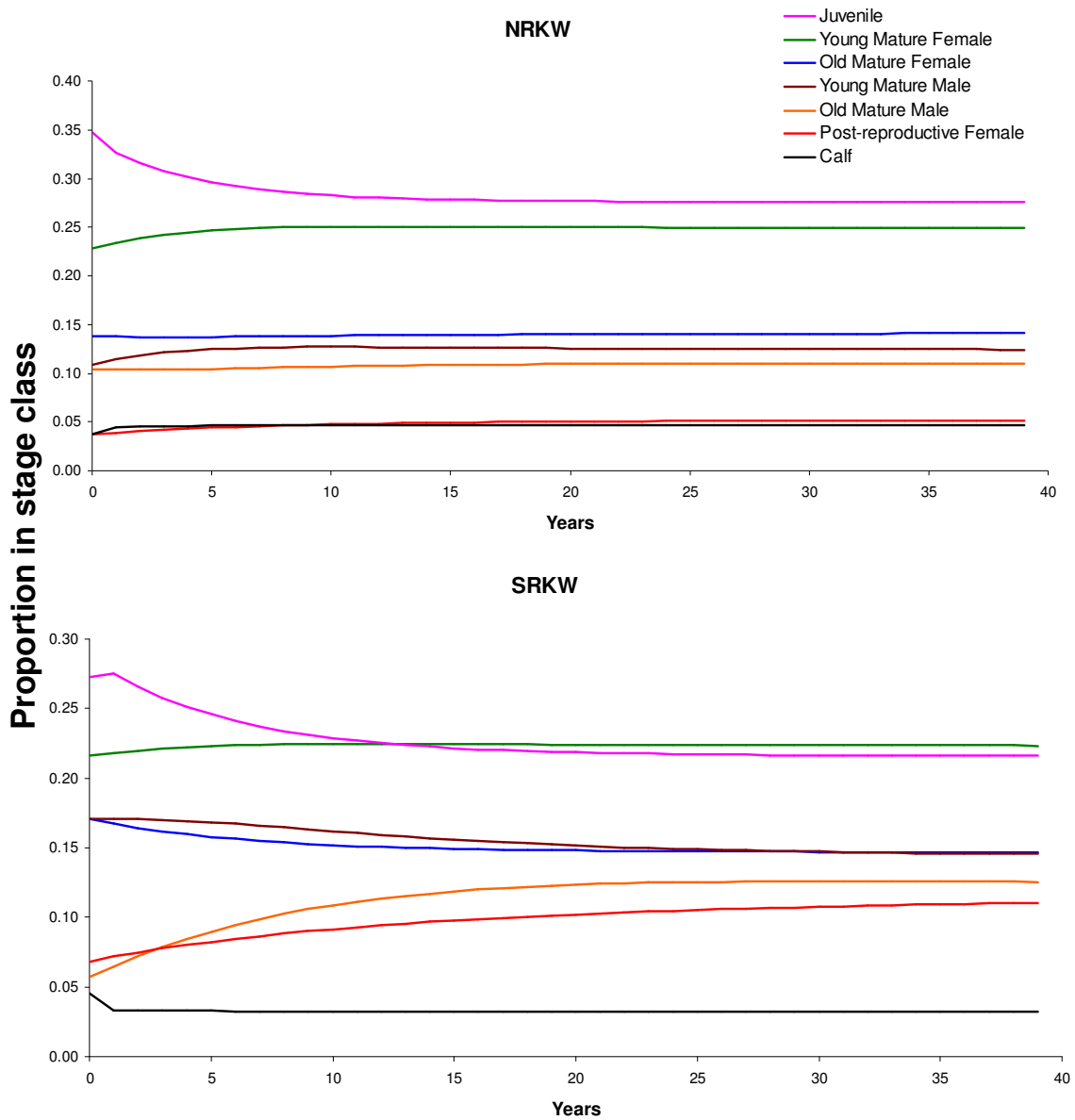
Figure 10. Stable-stage-distribution projections for NRKW and SRKW starting at stage distributions observed in 2011.
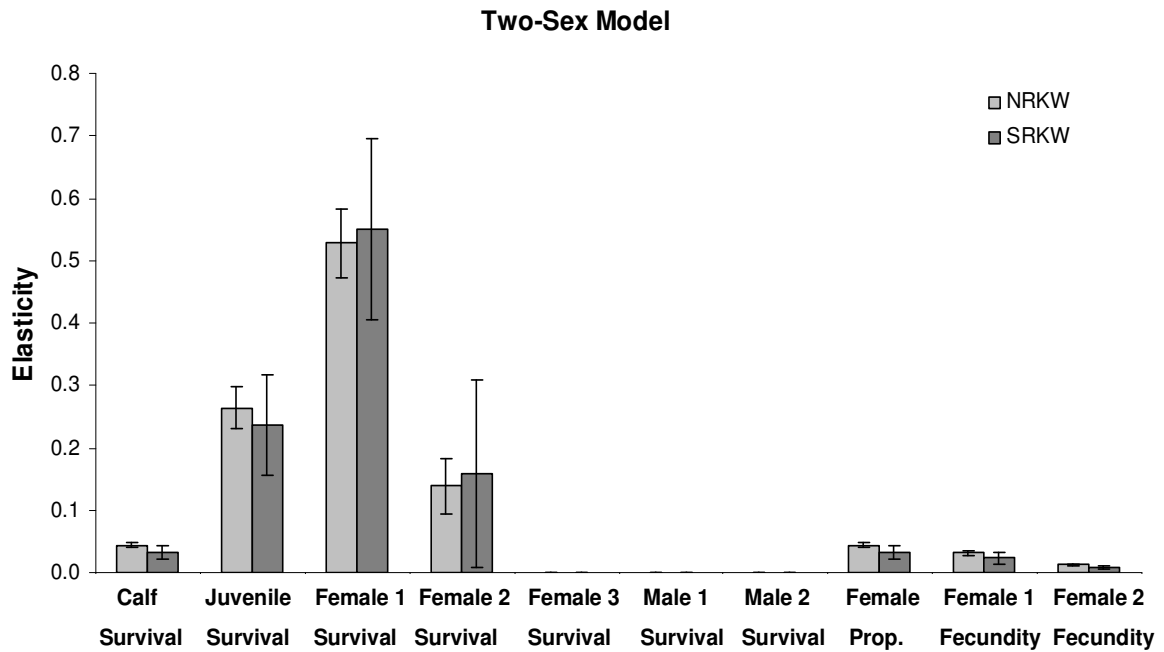
Figure 11. Vital-rate elasticities for NRKW and SRKW. Bars represent standard deviations. Female 1: young reproductive female; Female 2: old reproductive female; Female 3: post-reproductive female; Male 1: young mature male; Male 2: old mature male.
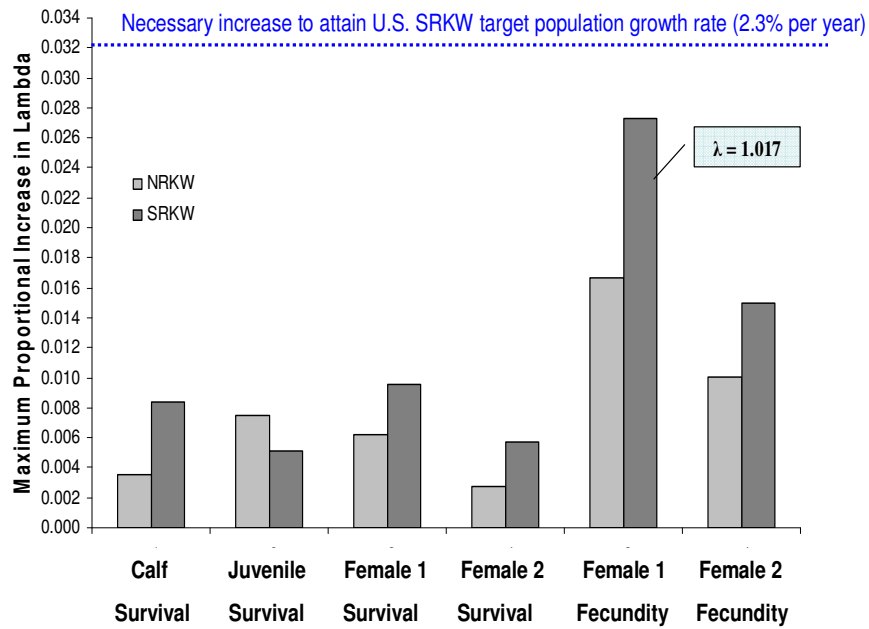
Figure 12. Maximum proportional increase in population growth resulting from maximization of individual vital rates (1.0 for survival and upper 95% C.L. for fecundity) in NRKW and SRKW. The proportional increase necessary to achieve the U.S. downlisting recovery goal is also shown. Female 1: young reproductive female; Female 2: old reproductive female. The maximization Female 1 fecundity is projected to produce a 1.7% annual increase in SRKW, which is still lower than the 2.3% U.S. downlisting recovery target
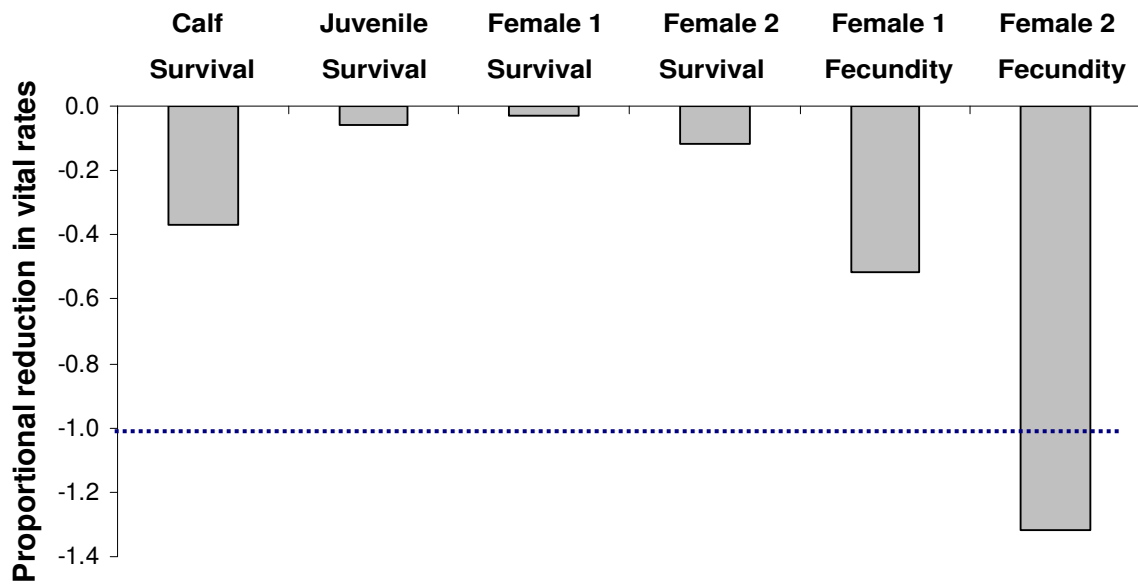
Figure 13. Proportional reduction in individual vital rates required to halt population growth (i.e., $\lambda = 1.0$) in NRKW. The horizontal line shows the maximum reduction in a vital rate. Female 1: young reproductive female; Female 2: old reproductive female.
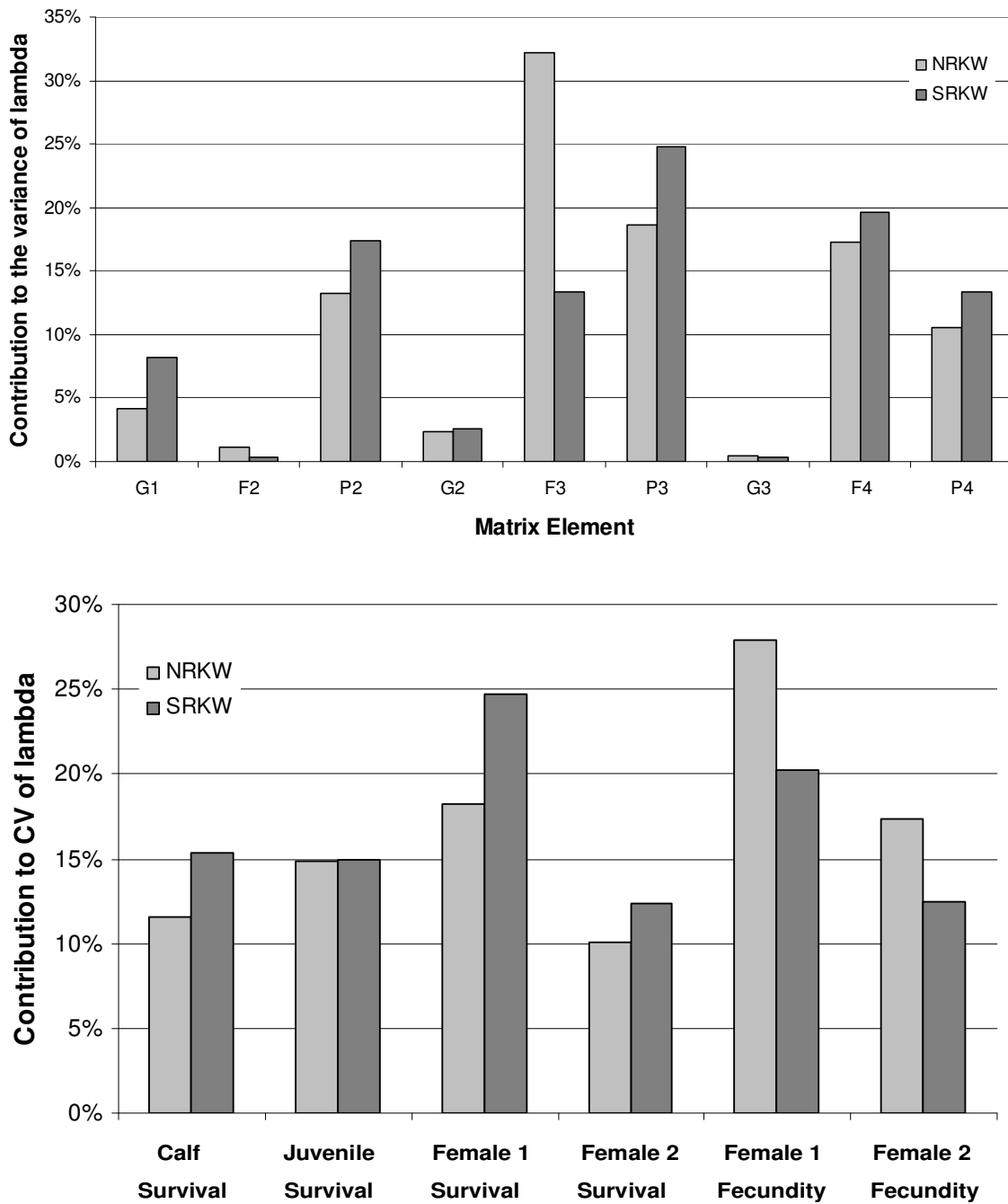
Figure 14. Contributions of matrix elements to the variance in population growth (top) and contributions of individual vital rates to the CV in population growth (bottom) for 1987-2011. Female 1: young reproductive female; Female 2: old reproductive female.

FIGURES
(3.2 Role of Chinook abundance on RKW population growth)
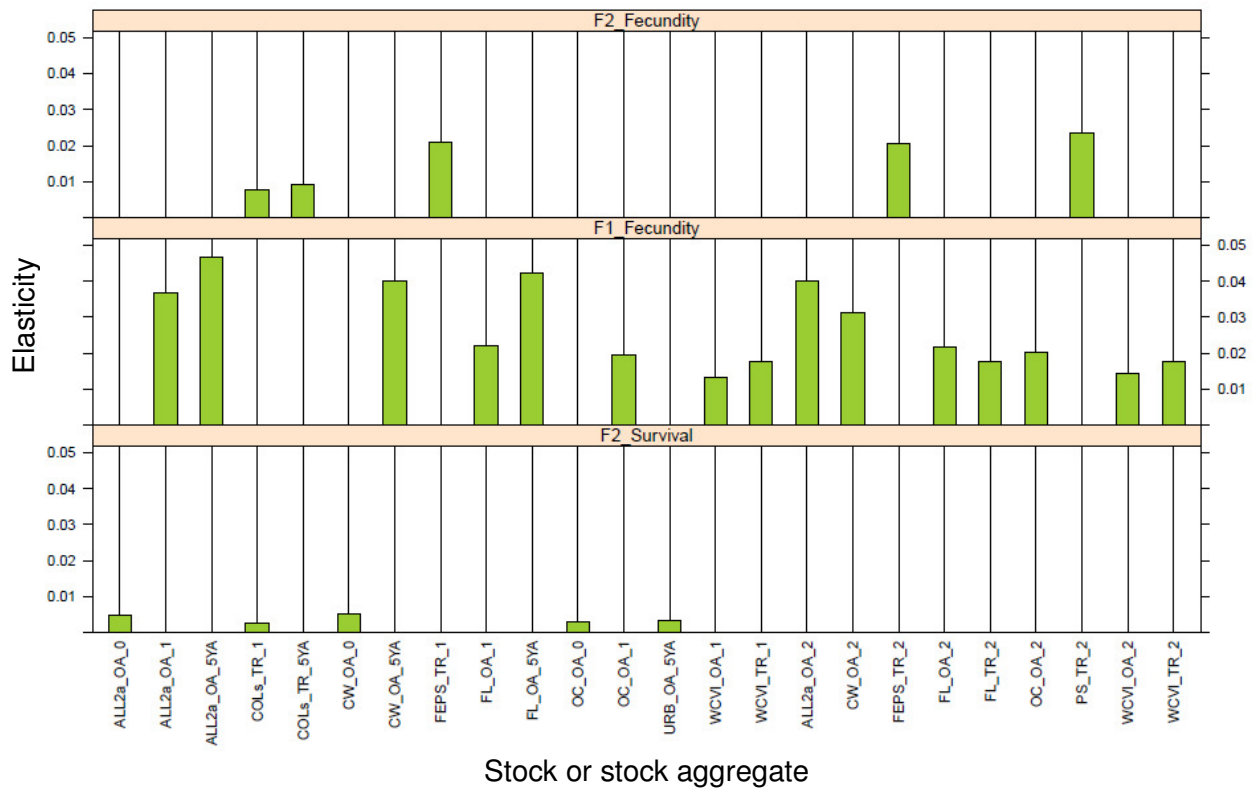
Figure 15. Mean stochastic elasticities of interactions between SRKW vital rates and Chinook salmon abundance for all significant regressions in Table 1. F1: young reproductive females; F2: old reproductive females. See Appendix 6 for a glossary of stock definitions.
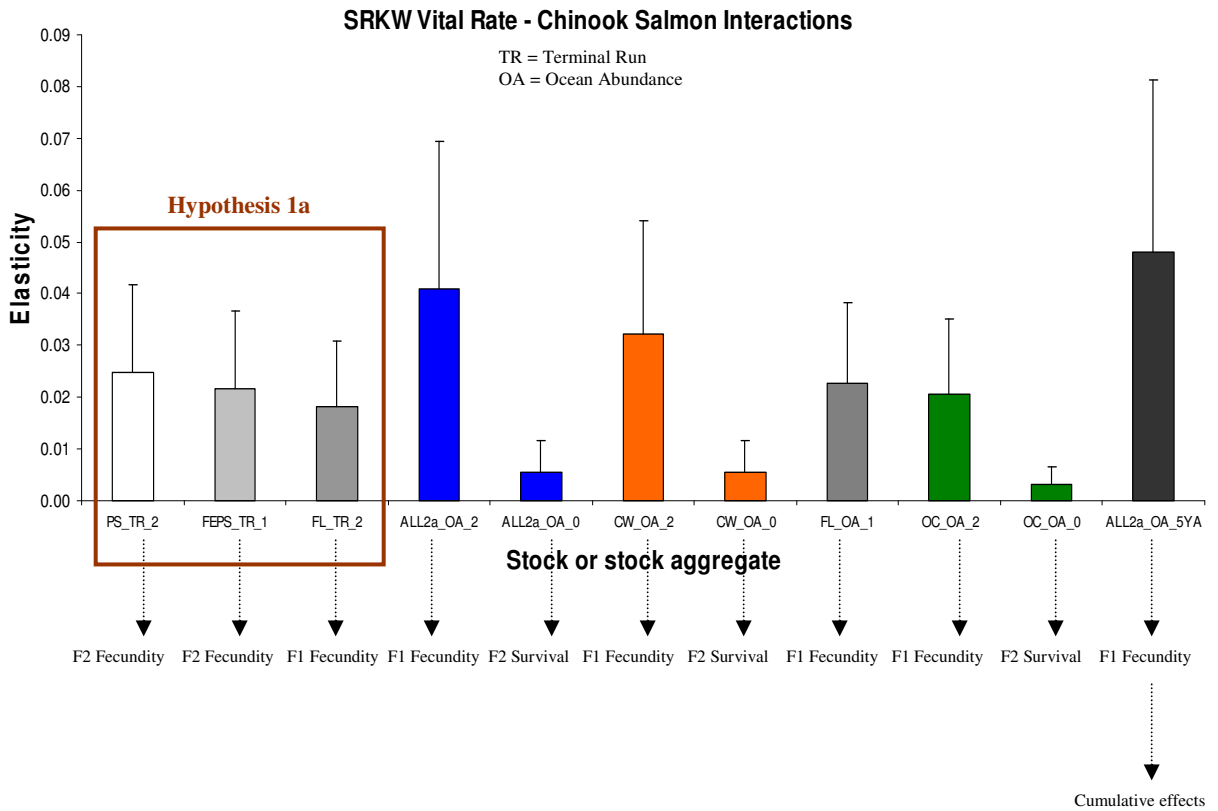
Figure 16. Elasticities of interactions between Chinook abundance and SRKW vital rates. Stock aggregates influencing more than one vital rate are color coded. Corresponding vital rates are shown at the bottom. The interactions corresponding to hypothesis 1a are highlighted. All other interactions correspond to hypothesis 2a. The interaction with the largest elasticity for cumulative effects is shown at the far right of the figure. F1: young reproductive female; F2: old reproductive female.

PS: Puget Sound; **FE:** Fraser Early; **FL:** Fraser Late; **ALL2a:** Columbia UpRiver Brights, OC, PS, FL, and WCVI; **CW:** Coastwide (excluding SEAK); **OC:** Oregon Coastal;
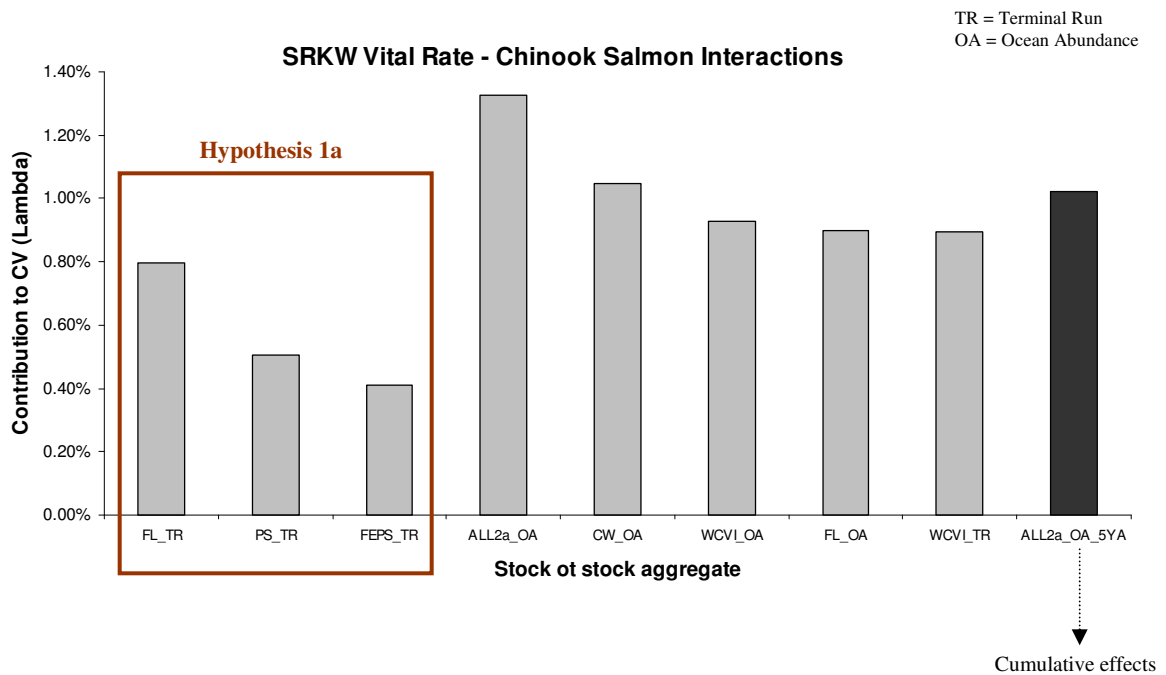
Figure 17. Contributions of SRKW vital rate - Chinook abundance interactions to the CV of population growth for years 1987-2011. The contributions of stock aggregates influencing more than one vital rate have been added to compute the total contribution to the CV in population growth. The interactions corresponding to hypothesis 1a are highlighted. All other interactions correspond to hypothesis 2a. The interaction with the largest elasticity for cumulative effects is shown at the far right of the figure.

FE: Fraser Early; **PS:** Puget Sound; **CW:** Coastwide (excluding SEAK); **WCVI:** West Coast Vancouver Island; **OC:** Oregon Coastal; **FL:** Fraser Late; **ALL2a:** Columbia UpRiver Brights, OC, PS, FL, and WCVI.
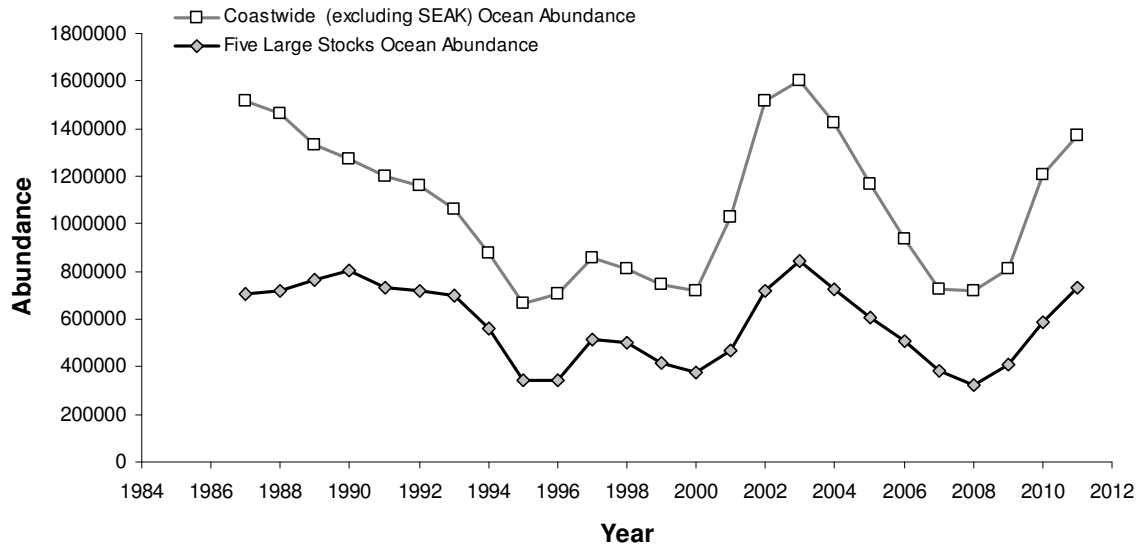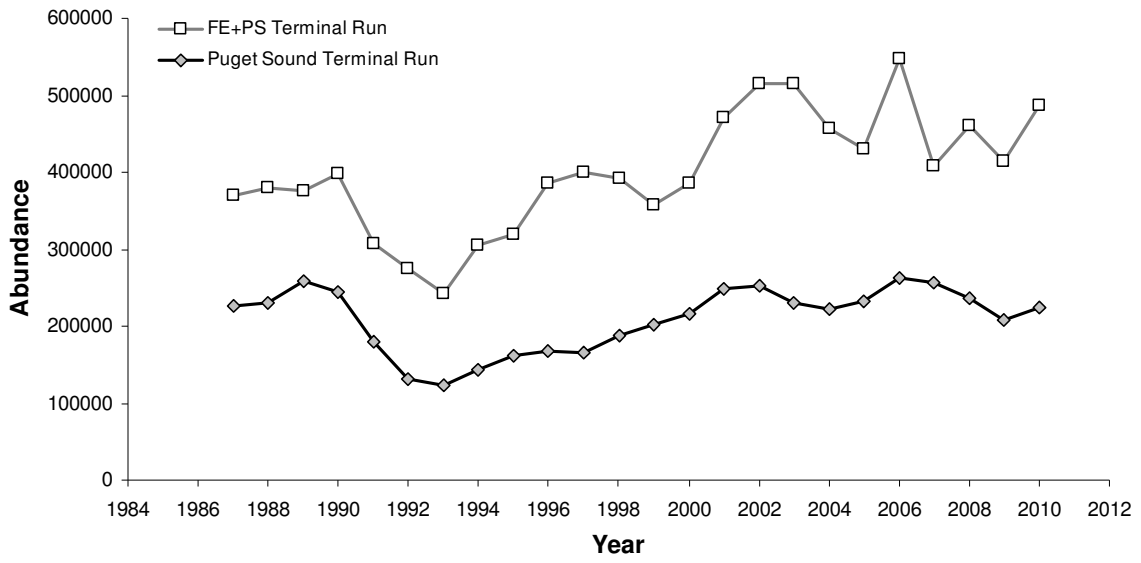
Figure 18. Time series of abundance for Chinook aggregates relevant for exploration of fishing scenarios under hypotheses 1a (top) and 2a (bottom).
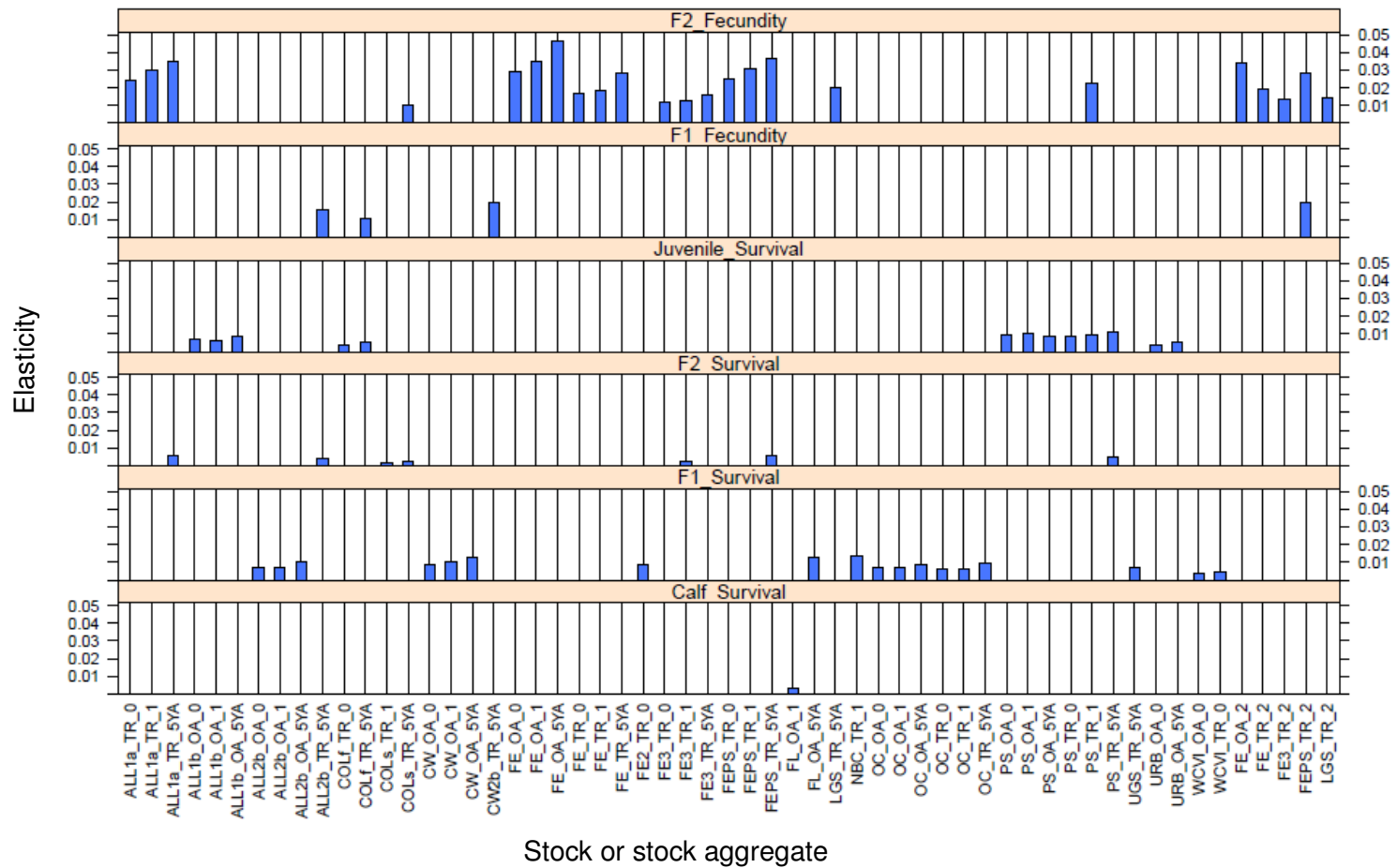
Figure 19. Mean stochastic elasticities of interactions between NRKW vital rates and Chinook salmon abundance for all significant regressions in Table 2. F1: young reproductive females; F2: old reproductive females. See Appendix 6 for a glossary of stock definitions.
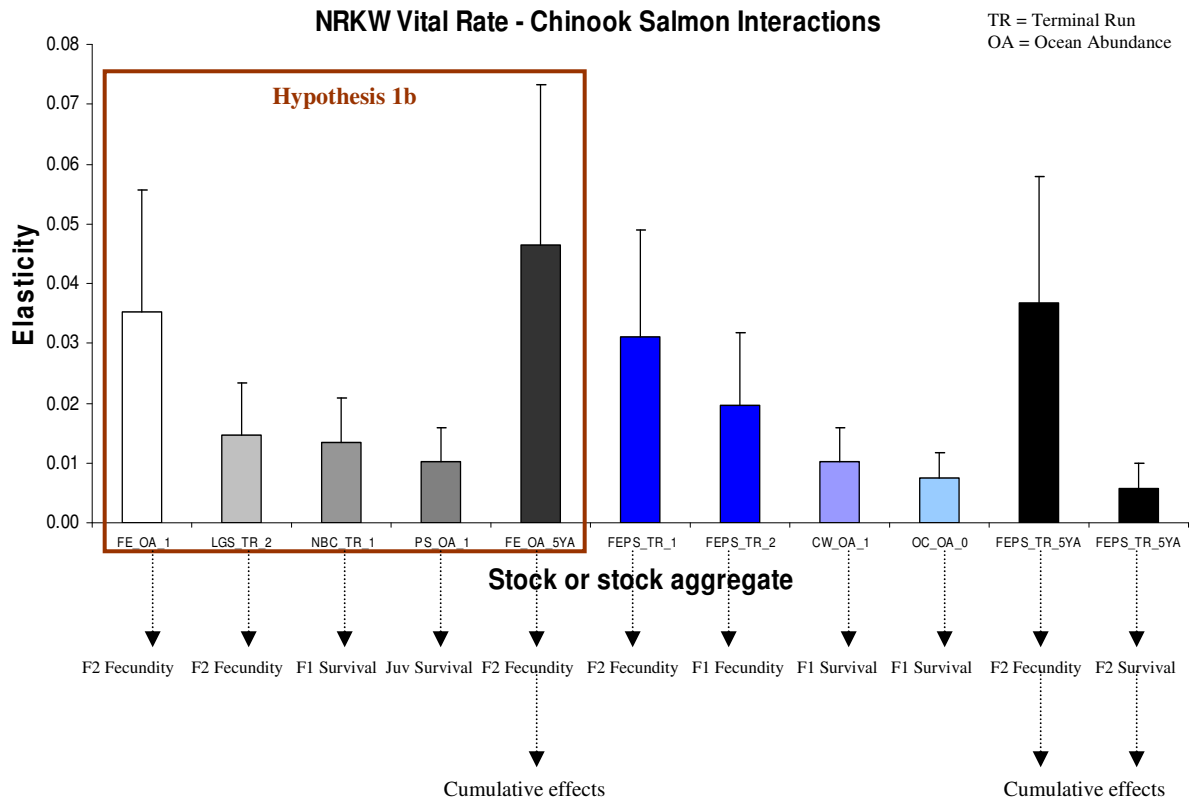
Figure 20. Elasticities of interactions between Chinook abundance and NRKW vital rates. Stock aggregates influencing more than one vital rate are color coded. Corresponding vital rates are shown at the bottom. The interaction corresponding to hypothesis 1b is highlighted. All other interactions correspond to hypothesis 2b. The interactions with the largest elasticities for cumulative effects are shown at the far right for each set of stock aggregates. F1: young reproductive female; F2: old reproductive female.

FE: Fraser Early; **LGS:** Lower Georgia Strait; **NBC:** Northern BC; **PS:** Puget Sound; **CW:** Coastwide; **OC:** Oregon Coastal
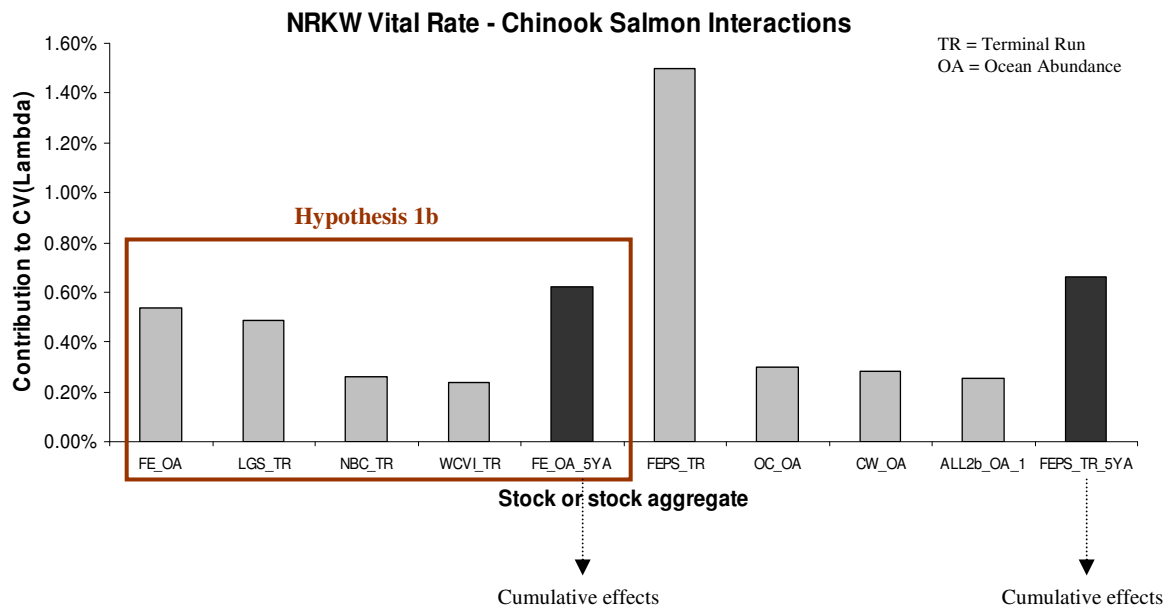
Figure 21. Contributions of NRKW vital rate - Chinook abundance interactions to the CV of population growth for years 1987-2011. The contributions of stock aggregates influencing more than one vital rate have been added to compute the total contribution to the CV in population growth. The interactions corresponding to hypothesis 1b are highlighted. All other interactions correspond to hypothesis 2b. The interactions with the largest elasticities for cumulative effects are shown at the far right of each set.

FE: Fraser Early; **LGS:** Lower Georgia Strait; **NBC:** Northern BC; **WCVI:** West Coast Vancouver Island; **PS:** Puget Sound; **OC:** Oregon Coastal; **CW:** Coastwide; **ALL2b:** Fraser Late, OC, and WCVI.
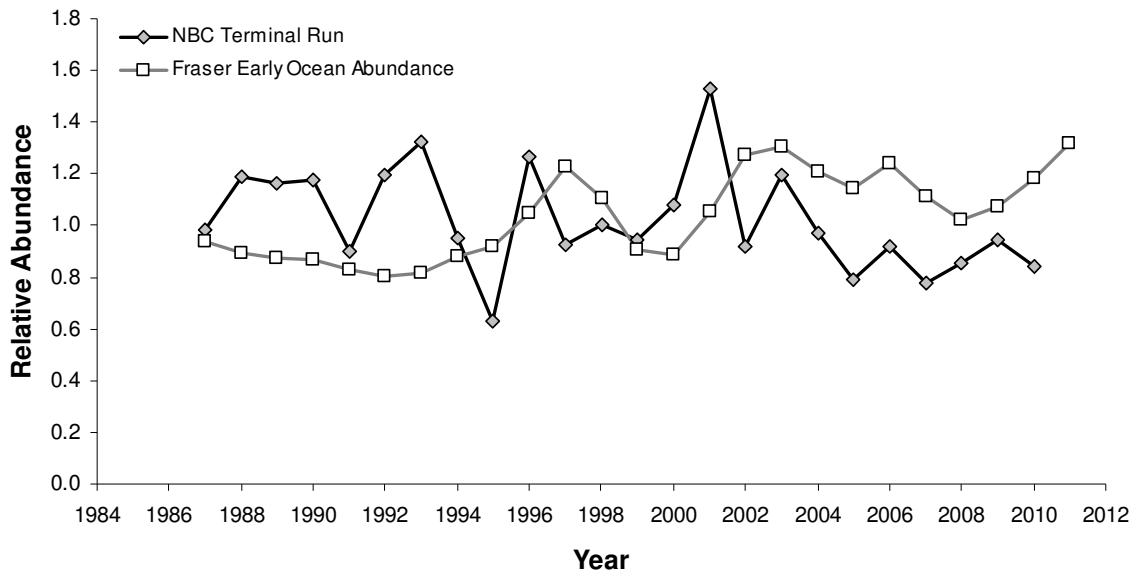
Figure 22. Time series of relative abundance for Chinook aggregates relevant for exploration of fishing scenarios under hypotheses 1b. Abundance was centralized (i.e., annual value divided by the long-term average) for this figure because abundance indices derived for terminal run and ocean abundance are in different units.

FIGURES
(3.3 Chum salmon as a covariate of RKW population growth)
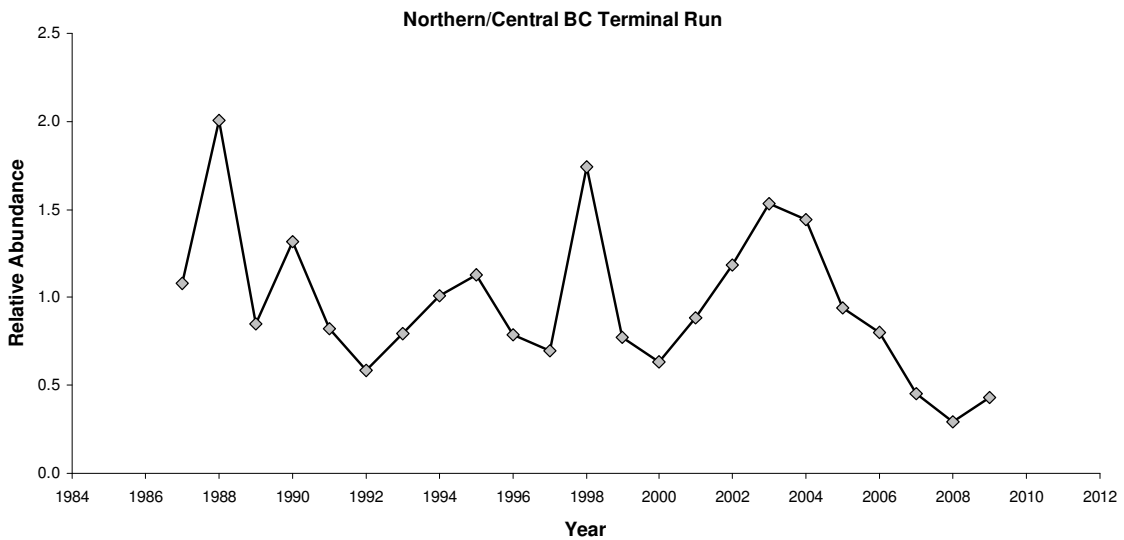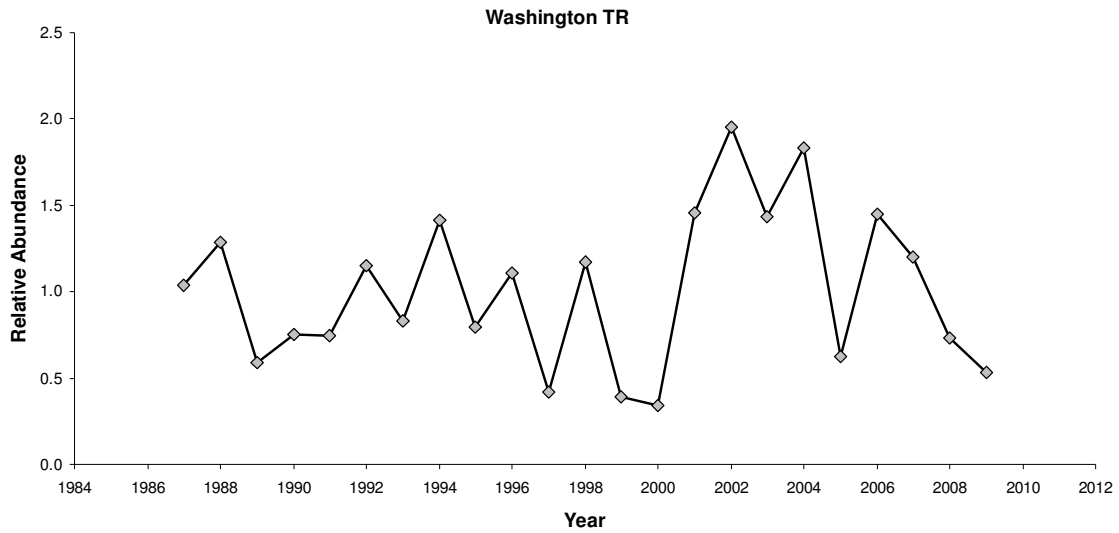
Figure 23. Time series of relative abundance (annual terminal run divided by the long-term average) for Chum salmon aggregates relevant for multiple beta-regression models meeting selection criteria and summarized in Table 3.
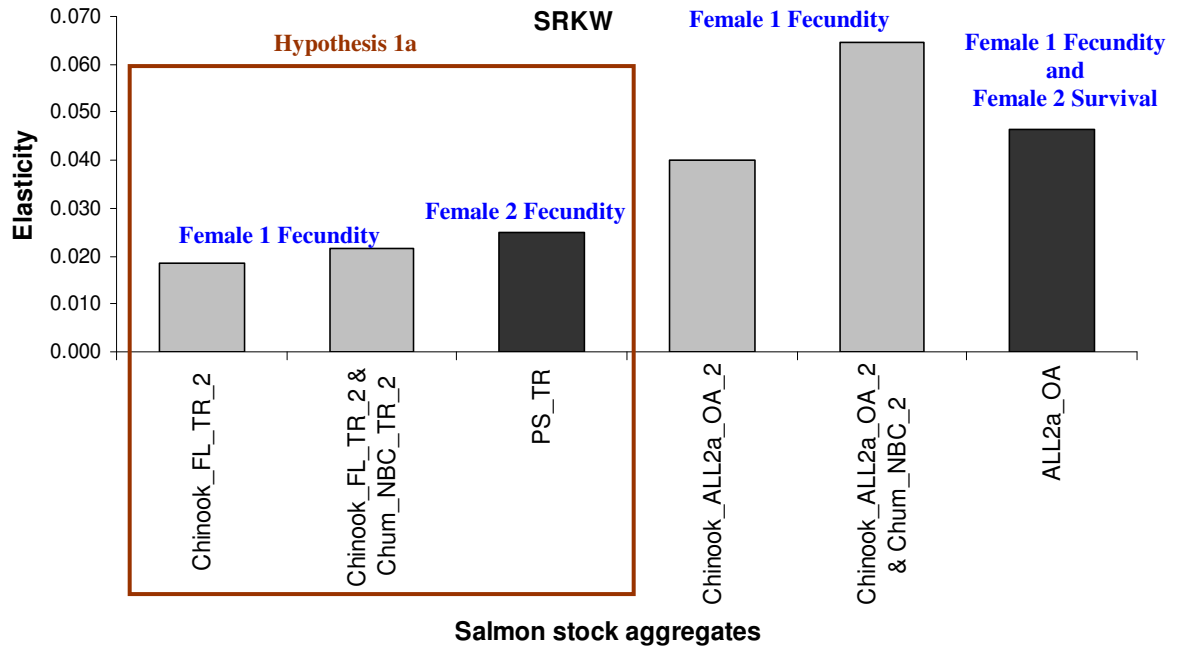
Figure 24. Elasticities of interactions between SRKW vital rates and Chinook abundance with and without Chum abundance as a covariate as identified in Table 4. Included in the figure are the Chinook interactions with the largest elasticities by hypothesis (dark bars) for comparison. The vital rates corresponding to each interaction are shown above the bars. See Appendix 6 for Chinook stock definitions and Appendix 7 for Chum stock definitions.
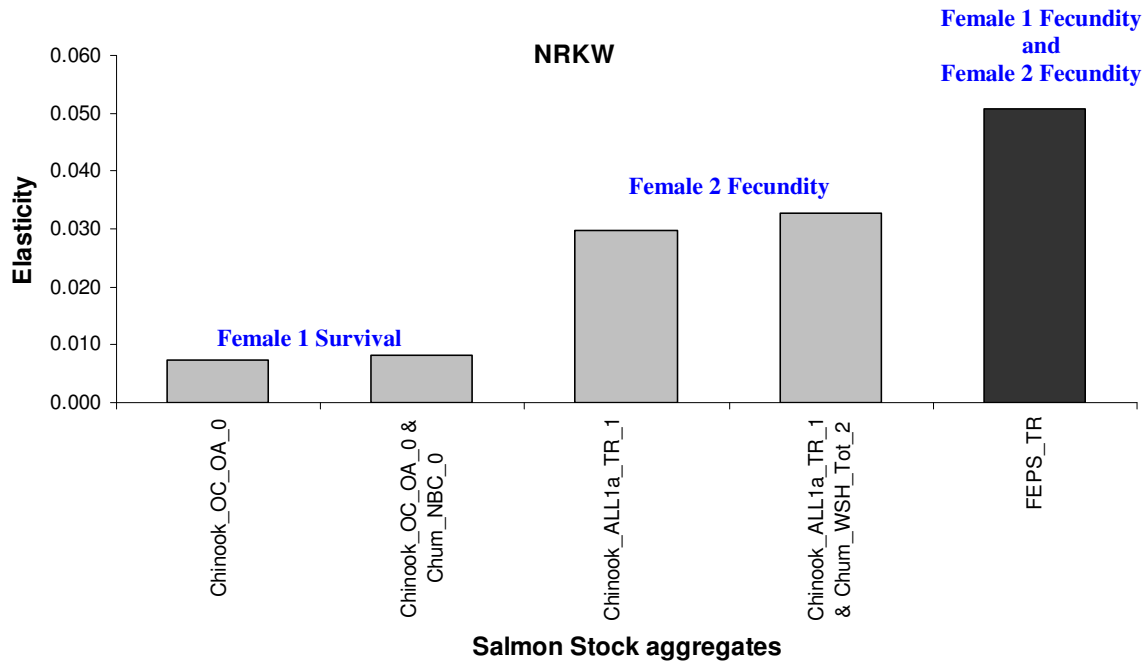
Figure 25. Elasticities of interactions between NRKW vital rates and Chinook abundance with and without Chum abundance as a covariate identified in Table 4. Included in the figure are the Chinook interactions with the largest elasticity for hypothesis 2b (dark bars) for comparison. There were no interactions with Chum abundance as a covariate meeting criteria for hypothesis 1b. The vital rates corresponding to each interaction are shown above the bars. See Appendix 6 for Chinook stock definitions and Appendix 7 for Chum stock definitions.

FIGURES
(3.4 RKW population viability under selected fishing scenarios)
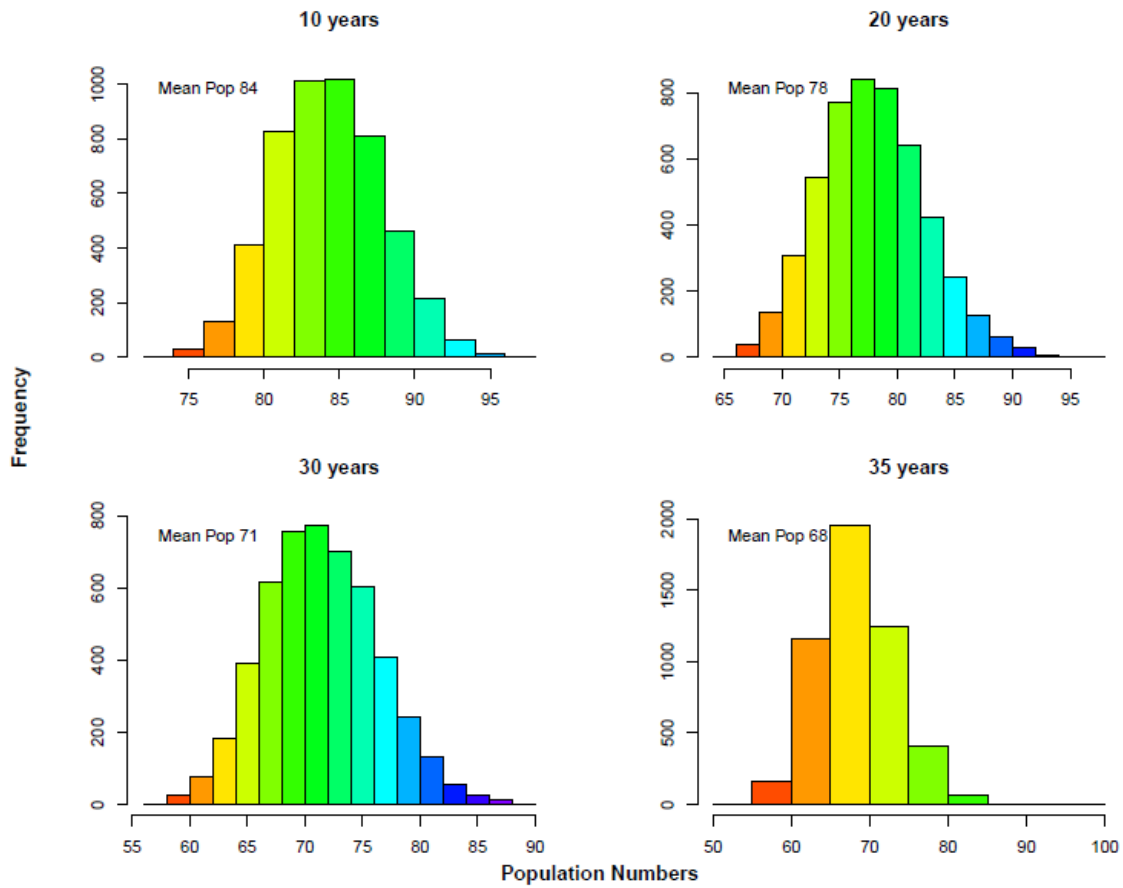
Figure 26. Projections of SRKW population size in an IID environment under status quo conditions (Scenario 1) at 10, 20, 30, and 35 years in the future (SRKW Damping Time = 35 years). Histograms and computation of stochastic population growth generated from 5000 realizations of population size.
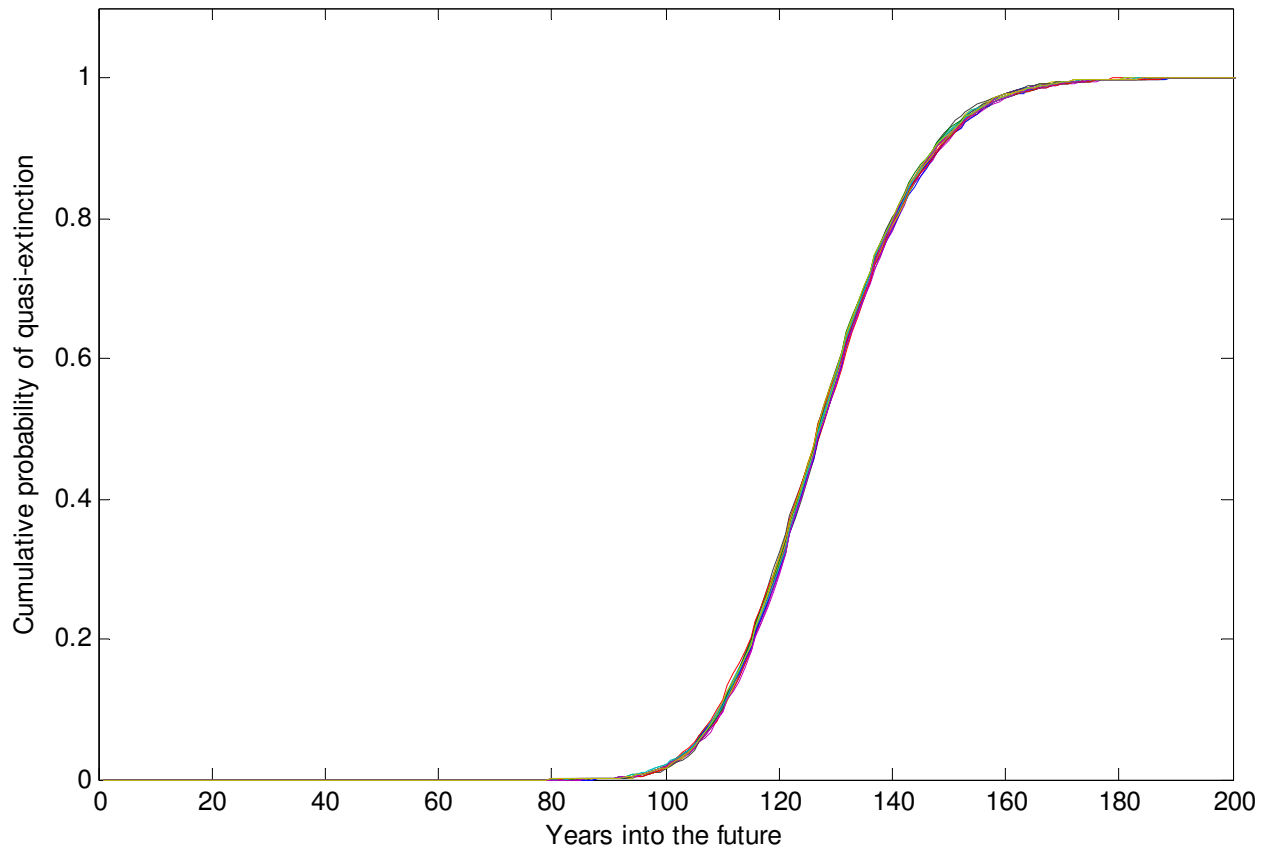
Figure 27. Cumulative probability of SRKW population size falling below 30 individuals in the future in an IID environment under status quo conditions (Scenario 1). Probabilities computed from 5000 realizations of population size. Twenty runs are shown in the figure.
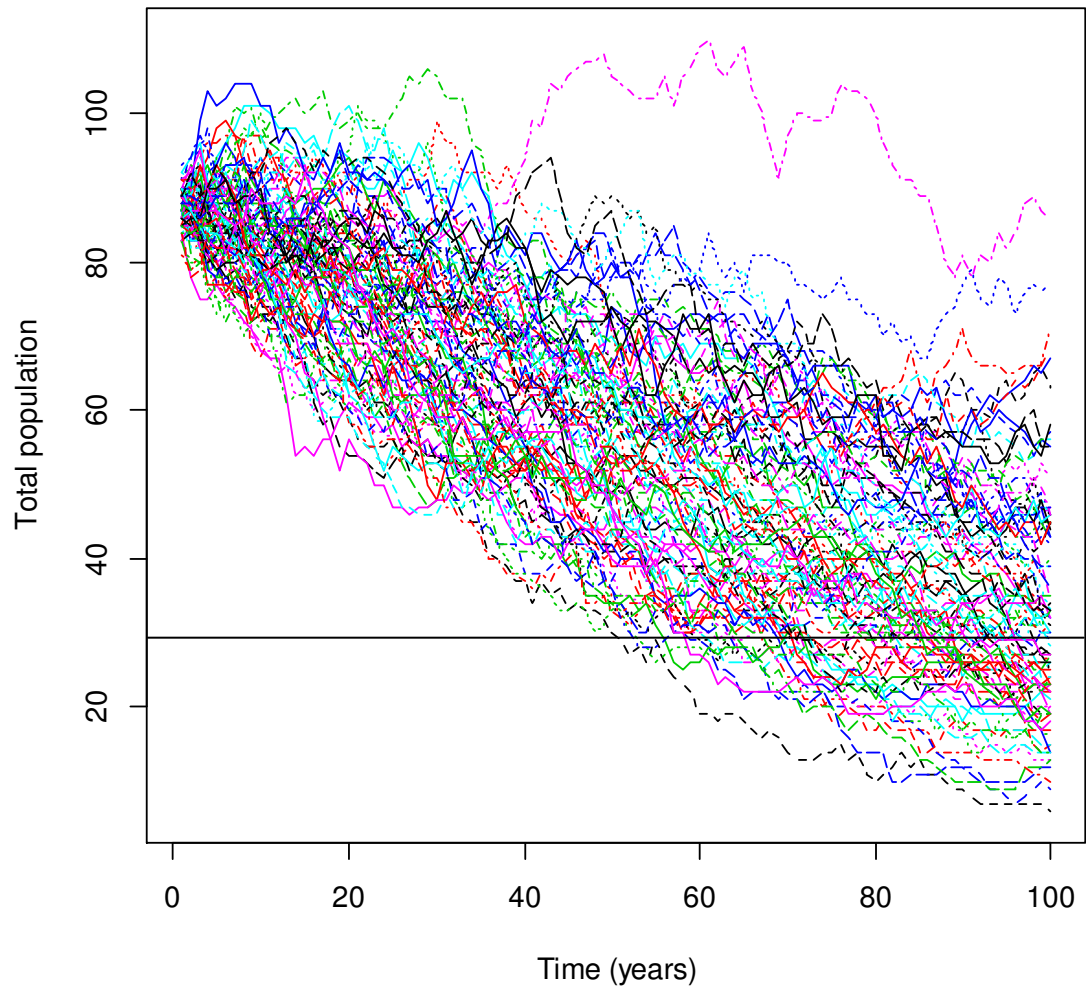
Figure 28. Projections (100) of SRKW population size under demographic stochasticity and status quo conditions (Scenario 1). Horizontal shows the 30-individual threshold used for Figure 27.
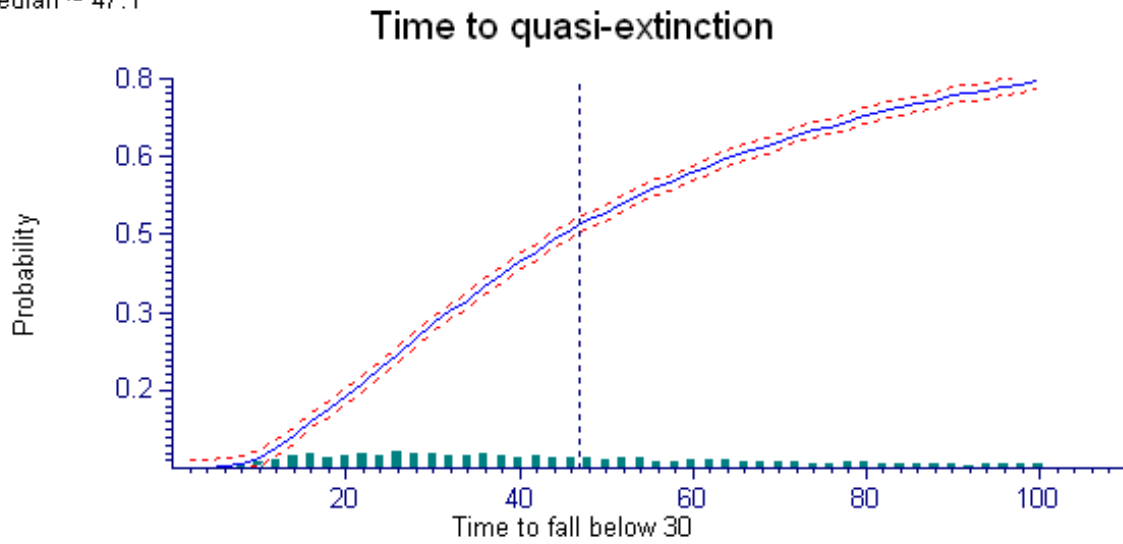
Figure 29. Probability of SRKW population falling below 30 individuals in the future under environmental and demographic stochasticity and status quo conditions (Scenario 1). Mean probability and 95% CIs generated from 5000 replications. Median is the number of years to reach a 0.5 probability of falling below 30 individuals.

Extinction risk ~ 0.493   Expected minimum abundance ~ 15.1
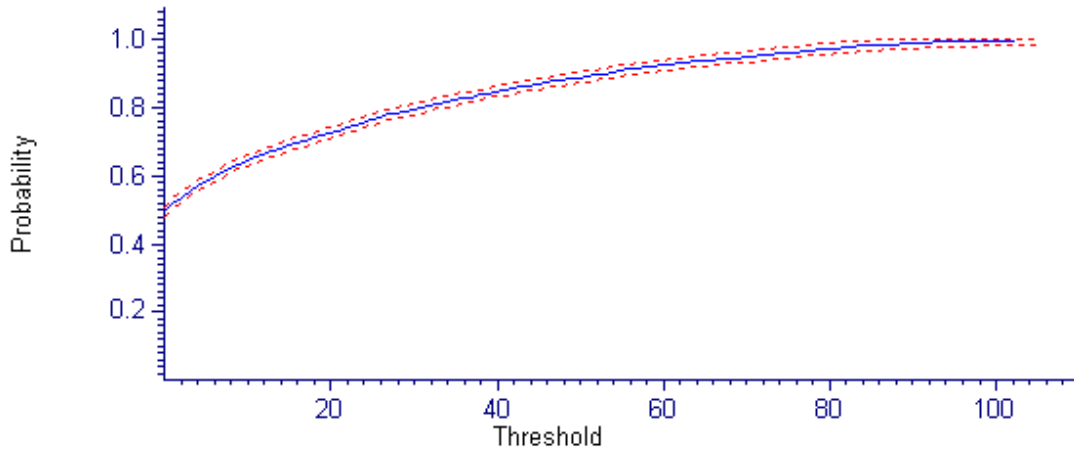
Figure 30. Probability of SRKW population size falling below a population threshold in 100 years under environmental and demographic stochasticity and status quo conditions (Scenario 1). Mean probability and 95% CIs generated from 5000 replications. Also shown are the extinction risk for $N_{Threshold} = 0$ and the expected minimum abundance, which is the average (over all replications) of the minimum population abundance of the trajectory.
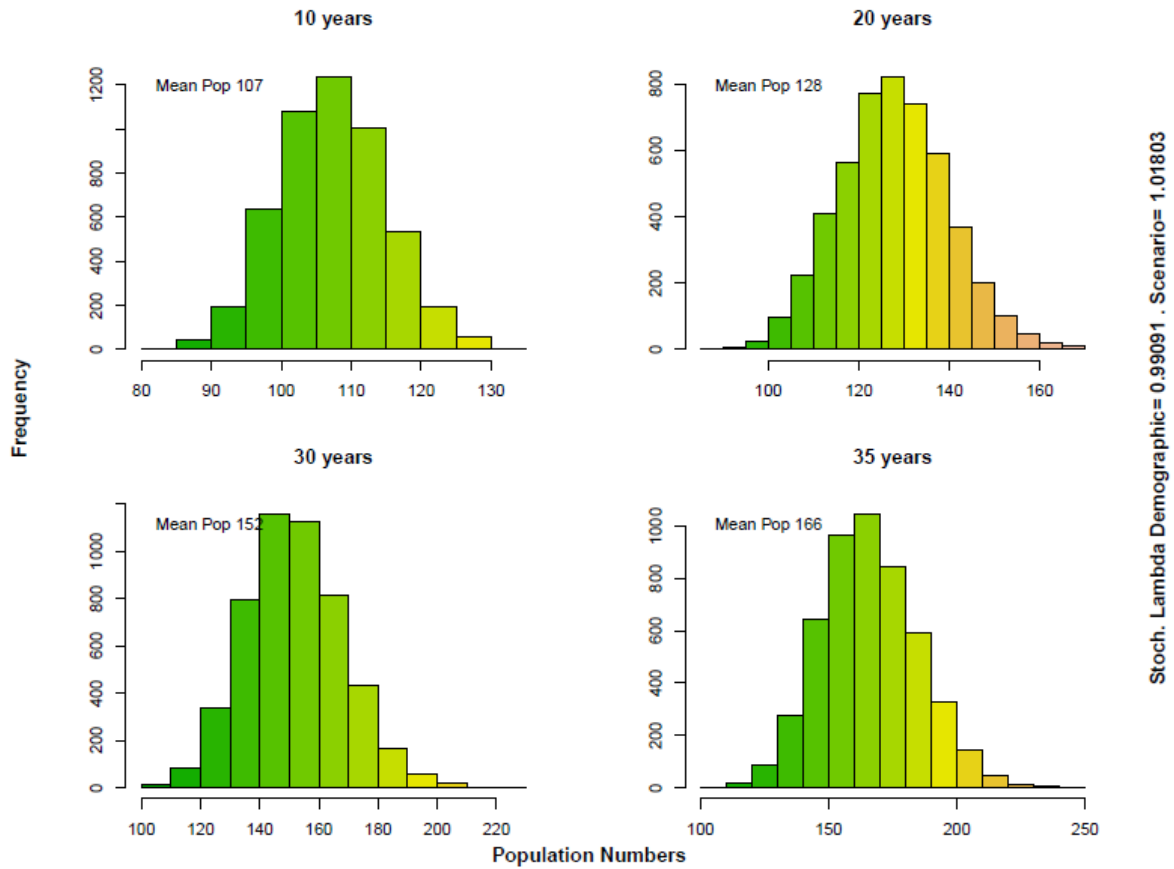
Figure 31. Projections of SRKW population size in an IID environment under Scenario 4 (51% reduction in the ocean harvest rates of the five large stocks WCVI/FL/PS/OC/URB) at 10, 20, 30, and 35 years in the future (SRKW Damping Time = 35 years). Histograms and computation of stochastic population growth generated from 5000 realizations of population size.
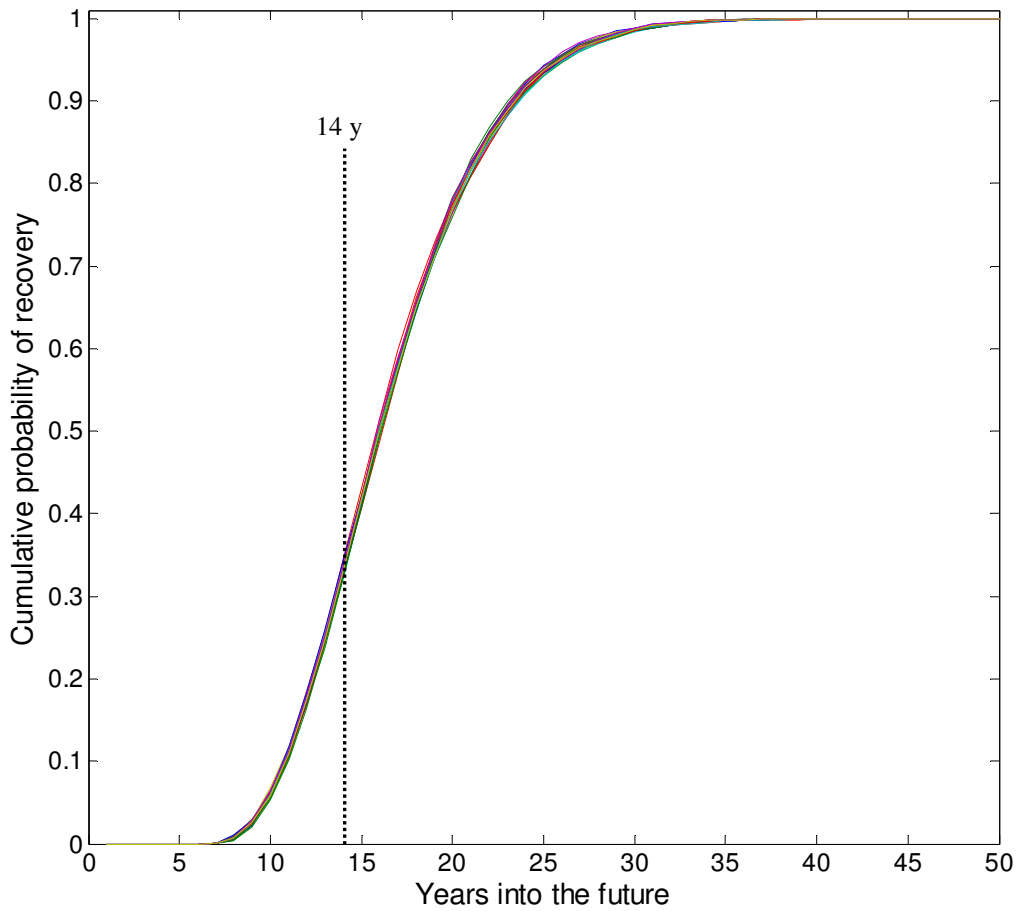
Figure 32. Cumulative probability of SRKW recovery (recovery target = downlisting population size = 120 individuals) in the future in an IID environment under Scenario 4 (51% reduction in the ocean harvest rates of the five large stocks WCVI/FL/PS/OC/URB). Probabilities computed from 5000 realizations of population size. Twenty runs are shown in the figure.
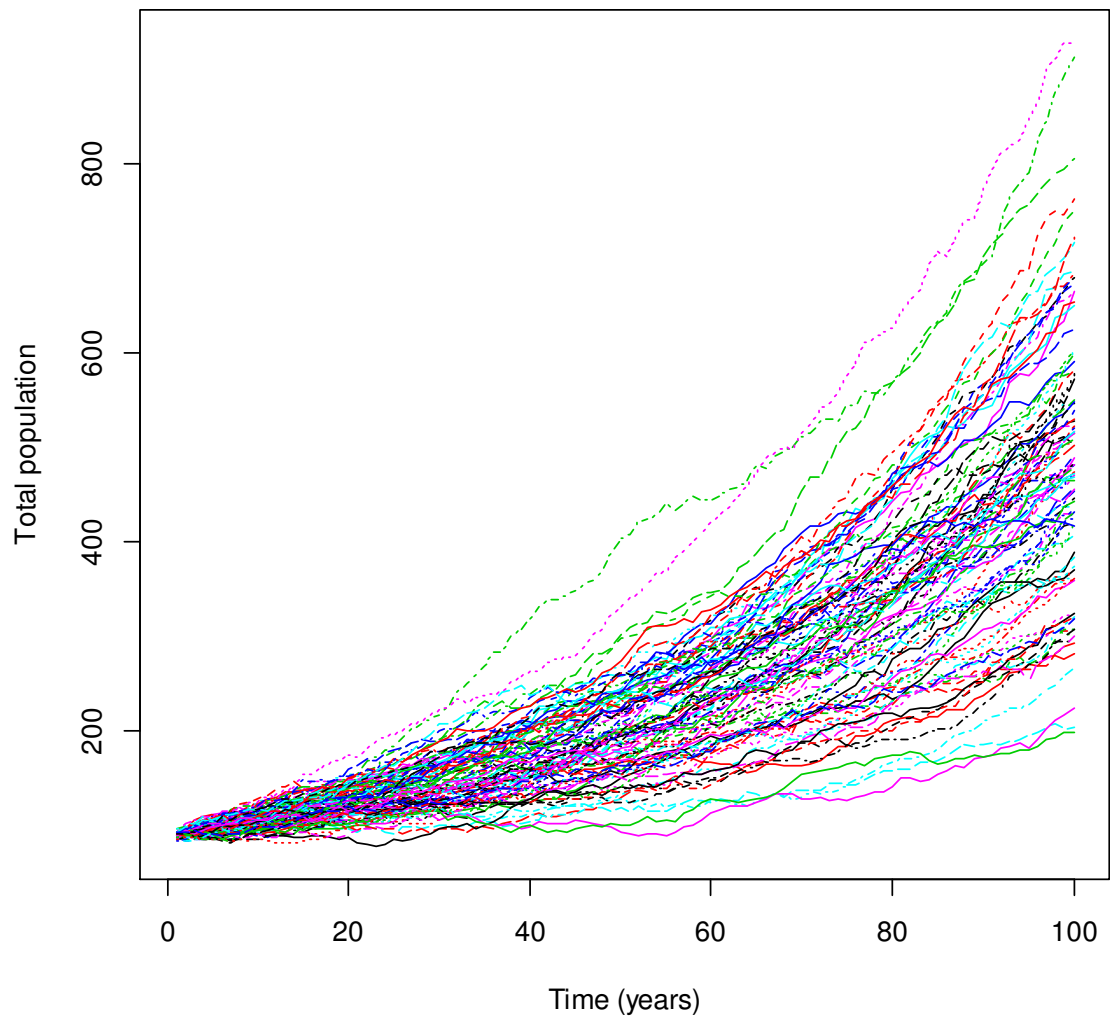
Figure 33. Projections (100) of SRKW population size under demographic stochasticity and under Scenario 4 (51% reduction in the ocean harvest rates on the five large stocks WCVI/FL/PS/OC/URB).

Median > 100 yr
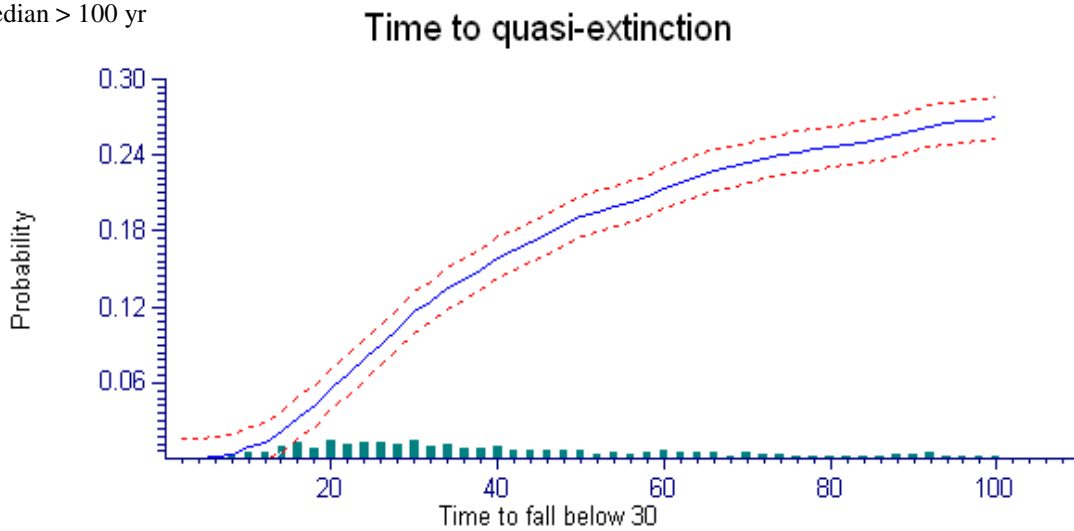
Figure 34. Probability of SRKW population falling below 30 individuals in the future under environmental and demographic stochasticity for Scenario 4 (51% reduction in the ocean harvest rates on the five large stocks WCVI/FL/PS/OC/URB). Median is the number of years to reach a 0.5 probability of falling below 30 individuals. Mean probability and 95% CIs generated from 5000 replications.
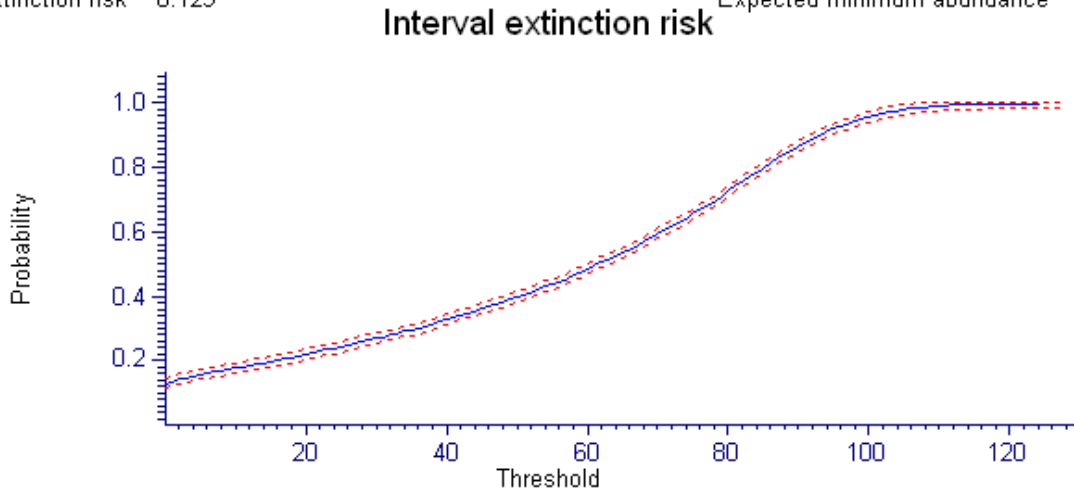
Figure 35. Probability of SRKW population size falling below a population threshold in 100 years under environmental and demographic stochasticity for Scenario 4 (51% reduction in the ocean harvest rates on the five large stocks WCVI/FL/PS/OC/URB). Mean probability and 95% CIs generated from 5000 replications. Also shown are the extinction risk for $N_{Threshold} = 0$ and the expected minimum abundance, which is the average (over all replications) of the minimum population abundance of the trajectory.
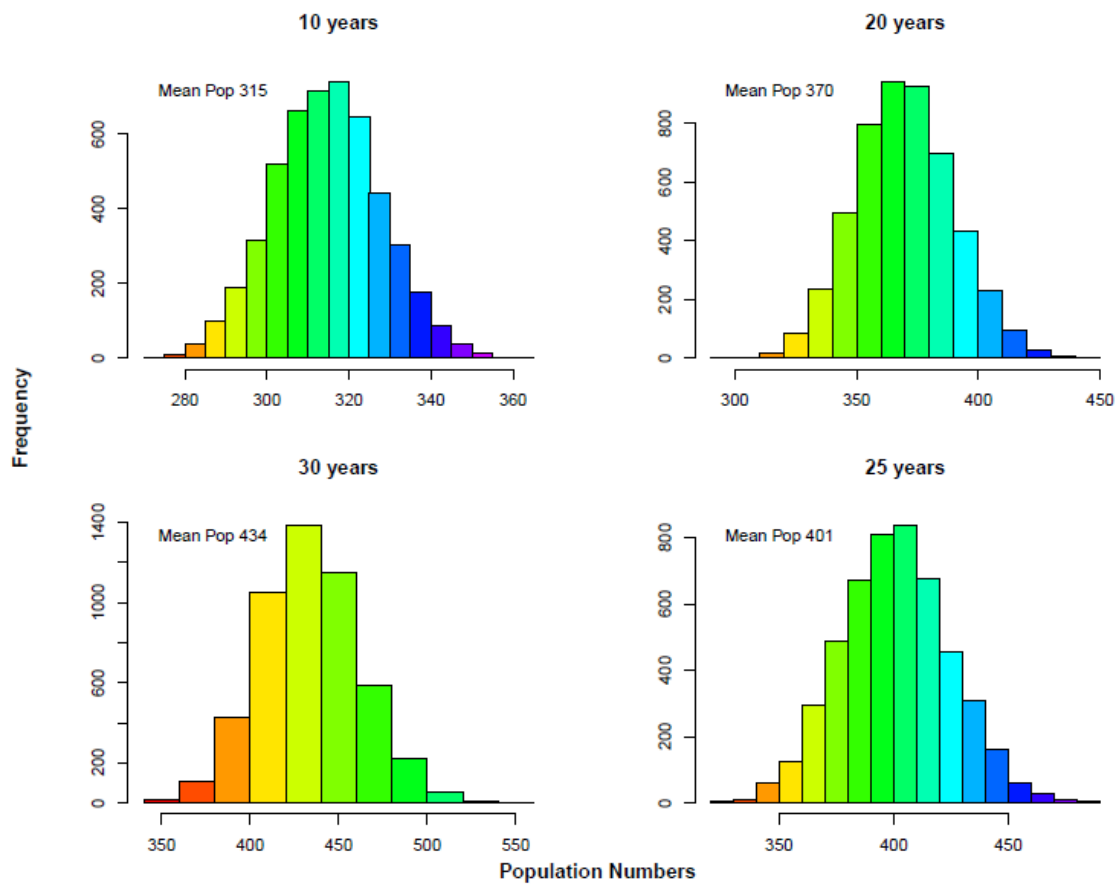
Figure 36. Projections of NRKW population size in an IID environment under status quo conditions (Scenario 7) at 10, 20, 30, and 25 years in the future (NRKW Damping Time = 25 years). Histograms and computation of stochastic population growth generated from 5000 realizations of population size.
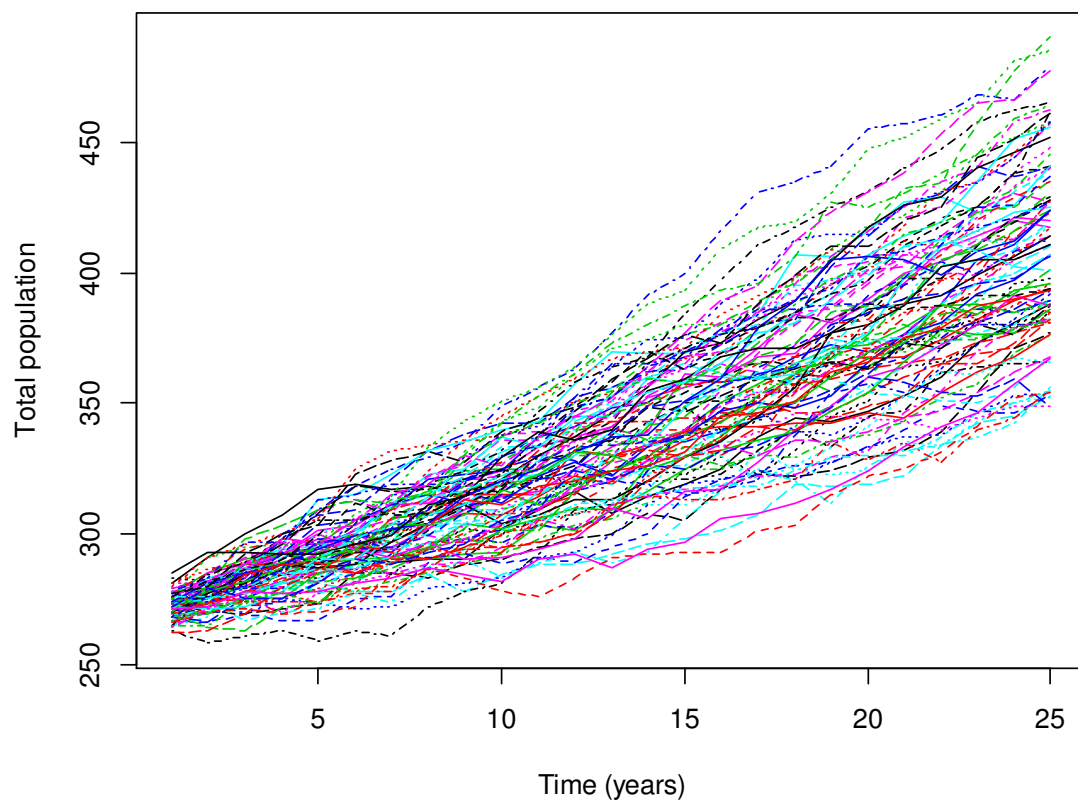
Figure 37. Projections (100) of NRKW population size under demographic stochasticity and status quo conditions (Scenario 7).
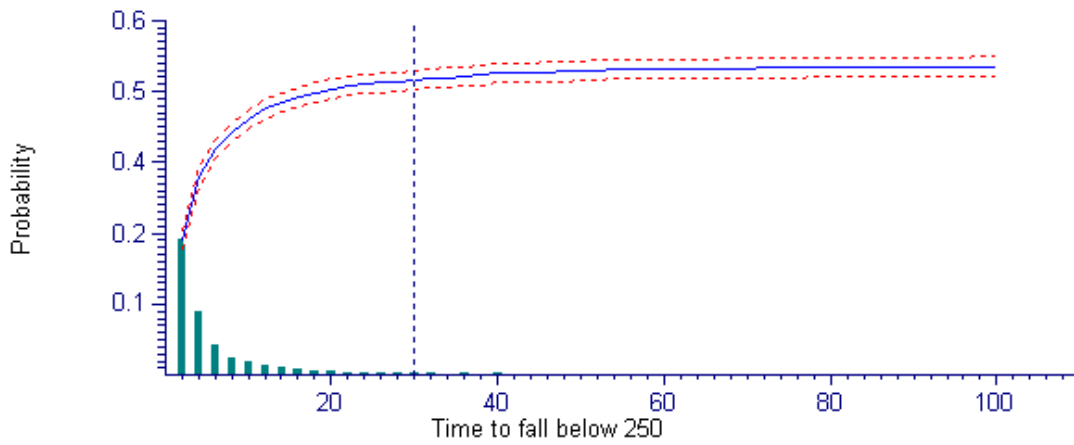
Figure 38. Probability of NRKW population falling below 250 individuals in the future under environmental and demographic stochasticity and status quo conditions (Scenario 7). Mean probability and 95% CIs generated from 5000 replications. Median is the number of years to reach a 0.5 probability of falling below 250 individuals.

Extinction risk ~ 0.000   Expected minimum abundance ~ 237.5

Interval extinction risk
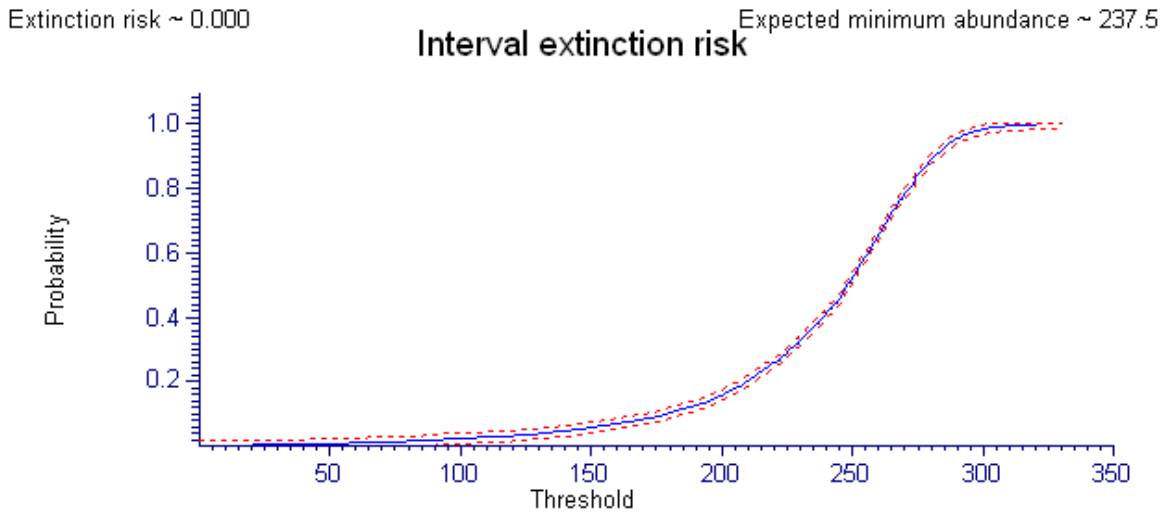
Figure 39. Probability of NRKW population size falling below a population threshold in 100 years under environmental and demographic stochasticity and status quo conditions (Scenario 7). Mean probability and 95% CIs generated from 5000 replications. Also shown are the extinction risk for $N_{Threshold} = 0$ and the expected minimum abundance, which is the average (over all replications) of the minimum population abundance of the trajectory.
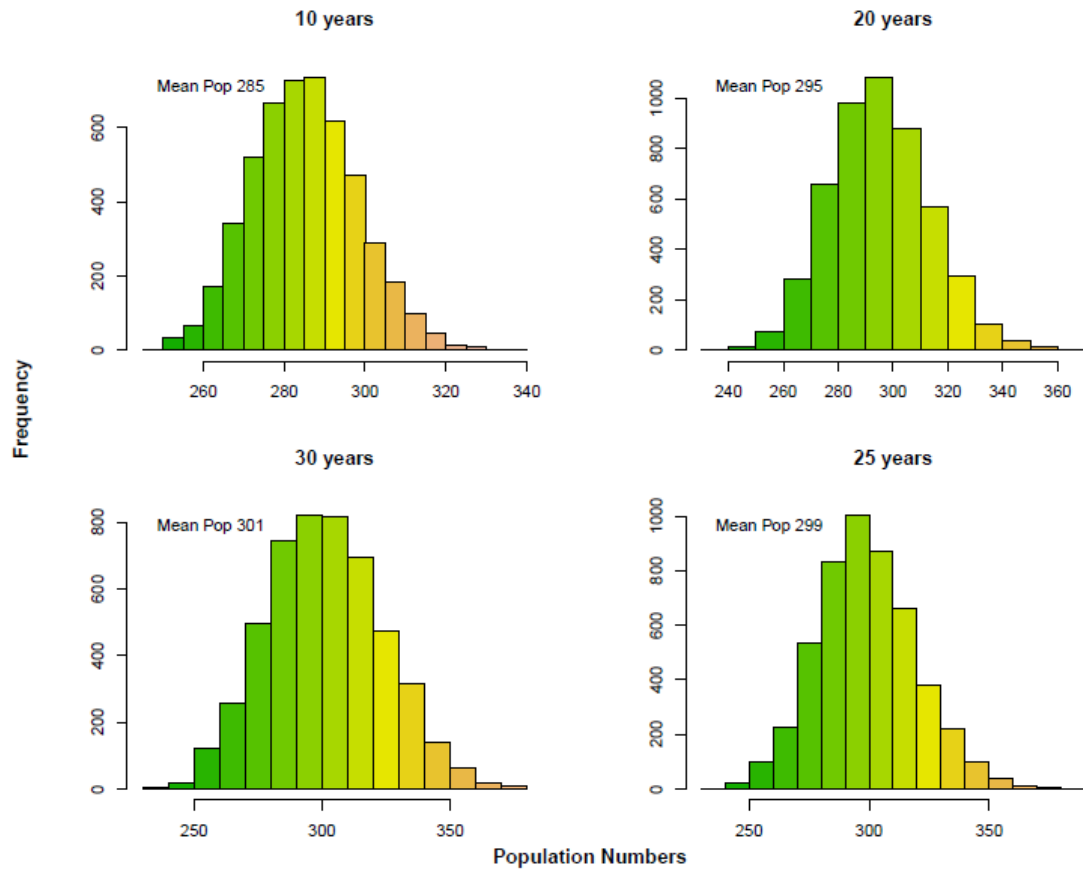
Figure 40. Projections of NRKW population size in an IID environment under Scenario 11 (66% increase of coastwide Chinook ocean harvest rates) at 10, 20, 30 and 25 years in the future (NRKW Damping Time = 25 years). Histograms and computation of stochastic population growth generated from 5000 realizations of population size.
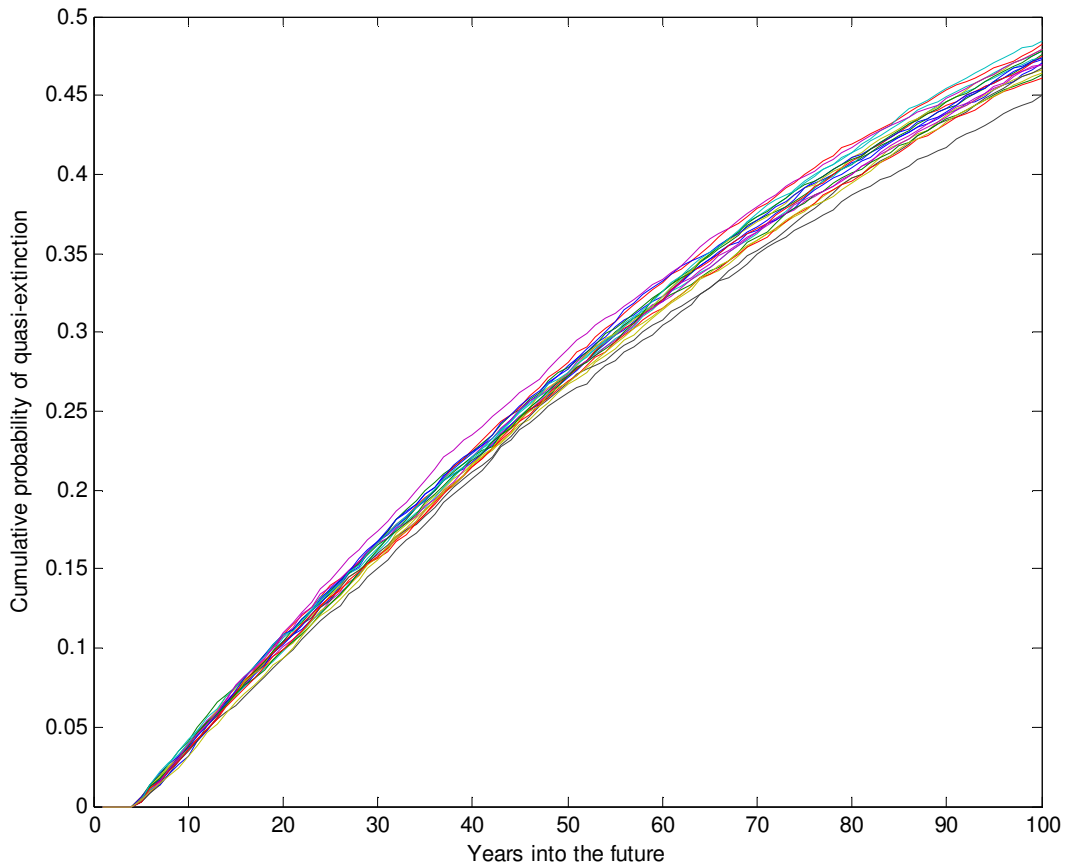
Figure 41. Cumulative probability of NRKW population size falling below 250 individuals in the future in an IID environment under Scenario 11 (66% increase of coastwide Chinook ocean harvest rates). Probabilities computed from 5000 realizations of population size. Twenty runs are shown in the figure.
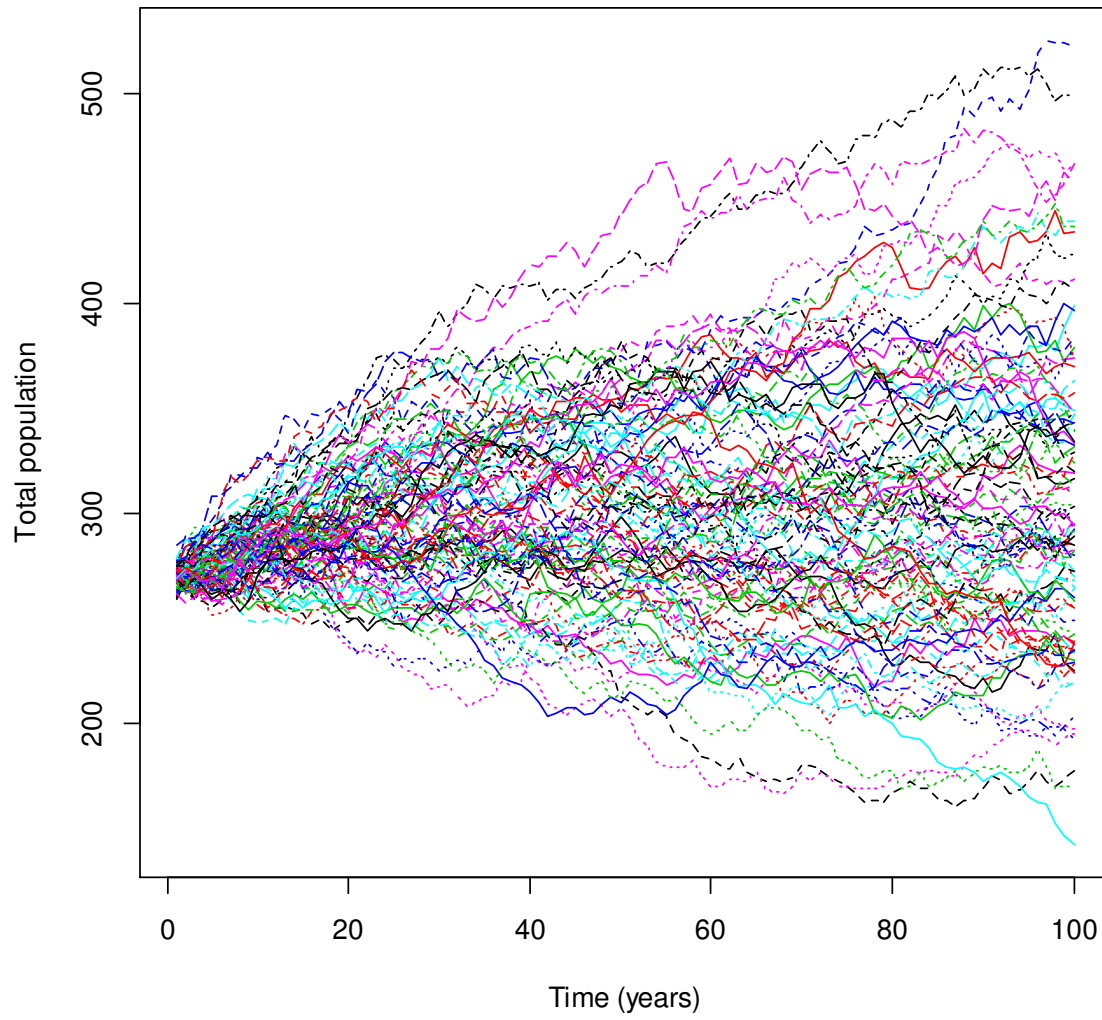
Figure 42. Projections (100) of NRKW population size under demographic stochasticity and Scenario 11 (66% increase of coastwide Chinook ocean harvest rates).
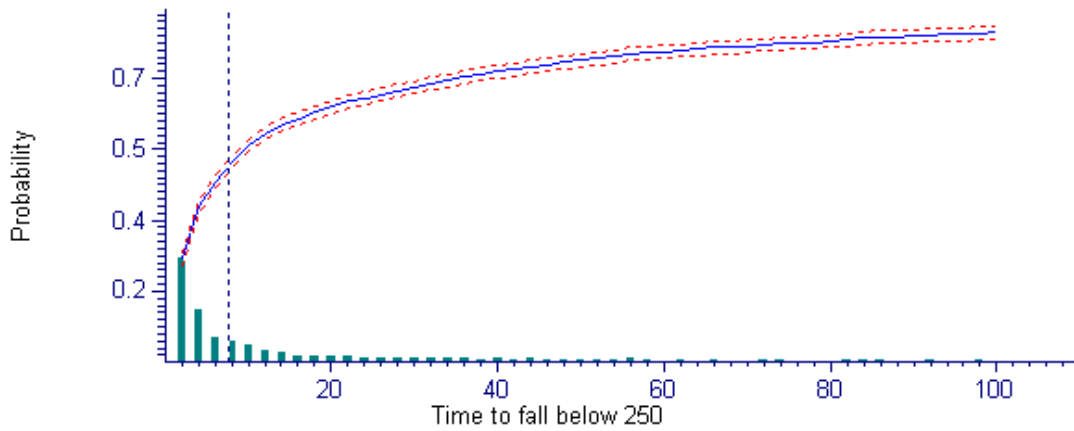
Figure 43. Probability of NRKW population falling below 250 individuals in the future under environmental and demographic stochasticity and Scenario 11 (66% increase of coastwide Chinook ocean harvest rates). Mean probability and 95% CIs generated from 5000 replications. Median is the number of years to reach a 0.5 probability of falling below 250 individuals.
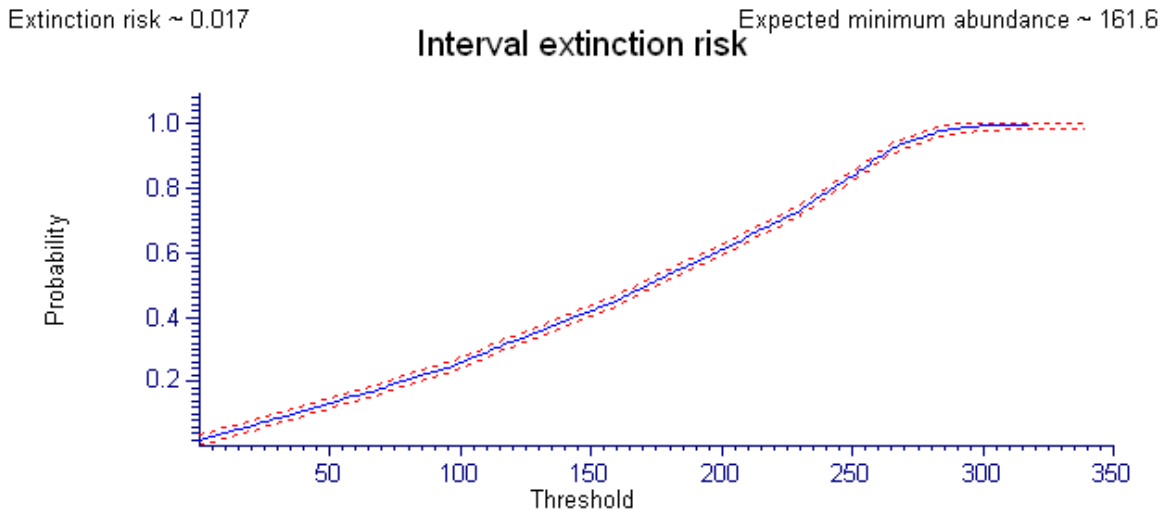
Figure 44. Probability of NRKW population size falling below a population threshold in 100 years under environmental and demographic stochasticity and Scenario 11 (66% increase of coastwide Chinook ocean harvest rates). Mean probability and 95% CIs generated from 5000 replications. Also shown are the extinction risk for $N_{Threshold} = 0$ and the expected minimum abundance, which is the average (over all replications) of the minimum population abundance of the trajectory.
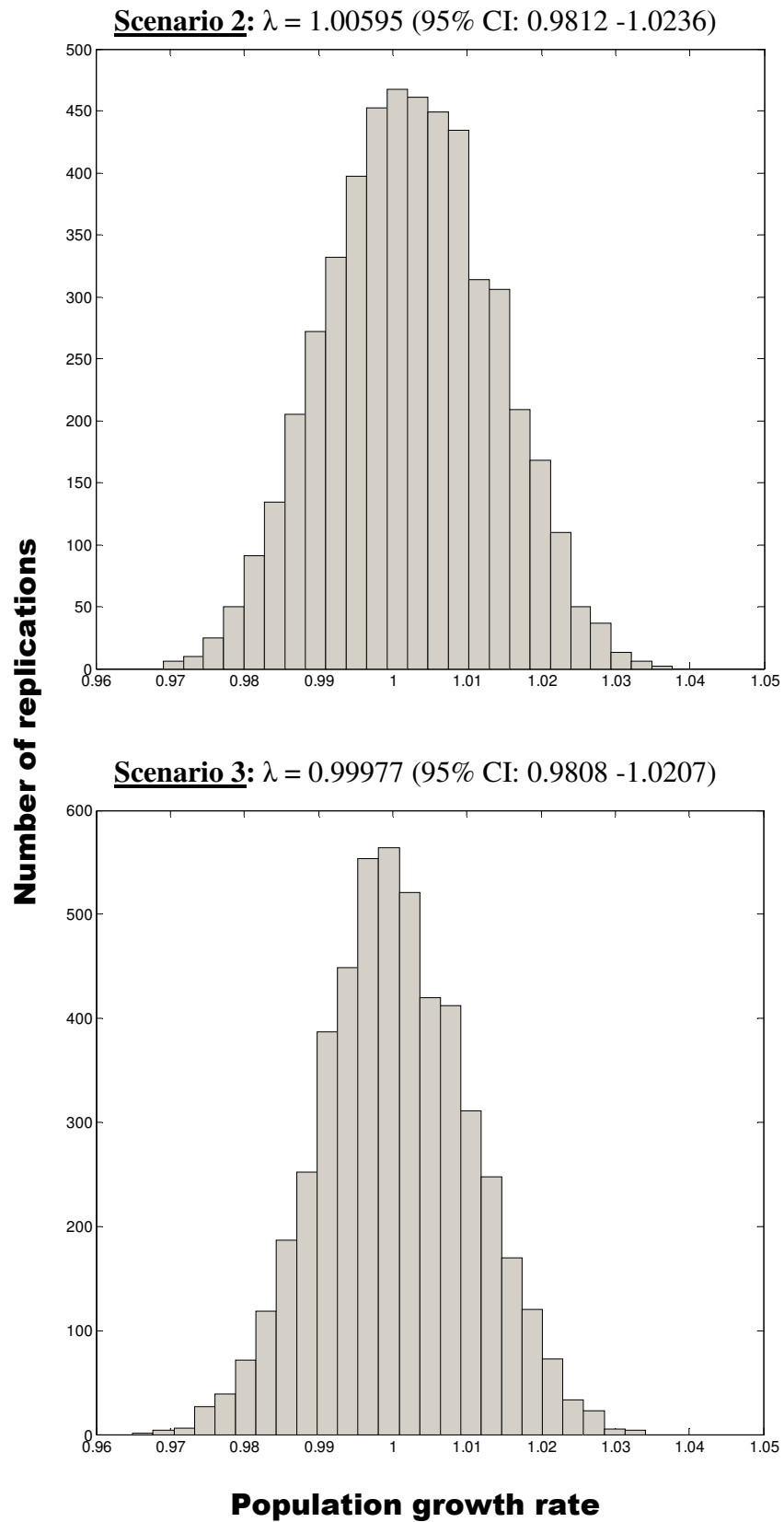
Figure 45. Frequency distribution of stochastic population growth for SRKW under fishing scenarios 2 (top) and 3 (bottom). See Table 5 for scenario characteristics.

FIGURES
(4. Discussion)
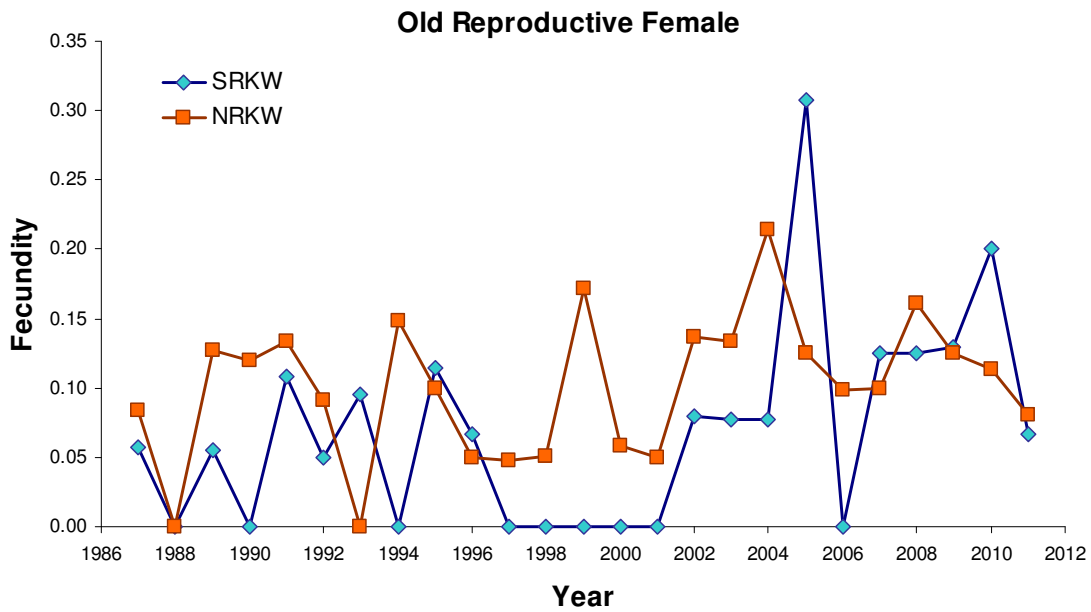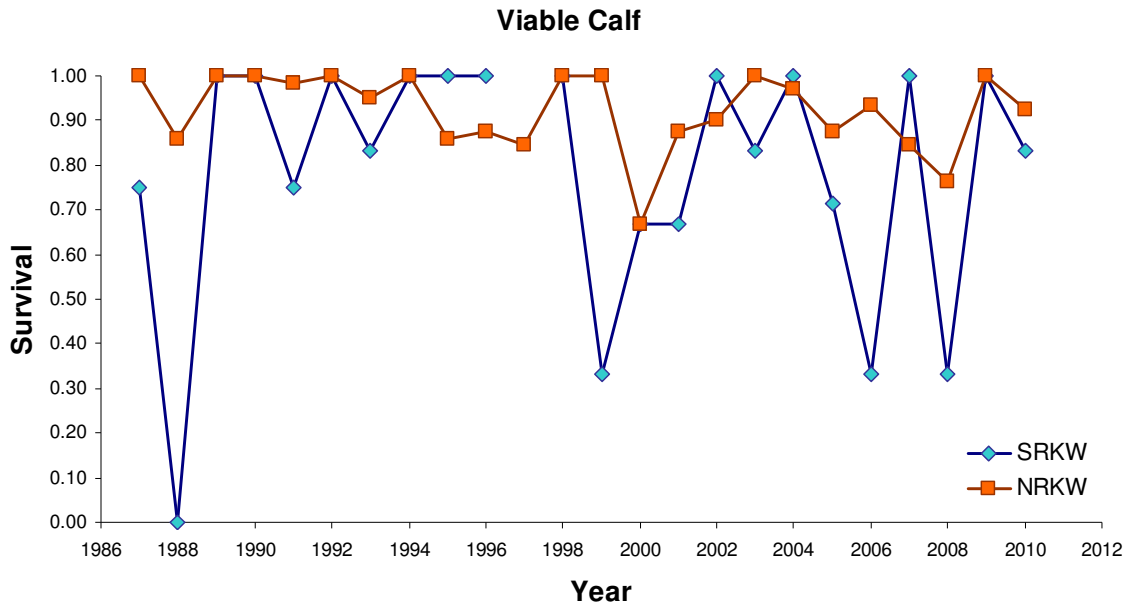
Figure 46. Viable calf survival (top) and fecundity of old reproductive females (bottom) for NRKW and SRKW for years 1987-2011. Viable calves are defined as those that survived to at least 0.5 years of age.
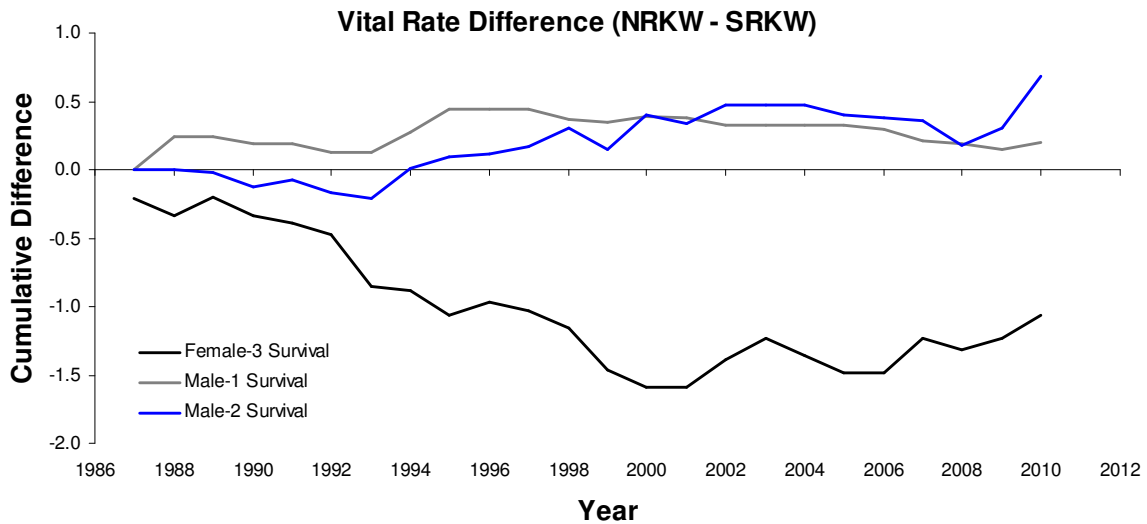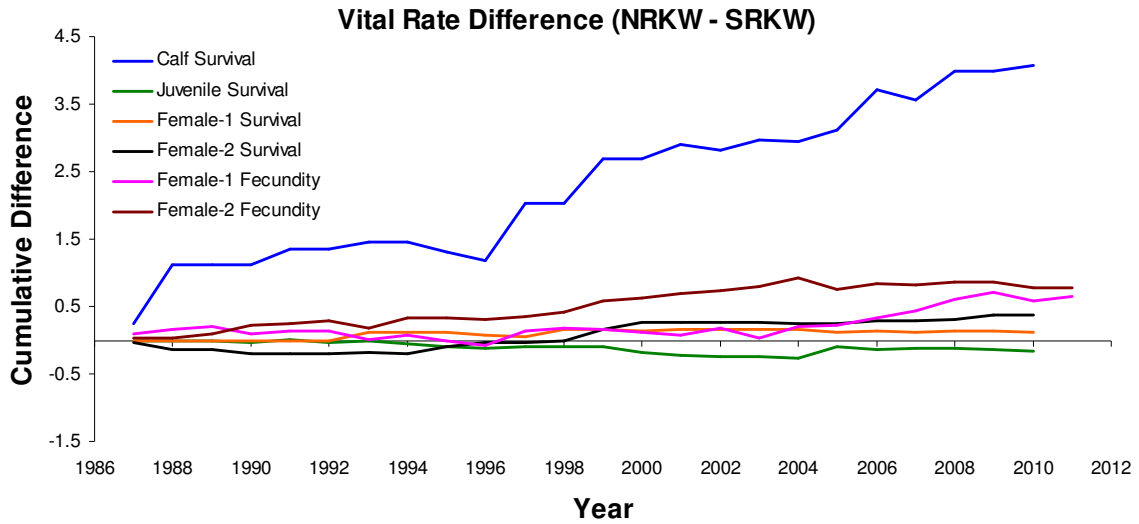
Figure 47. Cumulative difference between vital rates of NRKW and SRKW for years 1987-2011. The top panel shows the cumulative difference for vital rates contributing directly to population growth and the bottom panel for vital rates not contributing directly to population growth.

Puget Sound

Fraser Early

Fraser Late

Coastwide Total

Northern BC

Lower Georgia Strait
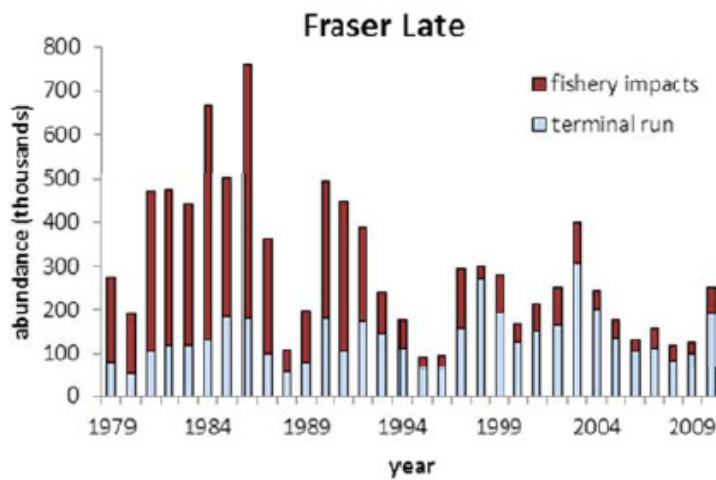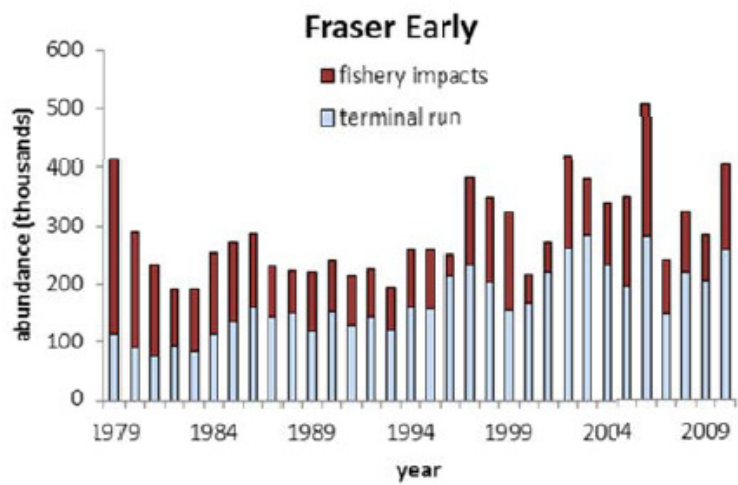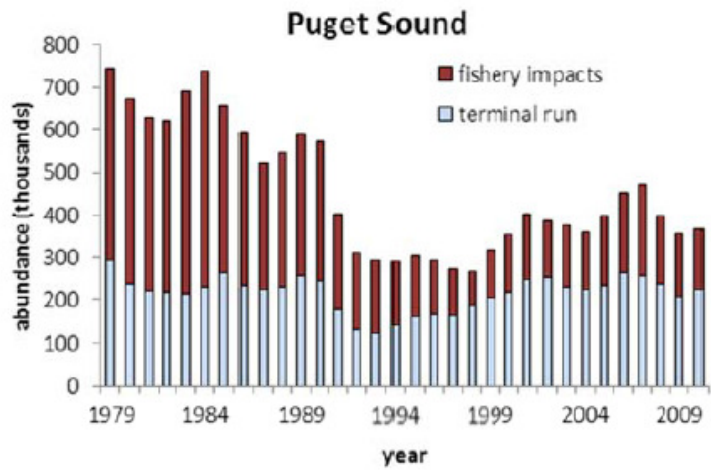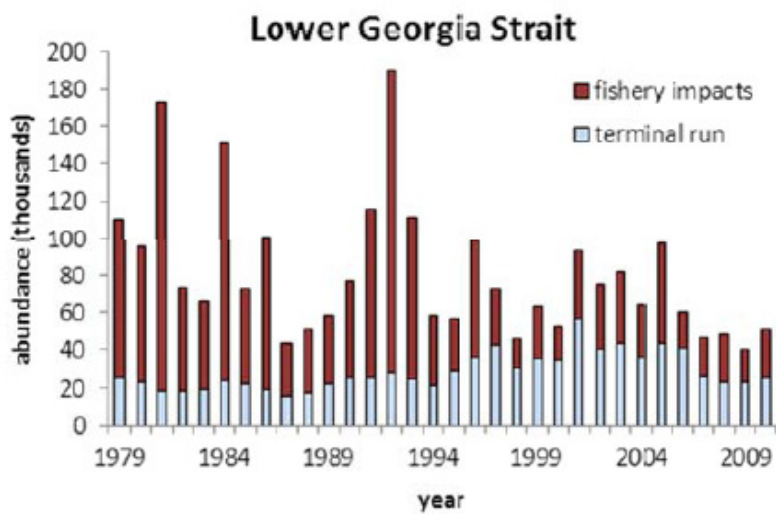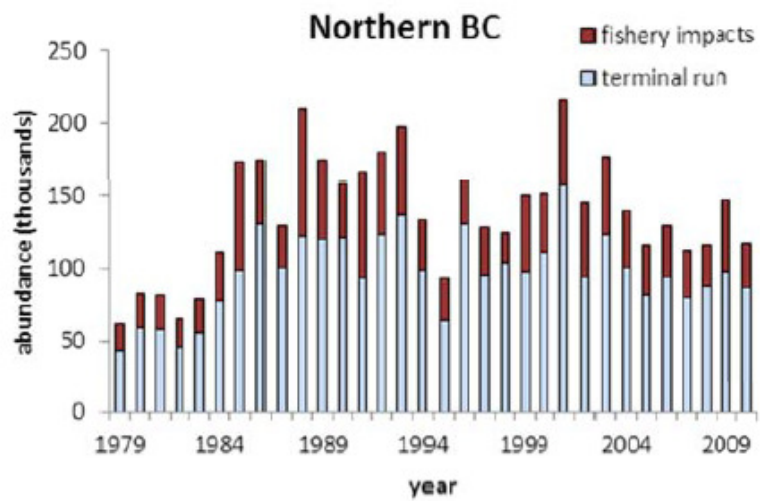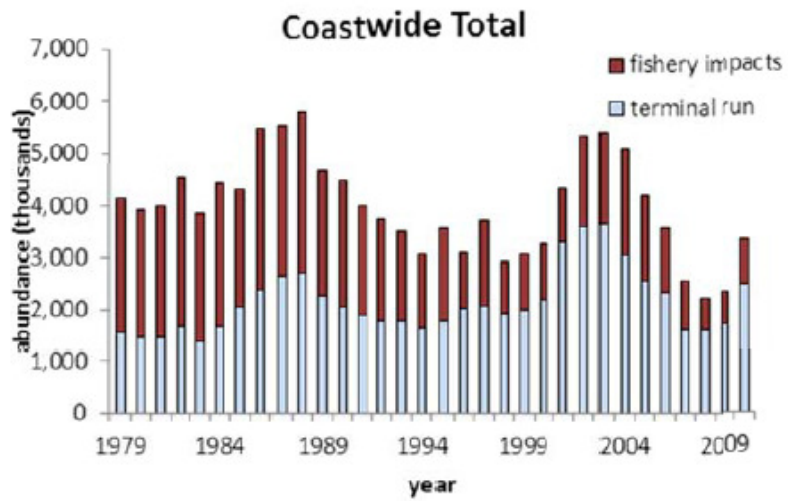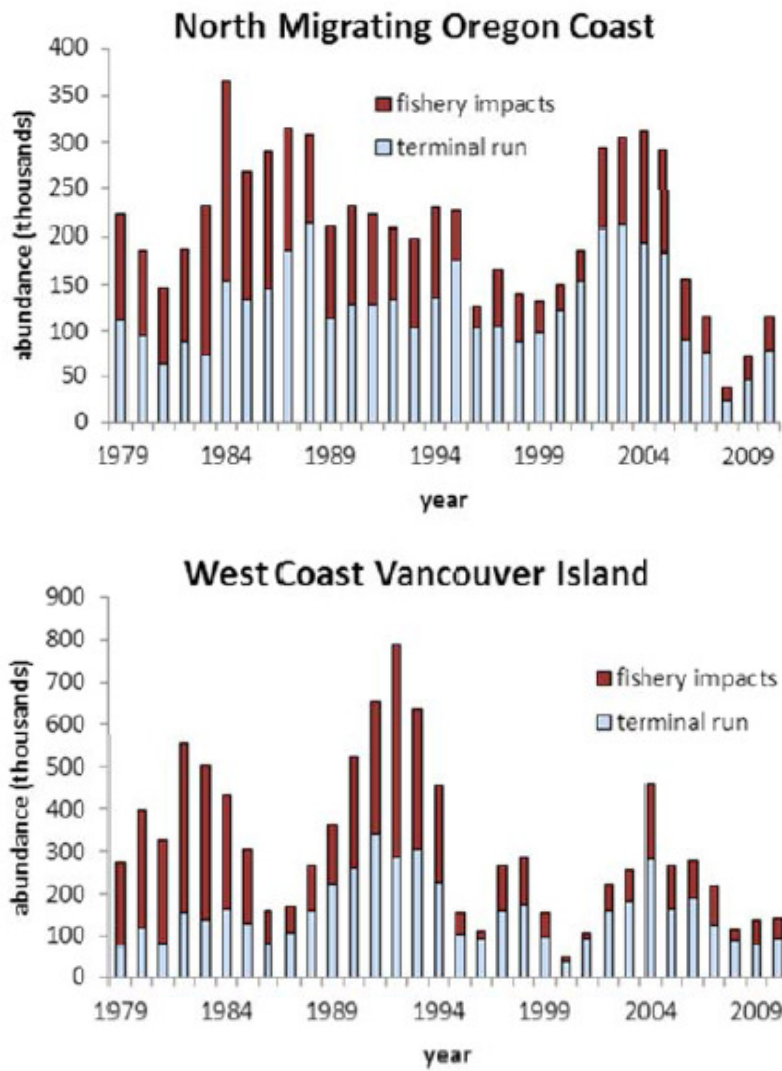
Figure 48. Terminal run and fishery impacts for Chinook stock aggregates with prominent interactions with RKW's vital rates (Kope and Parken, Appendix 3).

Appendix 1. Alternative RKW matrix population models used in this investigation included a model with gender identification at birth (below) and a truncated female-only model (shaded matrix elements) that excluded post-reproductive females.

Killer whale life cycle and projection matrix
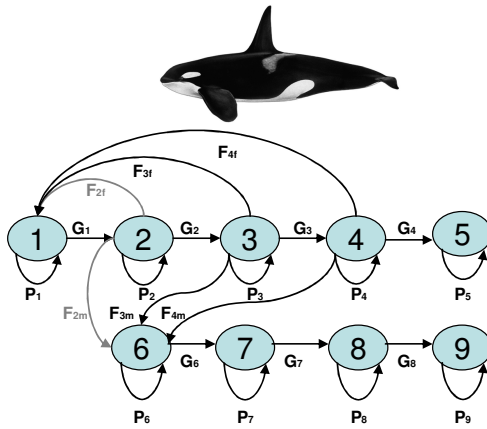
1: Female Calves
2: Female juveniles
3: Young reproductive females
4: Old reproductive females
5: Post-reproductive females
6: Male calves
7: Male juveniles
8: Young mature males
9: Old mature males

$$
M = \begin{pmatrix}
0 & F_{2f} & F_{3f} & F_{4f} & 0 & 0 & 0 & 0 & 0 \\
G_1 & P_2 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & G_2 & P_3 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & G_3 & P_4 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & G_4 & P_5 & 0 & 0 & 0 & 0 \\
0 & F_{2m} & F_{3m} & F_{4m} & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & G_6 & P_7 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & G_7 & P_8 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & G_8 & P_9
\end{pmatrix}
$$

Appendix 2. Projections of observed stage distributions towards stable stage distributions for SRKW and NRKW in the period between the end of the live-capture fishery and the first year used for the analyses in this report (1987). The projections represent the periods 1973-1976, 1977-1981, 1982-1986, and the entire period 1973-1986. Observed and stable stage distributions differ substantially from those in 1987-2011, particularly for SRKW. The live-capture fishery targeted mostly SRKW. Olesiuk et al. (1995) estimated 48 individuals (mostly juveniles and young males) were taken from the SRKW population between 1965 and 1973.

Stable Stage Projection from SRKW 1973 - 1976
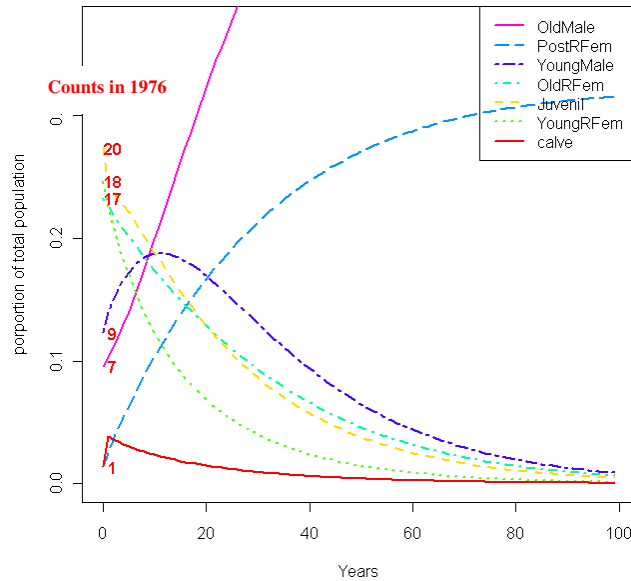
Stable Stage Projection from SRKW 1977 - 1981
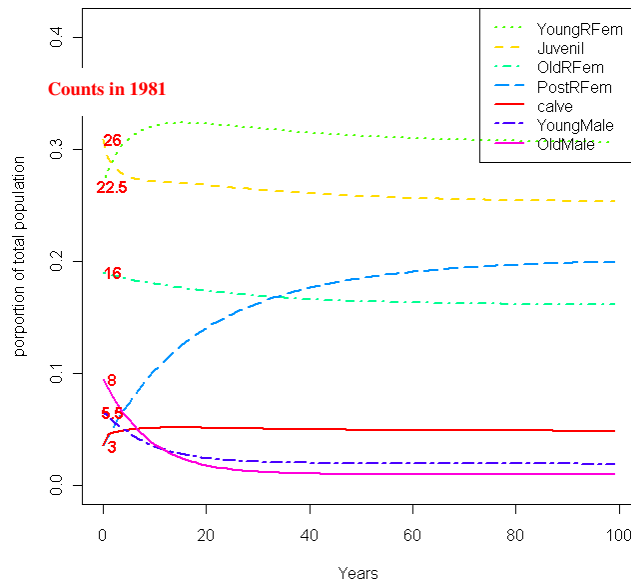
Stable Stage Projection from SRKW 1982 - 1986
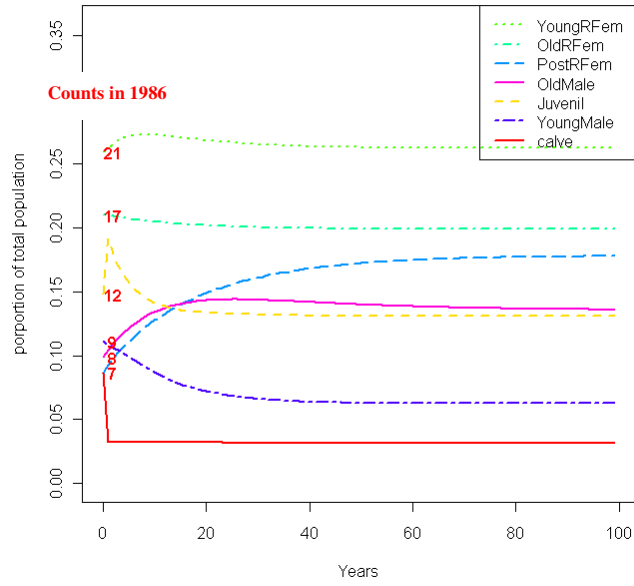
Stable Stage Projection from SRKW 1973 - 1986
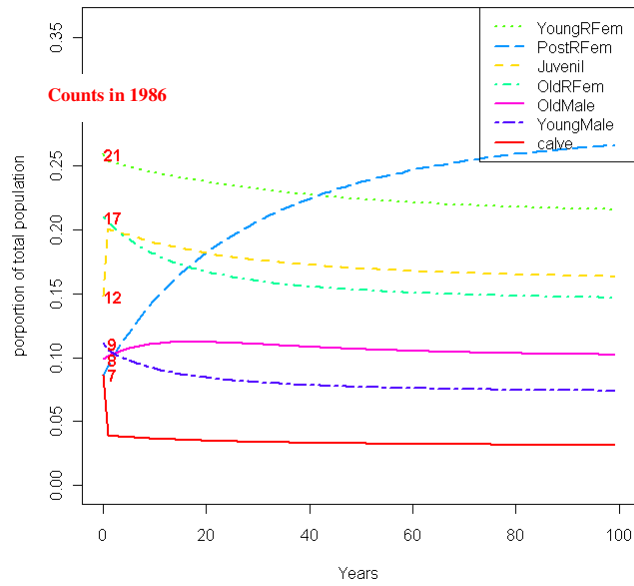
Stable Stage Projection from NRKW 1973 - 1976
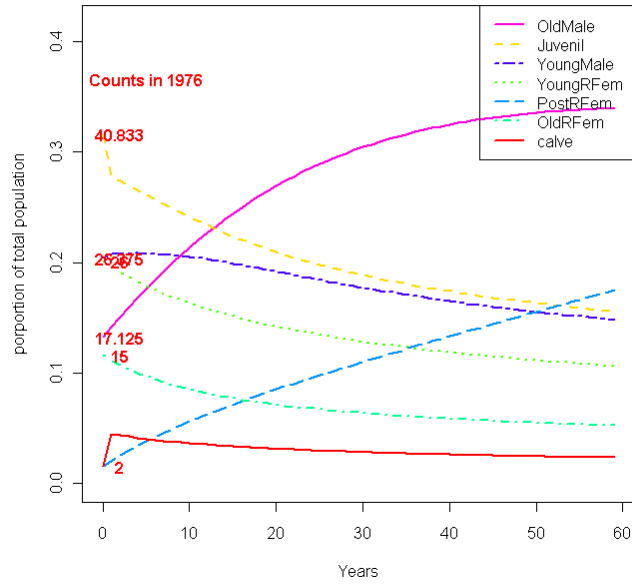
Stable Stage Projection from NRKW 1977 - 1981
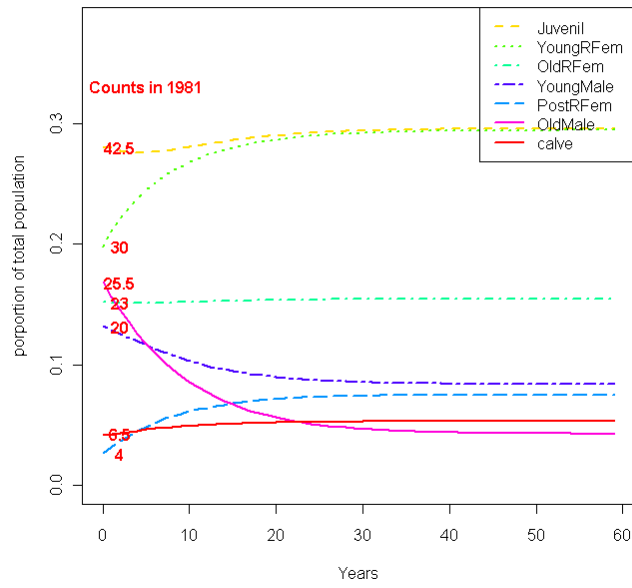
Stable Stage Projection from NRKW 1982 - 1986
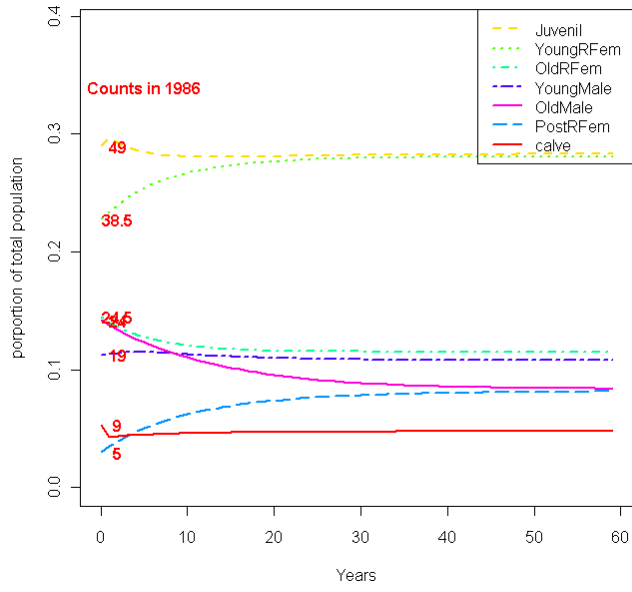
Stable Stage Projection from NRKW 1973 - 1986
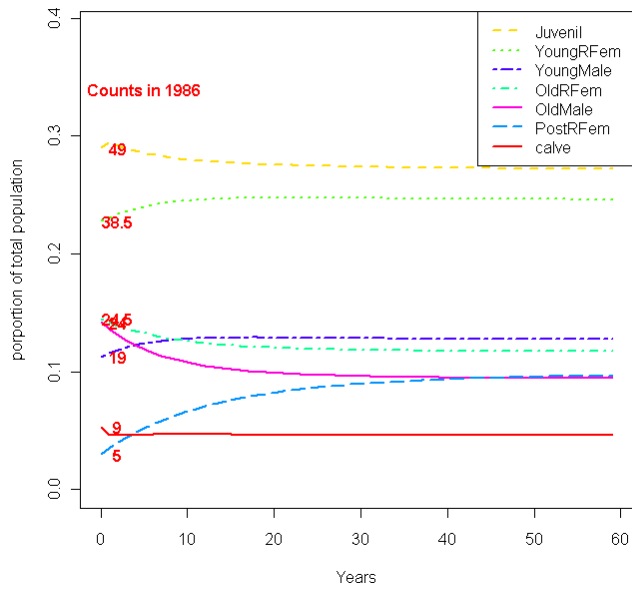
Appendix 3.

Recent trends in abundance of Chinook salmon stocks from British Columbia, Washington, Oregon, and California

Robert Kope
National Marine Fisheries Service
Northwest Fishery Science Center

Chuck Parken
Fisheries and Oceans Canada
Pacific Biological Station

Abundance data were compiled for Chinook salmon stocks from Northern British Columbia to the Sacramento River in California. This included terminal run size for fish of both hatchery and natural origin, and impacts in ocean fisheries. Data compilation focused on the Chinook Technical Committee's (CTC) Chinook Model. The CTC model was selected as a data source because it provides continuous coverage from 1979 through 2010, it includes both hatchery and natural production for stocks from Southeast Alaska to the central Oregon coast, and it gets around gaps in coverage of coded-wire tagging programs. Some smoothing of the terminal run data is done by the CTC model. For Canadian stocks, the model only has 8 stocks, some of which aggregate over different life history types and exploitation patterns, and only 4 CWT indicator stocks during the model base period. For these reasons, Canadian stocks were disaggregated to a finer scale than the CTC model stocks and 10 CWT indicator stocks were used, where possible, to account for the impacts of ocean fisheries.

For stocks not included in the CTC model, outside sources of data were used where available. These include Upper Columbia River spring Chinook, Klamath River fall Chinook, and Sacramento River fall Chinook.

These summaries are not exhaustive. All Canadian stock aggregates, except Fraser Late, do not include all production but they are suitable for describing abundance trends. Coastal Chinook stocks from the Umpqua River south, as well as spring Chinook from the Klamath River, spring, late-fall, and winter Chinook from the Sacramento River, and fall Chinook from the San Joaquin system are also omitted. In all cases, terminal runs and fishery impacts are of fish of ages 3 and older for ocean-type stocks, and ages 4 and older for stream-type stocks, and are presented on a calendar year basis. The abundance estimates (terminal run + fishery impacts) do not account for fish that do not mature, but remain at sea, and they also do not account for predation (e.g. by marine mammals); so they are minimum estimates. When RKW are in inside waters, the terminal run size of stocks is most representative of the availability of large Chinook salmon. When they are in outside marine waters, the sum of fishery impacts and terminal run is probably more representative.

Comparing the averages from the first 10 years of the times series to those of the last 10 years, there has been a modest decline in overall abundance of Chinook coastwide, but an increase in the terminal run size as a result of reductions in ocean salmon fisheries (Table 1). However abundance patterns differ greatly among the stocks. The stocks that figure most prominently in the diet studies of RKW in inside waters are the four aggregates of Fraser River spring and summer Chinook stocks, which are collectively incorporated in the CTC model as the "Fraser early" stock. This model stock includes both

stream-type (spring runs 1.2 and 1.3, and summer 1.3) as well as ocean-type (summer 0.3) life histories which have very different patterns of distribution, exploitation, and maturation. Stream-type stocks experience little impact from ocean fisheries and are harvested primarily in terminal fisheries, thus their availability to RKW is not substantially impacted by ocean fisheries. Ocean-type stocks are harvested primarily in ocean fisheries. While there has been a modest increase in the abundance and availability of stream-type Chinook from the Fraser River, there has been about a 50% increase in abundance and more than a 300% increase in terminal run size of ocean-type Chinook. This has resulted in more than doubling of the terminal runs size of Fraser River Chinook migrating through the inside marine waters during the spring and summer.

For other stocks coastwide, increases in abundance have been enhanced and declines in abundance have been mitigated or reversed in terminal runs by reductions in ocean fisheries.

Table 1. Average abundance and terminal run size, in thousands of adult fish, for Chinook stock aggregates from northern British Columbia south. Abundance is the sum of terminal run size and impacts in ocean fisheries by calendar year. Averages are presented for the first ten years (1979-1988) and last ten years (2001-2010) of the time series compiled for this report.

	Average Abundance			Average Terminal Run		
	79-88	01-10	change	79-88	01-10	change
Northern BC	117.2	41.7	21%	79.2	100.5	27%
Central BC	46.6	68.2	46%	31.6	46.7	48%
WCVI	39.5	220.0	-35%	121.8	45.3	19%
Upper Georgia Strait	118.2	35.2	-70%	30.1	20.8	-31%
Georgia Strait H & N	93.6	65.9	-30%	20.2	36.0	78%
Fraser late	425.7	207.2	-51%	112.6	154.9	38%
Fraser spring 1.2	11.2	22.8	103%	9.4	21.3	128%
Fraser spring 1.3	51.1	50.3	-2%	40.9	38.4	-6%
Fraser summer 1.3	48.5	53.6	11%	34.6	44.8	30%
Fraser summer 0.3	149.0	226.0	52%	30.4	128.7	324%
Puget Sound	641.1	396.9	-38%	36.7	37.6	0%
Washington coast	156.9	19.0	-24%	73.2	72.0	-2%
lower Col. River spring	130.0	18.8	-9%	101.8	102.5	1%
upper Col. River spring	80.9	222.8	176%	80.9	222.8	176%
Col. River summer	36.9	94.9	157%	19.2	64.4	236%
Col. River bright fall	369.0	495.0	34%	231.0	371.3	61%
Col. River tule fall	461.4	290.9	-37%	213.5	195.0	-9%
northern Oregon coast	252.0	188.4	-25%	126.3	126.6	0%
Klamath River fall	235.3	139.2	-41%	100.9	114.0	13%
Sacramento River fall	858.0	704.3	-18%	212.5	361.7	70%
Coastwide total	4,622.2	3,861.1	-16%	1,906.6	2,605.3	37%

Appendix 4. Use of terminal run equivalents (*TRE*s) for the exploration of fishing scenarios.

A4.1 Use of *TRE*s to compute the proportional increase in terminal run size in the absence of fishing (*PI_TR_NF*) in CTC exploitation rate indicator stocks and calculate the increase in terminal run of a stock of interest (*New_TR_{stock,y}*) for the exploration of fishing scenarios. See Table A4.1 for a summary of indicator stocks corresponding to each of the time series of Chinook abundance used for analysis.

$$PI\_TR\_NF_{indicator,y} = \frac{TRE_{indicator,y}}{TR_{indicator,y}} \tag{1}$$

$$New\_TR_{stock,y} = \left(1 + PI\_TR\_NF_{indicator,y}\right) TR_{stock,y} \tag{2}$$

A4.2 Sequence of equations necessary to compute the terminal run scalar (*TR_Scalar_y*) resulting from an specified change in the ocean harvest rate of a CTC exploitation rate indicator stock ($HR_{TRE_{preterminal},obs,y}$), where n_y is the number of fish necessary to produce that change. The following equations correspond to an increase in ocean harvest rate.

$$HR_{TRE_{indicator},obs,y} = \frac{TRE_{indicator,y}}{TRE_{indicator,y} + TR_{indicator,y}} \tag{3}$$

$$HR_{TRE_{indicator},new,y} = \frac{TRE_{indicator,y} + n_y}{(TRE_{indicator,y} + n_y) + (TR_{indicator,y} - n_y)} \tag{4}$$

$$HR_{TRE_{indicator},new,y} = \frac{TRE_{indicator,y} + n_y}{TRE_{indicator,y} + TR_{indicator,y}} \tag{5}$$

$$n_y = HR_{TRE_{indicator},new,y}\left(TRE_{indicator,y} + TR_{indicator,y}\right) - TRE_{indicator,y} \tag{6}$$

$$TR\_Scalar_y = \frac{TR_{indicator,y} - n_y}{TR_{indicator,y}} \tag{7}$$

TR_Scalar_y is then used to calculate the increase in terminal run of a stock of interest (*New_TR_{stock,y}*) for the exploration of fishing scenarios.

$$New\_TR_{stock,y} = TR\_Scalar_y * TR_{stock,y} \tag{8}$$

If more than one CTC exploitation rate indicator stock is used to represent the variability in catch and maturation rates within a stock aggregate, then the scalar in Equation 7 is computed as:

$$TR\_Scalar_{Aggregate,y} = \frac{\sum\limits_{indicator} \left(TR_{indicator,y} - n_y\right)}{\sum\limits_{indicator} TR_{indicator,y}} \quad\quad (9)$$

For the exploration of fishing scenarios, the time series average scalar was used for years without indicator stock information in a given stock aggregate.

Also notice that in the absence of fishing, $HR_{TRE_{indicator},new,y}$ is zero, $n_y = -TRE_{indicator,y}$, and

$$TR\_Scalar_y = \frac{TR_{indicator,y} + TRE_{indicator,y}}{TR_{indicator,y}}, \text{ which is equivalent to the term}$$

$\left(1 + PI\_TR\_NF_{indicator,y}\right)$ in Equation 2.

Table A4.1. List of CTC exploitation rate indicator stocks used to compute terminal run scalars (*TR_Scalar*$_{Aggregate t,y}$) for time series of Chinook stock aggregates. See Table A4.2 for indicator stock acronyms. Data required to generate *TRE*s for Sacramento Fall's SRFC and Klamath Fall's KRFC were obtained from PFMC 2012.

Time series	Stock or stock aggregate	Lag	ER Indicator Stocks
FE_TR_0	Fraser Early (Spring and Summer)	0	DOM,NIC,SHU
FE_TR_1	Fraser Early (Spring and Summer)	1	DOM,NIC,SHU
FE_TR_2	Fraser Early (Spring and Summer)	2	DOM,NIC,SHU
FE_TR_5YA	Fraser Early (Spring and Summer)	5YA	DOM,NIC,SHU
FE2_TR_0	Fraser Early (Spring)	0	DOM,NIC
FE2_TR_1	Fraser Early (Spring)	1	DOM,NIC
FE2_TR_2	Fraser Early (Spring)	2	DOM,NIC
FE2_TR_5YA	Fraser Early (Spring)	5YA	DOM,NIC
FE3_TR_0	Fraser Early (Summer)	0	SHU
FE3_TR_1	Fraser Early (Summer)	1	SHU
FE3_TR_2	Fraser Early (Summer)	2	SHU
FE3_TR_5YA	Fraser Early (Summer)	5YA	SHU
PS_TR_0	Puget Sound (Summer and Fall)	0	SPS,SAM,GAD
PS_TR_1	Puget Sound (Summer and Fall)	1	SPS,SAM,GAD
PS_TR_2	Puget Sound (Summer and Fall)	2	SPS,SAM,GAD
PS_TR_5YA	Puget Sound (Summer and Fall)	5YA	SPS,SAM,GAD
FEPS_TR_0	Fraser Early + Puget Sound	0	DOM,NIC,SHU,SPS,SAM,GAD
FEPS_TR_1	Fraser Early + Puget Sound	1	DOM,NIC,SHU,SPS,SAM,GAD
FEPS_TR_2	Fraser Early + Puget Sound	2	DOM,NIC,SHU,SPS,SAM,GAD
FEPS_TR_5YA	Fraser Early + Puget Sound	5YA	DOM,NIC,SHU,SPS,SAM,GAD
FL_TR_0	Fraser Late	0	CHE,CHI
FL_TR_1	Fraser Late	1	CHE,CHI
FL_TR_2	Fraser Late	2	CHE,CHI
FL_TR_5YA	Fraser Late	5YA	CHE,CHI
ALL1a_TR_0	Fraser Early+Puget Sound+Fraser Late	0	DOM,NIC,SHU,SPS,SAM,GAD,CHE,CHI
ALL1a_TR_1	Fraser Early+Puget Sound+Fraser Late	1	DOM,NIC,SHU,SPS,SAM,GAD,CHE,CHI
ALL1a_TR_2	Fraser Early+Puget Sound+Fraser Late	2	DOM,NIC,SHU,SPS,SAM,GAD,CHE,CHI
ALL1a_TR_5YA	Fraser Early+Puget Sound+Fraser Late	5YA	DOM,NIC,SHU,SPS,SAM,GAD,CHE,CHI
NBC_TR_0	Northern British Columbia (Areas 1-5)	0	KLM
NBC_TR_1	Northern British Columbia (Areas 1-5)	1	KLM
NBC_TR_2	Northern British Columbia (Areas 1-5)	2	KLM
NBC_TR_5YA	Northern British Columbia (Areas 1-5)	5YA	KLM
CBC_TR_0	Central British Columbia (Areas 6-10)	0	ATN
CBC_TR_1	Central British Columbia (Areas 6-10)	1	ATN
CBC_TR_2	Central British Columbia (Areas 6-10)	2	ATN
CBC_TR_5YA	Central British Columbia (Areas 6-10)	5YA	ATN
WCVI_TR_0	West Coast Vancouver Island	0	RBT
WCVI_TR_1	West Coast Vancouver Island	1	RBT
WCVI_TR_2	West Coast Vancouver Island	2	RBT
WCVI_TR_5YA	West Coast Vancouver Island	5YA	RBT
UGS_TR_0	Upper Georgia Strait	0	QUI
UGS_TR_1	Upper Georgia Strait	1	QUI
UGS_TR_2	Upper Georgia Strait	2	QUI
UGS_TR_5YA	Upper Georgia Strait	5YA	QUI
LGS_TR_0	Lower Georgia Strait	0	BQR,COW,NAN,PPS
LGS_TR_1	Lower Georgia Strait	1	BQR,COW,NAN,PPS
LGS_TR_2	Lower Georgia Strait	2	BQR,COW,NAN,PPS
LGS_TR_5YA	Lower Georgia Strait	5YA	BQR,COW,NAN,PPS
ALL1b_TR_0	NBC+CBC+WCVI+UGS+LGS	0	KLM,ATN,RBT,QUI,BQR,COW,NAN,PPS
ALL1b_TR_1	NBC+CBC+WCVI+UGS+LGS	1	KLM,ATN,RBT,QUI,BQR,COW,NAN,PPS
ALL1b_TR_2	NBC+CBC+WCVI+UGS+LGS	2	KLM,ATN,RBT,QUI,BQR,COW,NAN,PPS
ALL1b_TR_5YA	NBC+CBC+WCVI+UGS+LGS	5YA	KLM,ATN,RBT,QUI,BQR,COW,NAN,PPS
SF_TR_0	Sacramento Fall	0	SRFC
SF_TR_1	Sacramento Fall	1	SRFC
SF_TR_2	Sacramento Fall	2	SRFC
SF_TR_5YA	Sacramento Fall	5YA	SRFC
KLF_TR_0	Klamath Fall	0	KRFC
KLF_TR_1	Klamath Fall	1	KRFC
KLF_TR_2	Klamath Fall	2	KRFC
KLF_TR_5YA	Klamath Fall	5YA	KRFC
COLf_TR_0	Columbia Fall (UpRiver Brights+ Tule)	0	URB,LRH,SPR
COLf_TR_1	Columbia Fall (UpRiver Brights+ Tule)	1	URB,LRH,SPR
COLf_TR_2	Columbia Fall (UpRiver Brights+ Tule)	2	URB,LRH,SPR
COLf_TR_5YA	Columbia Fall (UpRiver Brights+ Tule)	5YA	URB,LRH,SPR
COLs_TR_0	Columbia Spring/Summer	0	WSH,SUM
COLs_TR_1	Columbia Spring/Summer	1	WSH,SUM
COLs_TR_2	Columbia Spring/Summer	2	WSH,SUM
COLs_TR_5YA	Columbia Spring/Summer	5YA	WSH,SUM
OC_TR_0	Oregon Coastal	0	SRH
OC_TR_1	Oregon Coastal	1	SRH
OC_TR_2	Oregon Coastal	2	SRH
OC_TR_5YA	Oregon Coastal	5YA	SRH
ALL2a_TR_0	SF+KLF+COLf+COLs+OC+WCVI	0	URB,LRH,SPR,WSH,SUM,SRH,RBT
ALL2a_TR_1	SF+KLF+COLf+COLs+OC+WCVI	1	URB,LRH,SPR,WSH,SUM,SRH,RBT
ALL2a_TR_2	SF+KLF+COLf+COLs+OC+WCVI	2	URB,LRH,SPR,WSH,SUM,SRH,RBT
ALL2a_TR_5YA	SF+KLF+COLf+COLs+OC+WCVI	5YA	URB,LRH,SPR,WSH,SUM,SRH,RBT
CW2a_TR_0	Coastwide (excluding SEAK, NBC and CBC)	0	RBT,QUI,BQR,COW,NAN,PPS,DOM,NIC,SHU,SPS,SAM,GAD,CHE,CHI,URB,LRH,SPR,WSH,SUM,SRH
CW2a_TR_1	Coastwide (excluding SEAK, NBC and CBC)	1	RBT,QUI,BQR,COW,NAN,PPS,DOM,NIC,SHU,SPS,SAM,GAD,CHE,CHI,URB,LRH,SPR,WSH,SUM,SRH
CW2a_TR_2	Coastwide (excluding SEAK, NBC and CBC)	2	RBT,QUI,BQR,COW,NAN,PPS,DOM,NIC,SHU,SPS,SAM,GAD,CHE,CHI,URB,LRH,SPR,WSH,SUM,SRH
CW2a_TR_5YA	Coastwide (excluding SEAK, NBC and CBC)	5YA	RBT,QUI,BQR,COW,NAN,PPS,DOM,NIC,SHU,SPS,SAM,GAD,CHE,CHI,URB,LRH,SPR,WSH,SUM,SRH
ALL2b_TR_0	FE+PS+FL+COLf+COLs+OC	0	DOM,NIC,SHU,SPS,SAM,GAD,CHE,CHI,URB,LRH,SPR,WSH,SUM,SRH
ALL2b_TR_1	FE+PS+FL+COLf+COLs+OC	1	DOM,NIC,SHU,SPS,SAM,GAD,CHE,CHI,URB,LRH,SPR,WSH,SUM,SRH
ALL2b_TR_2	FE+PS+FL+COLf+COLs+OC	2	DOM,NIC,SHU,SPS,SAM,GAD,CHE,CHI,URB,LRH,SPR,WSH,SUM,SRH
ALL2b_TR_5YA	FE+PS+FL+COLf+COLs+OC	5YA	DOM,NIC,SHU,SPS,SAM,GAD,CHE,CHI,URB,LRH,SPR,WSH,SUM,SRH
CW2b_TR_0	Coastwide (excluding Sacramento Fall and Klamath Fall)	0	KLM,ATN,RBT,QUI,BQR,COW,NAN,PPS,DOM,NIC,SHU,SPS,SAM,GAD,CHE,CHI,URB,LRH,SPR,WSH,SUM,SF
CW2b_TR_1	Coastwide (excluding Sacramento Fall and Klamath Fall)	1	KLM,ATN,RBT,QUI,BQR,COW,NAN,PPS,DOM,NIC,SHU,SPS,SAM,GAD,CHE,CHI,URB,LRH,SPR,WSH,SUM,SF
CW2b_TR_2	Coastwide (excluding Sacramento Fall and Klamath Fall)	2	KLM,ATN,RBT,QUI,BQR,COW,NAN,PPS,DOM,NIC,SHU,SPS,SAM,GAD,CHE,CHI,URB,LRH,SPR,WSH,SUM,SF
CW2b_TR_5YA	Coastwide (excluding Sacramento Fall and Klamath Fall)	5YA	KLM,ATN,RBT,QUI,BQR,COW,NAN,PPS,DOM,NIC,SHU,SPS,SAM,GAD,CHE,CHI,URB,LRH,SPR,WSH,SUM,SF

Table A4.2. Glossary of acronyms used for CTC exploitation rate indicator stocks.

Stock acronym	Description
ACI	Alaska Central Inside
AKS	Alaska Spring
ALP	Little Port Walter
ASI	Alaska Southern Inside
ATN	Atnarko Summer
BQR	Big Qualicum
CAP	Capilano Falls
CHE	Chehalis (Harrison Fall Stock)
CHI	Chilliwack (Harrison Fall Stock)
CKO	Chilko Spring
COW	Cowichan Fall
CWF	Cowlitz Fall Tule
CWS	Cowlitz Spring
DOM	Dome Creek Spring
ELK	Elk River
ELW	Elwha Fall Fingerling
GAD	George Adams Fall Fingerling
GRN	Green River Fall Fingerling
GRO	Grovers Creek Fall Fingerling
HAN	Hanford Wild
HOK	Hoko Fall Fingerling
ISS	Issaquah Fall Fingerling
KIT	Kitimat Spring
KLM	Kitsumkalum Summer
LRH	Columbia Lower River Hatchery
LRW	Lewis River Wild
LYF	Lyons Ferry
NAN	Nanaimo River Fall
NIC	Nicola River Spring
NIS	Nisqually Fall Fingerling
NKF	Nooksack Fall Fingerling
NKS	Nooksack Spring Yearling
NPY	North Puget Sound Fall Yearling
NSF	Nooksack Spring Fingerling
PPS	Puntledge Summer
QNT	Quinault Fall Fingerling
QUE	Queets Fall Fingerling
QUI	Quinsam Fall
RBT	Robertson Creek
SAM	Samish Fall Fingerling
SHU	Lower Shuswap River Summers
SKE	Skeena Summer
SKF	Skagit Spring Fingerling
SKS	Skagit Spring Yearling
SKY	Skykomish Fall Fingerling
SOO	Sooes Fall Fingerling
SPR	Spring Creek Tule
SPS	South Puget Sound Fall Fingerling
SPY	South Puget Sound Fall Yearling
SQP	Squaxin Pens Fall Yearling
SRH	Salmon River
SSF	Skagit Summer Fingerling
STL	Stillaguamish Fall Fingerling
SUM	Columbia Summers
URB	Upriver Brights
UWA	University of Washington Accelerated
WHF	White River Hatchery Fingerling
WHY	White River Hatchery Yearling
WRF	White River Fall Fingerling
WRY	White River Spring Yearling
WSH	Willamette Spring

Appendix 5. Time series of vital rates and total population abundance for SRKW and NRKW (1987-2011). Female 1: young reproductive female; Female 2: old reproductive female; Female 3: post-reproductive female; Male 1: young mature male; Male 2: old mature male.

Year	Pop	Calf Surv.	Juvenile Surv.	Female 1 Surv.	Female 2 Surv.	Female 3 Surv.	Male 1 Surv.	Male 2 Surv.	Female 1 Fec.	Female 2 Fec.	Abundance
1987	SRKW	0.7500	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	0.1500	0.0571	84
1988	SRKW	0.0000	1.0000	1.0000	1.0000	1.0000	0.7619	1.0000	0.0952	0.0000	85
1989	SRKW	1.0000	1.0000	1.0000	1.0000	0.8571	1.0000	1.0000	0.0500	0.0556	83
1990	SRKW	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	0.2500	0.0000	87
1991	SRKW	0.7500	0.9444	1.0000	1.0000	1.0000	1.0000	0.9500	0.1000	0.1081	91
1992	SRKW	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	0.1111	0.0500	91
1993	SRKW	0.8333	0.9510	0.8750	0.9524	1.0000	1.0000	1.0000	0.2222	0.0952	97
1994	SRKW	1.0000	1.0000	1.0000	1.0000	1.0000	0.8571	0.7727	0.1000	0.0000	94
1995	SRKW	1.0000	1.0000	1.0000	0.8750	1.0000	0.8333	0.9000	0.1818	0.1143	96
1996	SRKW	1.0000	1.0000	1.0000	0.9157	0.6250	1.0000	0.9000	0.1667	0.0667	97
1997	SRKW	NA	0.9438	1.0000	1.0000	1.0000	1.0000	0.7500	0.0000	0.0000	91
1998	SRKW	1.0000	0.9405	0.9000	0.9537	1.0000	1.0000	0.6667	0.0833	0.0000	89
1999	SRKW	0.3333	1.0000	0.9550	0.8083	1.0000	1.0000	0.9286	0.1200	0.0000	85
2000	SRKW	0.6667	1.0000	1.0000	0.8571	1.0000	0.9000	0.5714	0.1200	0.0000	82
2001	SRKW	0.6667	1.0000	0.9750	1.0000	1.0000	1.0000	1.0000	0.1702	0.0000	80
2002	SRKW	1.0000	1.0000	1.0000	1.0000	0.8000	1.0000	0.8000	0.0000	0.0800	80
2003	SRKW	0.8333	1.0000	1.0000	1.0000	0.7778	1.0000	1.0000	0.2273	0.0769	84
2004	SRKW	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	0.0435	0.0769	84
2005	SRKW	0.7143	0.7857	1.0000	1.0000	0.8750	1.0000	1.0000	0.1667	0.3077	91
2006	SRKW	0.3333	1.0000	0.9545	0.9375	1.0000	0.9688	1.0000	0.1250	0.0000	89
2007	SRKW	1.0000	0.9714	1.0000	1.0000	0.7500	1.0000	1.0000	0.0526	0.1250	87
2008	SRKW	0.3333	1.0000	0.9697	0.9750	0.8333	1.0000	1.0000	0.0000	0.1250	88
2009	SRKW	1.0000	1.0000	1.0000	0.9375	0.9167	1.0000	0.6667	0.0556	0.1290	87
2010	SRKW	0.8333	1.0000	1.0000	1.0000	0.8333	0.9286	0.6000	0.2632	0.2000	88
2011	SRKW	NA	NA	NA	NA	NA	NA	NA	0.0526	0.0667	88
1987	NRKW	1.0000	0.9931	1.0000	0.9702	0.7857	1.0000	1.0000	0.2368	0.0833	177
1988	NRKW	0.8571	0.9926	1.0000	0.8821	0.8750	1.0000	1.0000	0.1647	0.0000	182
1989	NRKW	1.0000	0.9990	1.0000	1.0000	1.0000	1.0000	0.9744	0.0870	0.1277	185
1990	NRKW	1.0000	0.9875	1.0000	0.9484	0.8571	0.9484	0.8974	0.1489	0.1200	194
1991	NRKW	0.9833	0.9899	0.9917	0.9872	0.9524	1.0000	1.0000	0.1443	0.1333	197
1992	NRKW	1.0000	0.9410	0.9900	1.0000	0.9125	0.9444	0.9099	0.1176	0.0909	203
1993	NRKW	0.9500	0.9726	1.0000	0.9904	0.6238	1.0000	0.9589	0.0926	0.0000	200
1994	NRKW	1.0000	0.9609	1.0000	0.9694	0.9673	1.0000	0.9952	0.1622	0.1481	207
1995	NRKW	0.8571	0.9721	1.0000	0.9881	0.8242	1.0000	0.9853	0.0877	0.1000	210
1996	NRKW	0.8750	0.9694	0.9664	0.9857	0.7148	0.9991	0.9144	0.1152	0.0494	213
1997	NRKW	0.8462	0.9708	0.9895	0.9852	0.9391	0.9990	0.8087	0.2062	0.0476	218
1998	NRKW	1.0000	0.9417	0.9893	0.9775	0.8738	0.9330	0.8000	0.1203	0.0513	215
1999	NRKW	1.0000	0.9830	0.9707	0.9793	0.6896	0.9796	0.7731	0.1131	0.1714	215
2000	NRKW	0.6667	0.9223	0.9700	0.9667	0.8750	0.9417	0.8196	0.0775	0.0588	209
2001	NRKW	0.8750	0.9694	0.9867	1.0000	1.0000	0.9890	0.9375	0.1156	0.0500	201
2002	NRKW	0.9000	0.9709	1.0000	1.0000	1.0000	0.9444	0.9412	0.1186	0.1364	204
2003	NRKW	1.0000	0.9946	1.0000	1.0000	0.9375	1.0000	1.0000	0.0781	0.1333	205
2004	NRKW	0.9714	0.9854	1.0000	0.9861	0.8750	1.0000	1.0000	0.2015	0.2143	222
2005	NRKW	0.8750	0.9441	0.9690	0.9815	0.7500	0.9977	0.9211	0.1976	0.1250	236
2006	NRKW	0.9333	0.9740	0.9835	1.0000	1.0000	0.9429	0.9825	0.2180	0.0984	240
2007	NRKW	0.8462	0.9842	0.9728	1.0000	1.0000	0.9167	0.9750	0.1686	0.1000	246
2008	NRKW	0.7647	0.9969	0.9932	0.9889	0.7500	0.9697	0.8254	0.1770	0.1613	256
2009	NRKW	1.0000	0.9783	0.9926	1.0000	1.0000	0.9621	0.7895	0.1443	0.1250	258
2010	NRKW	0.9231	0.9767	0.9709	0.9967	1.0000	0.9818	0.9792	0.1505	0.1135	264
2011	NRKW	NA	NA	NA	NA	NA	NA	NA	0.1139	0.0811	268

Appendix 6. Glossary of Chinook abundance definitions by stock aggregate, abundance type, time lag (5YA: 5-year running average), and hypothesis (SR: Southern Resident Killer Whale; NR: Northern Resident Killer Whale).

Time series	Stock or stock aggregate	Abundance type	Time lag	SR Hypothesis	NR Hypothesis
FE_TR_0	Fraser Early (Spring and Summer)	Terminal run	0	1a	2b
FE_TR_1	Fraser Early (Spring and Summer)	Terminal run	1	1a	2b
FE_TR_2	Fraser Early (Spring and Summer)	Terminal run	2	1a	2b
FE_TR_5YA	Fraser Early (Spring and Summer)	Terminal run	5YA	1a	2b
FE2_TR_0	Fraser Early (Spring)	Terminal run	0	1a	2b
FE2_TR_1	Fraser Early (Spring)	Terminal run	1	1a	2b
FE2_TR_2	Fraser Early (Spring)	Terminal run	2	1a	2b
FE2_TR_5YA	Fraser Early (Spring)	Terminal run	5YA	1a	2b
FE3_TR_0	Fraser Early (Summer)	Terminal run	0	1a	2b
FE3_TR_1	Fraser Early (Summer)	Terminal run	1	1a	2b
FE3_TR_2	Fraser Early (Summer)	Terminal run	2	1a	2b
FE3_TR_5YA	Fraser Early (Summer)	Terminal run	5YA	1a	2b
PS_TR_0	Puget Sound (Summer and Fall)	Terminal run	0	1a	2b
PS_TR_1	Puget Sound (Summer and Fall)	Terminal run	1	1a	2b
PS_TR_2	Puget Sound (Summer and Fall)	Terminal run	2	1a	2b
PS_TR_5YA	Puget Sound (Summer and Fall)	Terminal run	5YA	1a	2b
FEPS_TR_0	Fraser Early + Puget Sound	Terminal run	0	1a	2b
FEPS_TR_1	Fraser Early + Puget Sound	Terminal run	1	1a	2b
FEPS_TR_2	Fraser Early + Puget Sound	Terminal run	2	1a	2b
FEPS_TR_5YA	Fraser Early + Puget Sound	Terminal run	5YA	1a	2b
FL_TR_0	Fraser Late	Terminal run	0	1a	2b
FL_TR_1	Fraser Late	Terminal run	1	1a	2b
FL_TR_2	Fraser Late	Terminal run	2	1a	2b
FL_TR_5YA	Fraser Late	Terminal run	5YA	1a	2b
ALL1a_TR_0	Fraser Early+Puget Sound+Fraser Late	Terminal run	0	1a	2b
ALL1a_TR_1	Fraser Early+Puget Sound+Fraser Late	Terminal run	1	1a	2b
ALL1a_TR_2	Fraser Early+Puget Sound+Fraser Late	Terminal run	2	1a	2b
ALL1a_TR_5YA	Fraser Early+Puget Sound+Fraser Late	Terminal run	5YA	1a	2b
NBC_TR_0	Northern British Columbia (Areas 1-5)	Terminal run	0	NA	1b
NBC_TR_1	Northern British Columbia (Areas 1-5)	Terminal run	1	NA	1b
NBC_TR_2	Northern British Columbia (Areas 1-5)	Terminal run	2	NA	1b
NBC_TR_5YA	Northern British Columbia (Areas 1-5)	Terminal run	5YA	NA	1b
CBC_TR_0	Central British Columbia (Areas 6-10)	Terminal run	0	NA	1b
CBC_TR_1	Central British Columbia (Areas 6-10)	Terminal run	1	NA	1b
CBC_TR_2	Central British Columbia (Areas 6-10)	Terminal run	2	NA	1b
CBC_TR_5YA	Central British Columbia (Areas 6-10)	Terminal run	5YA	NA	1b
WCVI_TR_0	West Coast Vancouver Island	Terminal run	0	2a	1b
WCVI_TR_1	West Coast Vancouver Island	Terminal run	1	2a	1b
WCVI_TR_2	West Coast Vancouver Island	Terminal run	2	2a	1b
WCVI_TR_5YA	West Coast Vancouver Island	Terminal run	5YA	2a	1b
UGS_TR_0	Upper Georgia Strait	Terminal run	0	NA	1b
UGS_TR_1	Upper Georgia Strait	Terminal run	1	NA	1b
UGS_TR_2	Upper Georgia Strait	Terminal run	2	NA	1b
UGS_TR_5YA	Upper Georgia Strait	Terminal run	5YA	NA	1b
LGS_TR_0	Lower Georgia Strait	Terminal run	0	NA	1b
LGS_TR_1	Lower Georgia Strait	Terminal run	1	NA	1b
LGS_TR_2	Lower Georgia Strait	Terminal run	2	NA	1b
LGS_TR_5YA	Lower Georgia Strait	Terminal run	5YA	NA	1b
ALL1b_TR_0	NBC+CBC+WCVI+UGS+LGS	Terminal run	0	NA	1b
ALL1b_TR_1	NBC+CBC+WCVI+UGS+LGS	Terminal run	1	NA	1b
ALL1b_TR_2	NBC+CBC+WCVI+UGS+LGS	Terminal run	2	NA	1b
ALL1b_TR_5YA	NBC+CBC+WCVI+UGS+LGS	Terminal run	5YA	NA	1b
FE_OA_0	Fraser Early	Ocean Abundance	0	NA	1b
FE_OA_1	Fraser Early	Ocean Abundance	1	NA	1b
FE_OA_2	Fraser Early	Ocean Abundance	2	NA	1b
FE_OA_5YA	Fraser Early	Ocean Abundance	5YA	NA	1b
PS_OA_0	Puget Sound	Ocean Abundance	0	2a	1b
PS_OA_1	Puget Sound	Ocean Abundance	1	2a	1b
PS_OA_2	Puget Sound	Ocean Abundance	2	2a	1b
PS_OA_5YA	Puget Sound	Ocean Abundance	5YA	2a	1b

URB_OA_0	Columbia UpRiver Brights	Ocean Abundance	0	2a	1b
URB_OA_1	Columbia UpRiver Brights	Ocean Abundance	1	2a	1b
URB_OA_2	Columbia UpRiver Brights	Ocean Abundance	2	2a	1b
URB_OA_5YA	Columbia UpRiver Brights	Ocean Abundance	5YA	2a	1b
ALL1b_OA_0	Fraser Early+Puget Sound+Columbia UpRiver Brights	Ocean Abundance	0	NA	1b
ALL1b_OA_1	Fraser Early+Puget Sound+Columbia UpRiver Brights	Ocean Abundance	1	NA	1b
ALL1b_OA_2	Fraser Early+Puget Sound+Columbia UpRiver Brights	Ocean Abundance	2	NA	1b
ALL1b_OA_5YA	Fraser Early+Puget Sound+Columbia UpRiver Brights	Ocean Abundance	5YA	NA	1b
SF_TR_0	Sacramento Fall	Terminal run	0	2a	NA
SF_TR_1	Sacramento Fall	Terminal run	1	2a	NA
SF_TR_2	Sacramento Fall	Terminal run	2	2a	NA
SF_TR_5YA	Sacramento Fall	Terminal run	5YA	2a	NA
KLF_TR_0	Klamath Fall	Terminal run	0	2a	NA
KLF_TR_1	Klamath Fall	Terminal run	1	2a	NA
KLF_TR_2	Klamath Fall	Terminal run	2	2a	NA
KLF_TR_5YA	Klamath Fall	Terminal run	5YA	2a	NA
COLf_TR_0	Columbia Fall (UpRiver Brights+ Tule)	Terminal run	0	2a	2b
COLf_TR_1	Columbia Fall (UpRiver Brights+ Tule)	Terminal run	1	2a	2b
COLf_TR_2	Columbia Fall (UpRiver Brights+ Tule)	Terminal run	2	2a	2b
COLf_TR_5YA	Columbia Fall (UpRiver Brights+ Tule)	Terminal run	5YA	2a	2b
COLs_TR_0	Columbia Spring/Summer	Terminal run	0	2a	2b
COLs_TR_1	Columbia Spring/Summer	Terminal run	1	2a	2b
COLs_TR_2	Columbia Spring/Summer	Terminal run	2	2a	2b
COLs_TR_5YA	Columbia Spring/Summer	Terminal run	5YA	2a	2b
OC_TR_0	Oregon Coastal	Terminal run	0	2a	2b
OC_TR_1	Oregon Coastal	Terminal run	1	2a	2b
OC_TR_2	Oregon Coastal	Terminal run	2	2a	2b
OC_TR_5YA	Oregon Coastal	Terminal run	5YA	2a	2b
ALL2a_TR_0	SF+KLF+COLf+COLs+OC+WCVI	Terminal run	0	2a	NA
ALL2a_TR_1	SF+KLF+COLf+COLs+OC+WCVI	Terminal run	1	2a	NA
ALL2a_TR_2	SF+KLF+COLf+COLs+OC+WCVI	Terminal run	2	2a	NA
ALL2a_TR_5YA	SF+KLF+COLf+COLs+OC+WCVI	Terminal run	5YA	2a	NA
CW2a_TR_0	Coastwide (excluding SEAK, NBC and CBC)	Terminal run	0	2a	NA
CW2a_TR_1	Coastwide (excluding SEAK, NBC and CBC)	Terminal run	1	2a	NA
CW2a_TR_2	Coastwide (excluding SEAK, NBC and CBC)	Terminal run	2	2a	NA
CW2a_TR_5YA	Coastwide (excluding SEAK, NBC and CBC)	Terminal run	5YA	2a	NA
WCVI_OA_0	West Coast Vancouver Island	Ocean Abundance	0	2a	2b
WCVI_OA_1	West Coast Vancouver Island	Ocean Abundance	1	2a	2b
WCVI_OA_2	West Coast Vancouver Island	Ocean Abundance	2	2a	2b
WCVI_OA_5YA	West Coast Vancouver Island	Ocean Abundance	5YA	2a	2b
FL_OA_0	Fraser Late	Ocean Abundance	0	2a	2b
FL_OA_1	Fraser Late	Ocean Abundance	1	2a	2b
FL_OA_2	Fraser Late	Ocean Abundance	2	2a	2b
FL_OA_5YA	Fraser Late	Ocean Abundance	5YA	2a	2b
OC_OA_0	Oregon Coastal	Ocean Abundance	0	2a	2b
OC_OA_1	Oregon Coastal	Ocean Abundance	1	2a	2b
OC_OA_2	Oregon Coastal	Ocean Abundance	2	2a	2b
OC_OA_5YA	Oregon Coastal	Ocean Abundance	5YA	2a	2b
ALL2a_OA_0	WCVI+URB+FL+OC+PS	Ocean Abundance	0	2a	NA
ALL2a_OA_1	WCVI+URB+FL+OC+PS	Ocean Abundance	1	2a	NA
ALL2a_OA_2	WCVI+URB+FL+OC+PS	Ocean Abundance	2	2a	NA
ALL2a_OA_5YA	WCVI+URB+FL+OC+PS	Ocean Abundance	5YA	2a	NA
CW_OA_0	Coastwide (excluding SEAK)	Ocean Abundance	0	2a	2b
CW_OA_1	Coastwide (excluding SEAK)	Ocean Abundance	1	2a	2b
CW_OA_2	Coastwide (excluding SEAK)	Ocean Abundance	2	2a	2b
CW_OA_5YA	Coastwide (excluding SEAK)	Ocean Abundance	5YA	2a	2b
ALL2b_TR_0	FE+PS+FL+COLf+COLs+OC	Terminal run	0	NA	2b
ALL2b_TR_1	FE+PS+FL+COLf+COLs+OC	Terminal run	1	NA	2b
ALL2b_TR_2	FE+PS+FL+COLf+COLs+OC	Terminal run	2	NA	2b
ALL2b_TR_5YA	FE+PS+FL+COLf+COLs+OC	Terminal run	5YA	NA	2b
ALL2b_OA_0	WCVI+FL+OC	Ocean Abundance	0	NA	2b
ALL2b_OA_1	WCVI+FL+OC	Ocean Abundance	1	NA	2b
ALL2b_OA_2	WCVI+FL+OC	Ocean Abundance	2	NA	2b
ALL2b_OA_5YA	WCVI+FL+OC	Ocean Abundance	5YA	NA	2b
CW2b_TR_0	Coastwide (excluding Sacramento Fall and Klamath Fall)	Terminal run	0	NA	2b
CW2b_TR_1	Coastwide (excluding Sacramento Fall and Klamath Fall)	Terminal run	1	NA	2b
CW2b_TR_2	Coastwide (excluding Sacramento Fall and Klamath Fall)	Terminal run	2	NA	2b
CW2b_TR_5YA	Coastwide (excluding Sacramento Fall and Klamath Fall)	Terminal run	5YA	NA	2b

Appendix 7. Glossary of Chum salmon terminal run definitions by stock aggregate and time lag. Northern/Central BC includes both summer and fall run types. Southern BC Chum includes only fall run type.

Time series	Stock aggregate	Time lag
NBC_0	Northern/Central Brittish Columbia	0
NBC_1	Northern/Central Brittish Columbia	1
NBC_2	Northern/Central Brittish Columbia	2
SBC_0	Southern British Columbia	0
SBC_1	Southern British Columbia	1
SBC_2	Southern British Columbia	2
WSH_Fa_0	Washington Fall	0
WSH_Fa_1	Washington Fall	1
WSH_Fa_2	Washington Fall	2
WSH_Tot_0	Washington Summer, Fall and Winter	0
WSH_Tot_1	Washington Summer, Fall and Winter	1
WSH_Tot_2	Washington Summer, Fall and Winter	2
SBCWSH__Fa_0	Southern BC and Washington Fall	0
SBCWSH__Fa_1	Southern BC and Washington Fall	1
SBCWSH__Fa_2	Southern BC and Washington Fall	2
SBCWSH_Tot_0	Southern BC and Washington Su/Fa/Wi	0
SBCWSH_Tot_1	Southern BC and Washington Su/Fa/Wi	1
SBCWSH_Tot_2	Southern BC and Washington Su/Fa/Wi	2

Appendix 8. R code for the study of RKW demography, evaluation of interactions with Chinook abundance, and exploration of effects of Chinook fishing scenarios on RKW population viability.

A 8.1. R-code modules

```
KW R-CODE MODULES
FUNCTIONS : SOURCE (MONSTERCAVE)
1.   SETTINGS
2.   DEMOGRAPHIC DATA PROCESSING
3.   ESTIMATING SURVIVALS & FECUNDITIES
4.   DETERMINISTIC MATRIX ELEMENTS AND MEAN MATRIX
5.   ALIVE IN LAST YEAR
6.   BASIC MATRIX ESTIMATES
7.   DETERMINISTIC VITAL RATE ELASTICITY AND SENSITIVITY
8.   STOCHASTIC VITAL RATE ELASTICITY AND SENSITIVITY
9.   CHINOOK REGRESSION MODELS
10. NORMAL ERROR STRUCTURE TESTS
11. ELASTICITIES OF INTERACTIONS- MATRIX PERT.
12. PLOTTING BETA DIAGNOSTICS AND AIC
13. RESTROSPECTIVE ANALYSES
14. STOCHASTIC POPULATION GROWTH
15. PROJECTING POPULATION SIZE
16. FISHING SCENARIOS - TERMINAL RUN
17. FISHING SCENARIOS - OCEAN ABUNDANCE
18. REGRESSIONS KW ABUNDANCE ~ CHINOOK ABUNDANCE
19. CHUM MULTIPLE REGRESSIONS
20. ELASTICITY OF INTERACTION FOR CHUM MR


#<<<@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@>>>
#<<<@@@@@@@@@@@@@@@@@@@@@@@@@@@        1.SETTINGS        @@@@@@@@@@@@@@@@@@@@@@@@@@@>>>
#<<<@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@>>>
getwd()    #Where are we working exactly?
#setwd()  #Uncomment(#) to change workfolder, if needed. E.G.
setwd("C:/KillerWhales/R_code)


#Defines the population to be used in the analyses: Northern (NRKW) or Southern
(SRKW)
Population<- c('SRKW')


#Period for Demographic analyses. Note: Double check IID periods is this  setting
is changed (earliest year is 1973)
Period<- c(1987,2011)


#Seed for Stochastic simulations
set.seed= pi*pi


#Select "YES" to install packages if it is the first time running the code
install_pcks = "NO"


#Options to control R output
options(width = 200, digits = 5, prompt = ">", continue = "+")


#File with Functions
source('MonsterCave.r')


#Recommended Tinn-R version:
#<<< http://sourceforge.net/projects/tinn-r/files/Tinn-R%20setup/1.19.1.9/ >>>


#@@@@@@@@@@@@@@@@@        Defining  Age Categories        @@@@@@@@@@@@@@@@@@@
```

```r
#These age categories can be changed according to the user needs, except for
#Juveniles
#Starting age for young males and females must be 10. Age groups must be
# continuous
#(e.g. no gaps in ages). See section 2.2 Killer Whale matrix population modeling
# of the report for more information.

CalfAges <- c(0,1)          #   calves age range                   (default 0 to
1)
JuvsAges <- c(2,9)          #   juveniles age range                (default 2 to
9)
YRFemAges<- c(10,30)        #   young reproductive females age range(default 10 to
30)
ORFemAges<- c(31,50)        #   old reproductive females age range  (default 31 to
50)
PRFemAges<- c(51,200)       #   post reproductive females age range (default 51 to
200)
YMMalAges<- c(10,21)        #   young mature males                  (default 10 to
21)
OMMalAges<- c(22,200)       #   old mature males                    (default 22 to
200)

#_____
#-----------------------------------------------------------------------------

#<<<@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@>>>
#<<<@@@@@@@@@@@                2. DEMOGRAPHIC DATA PROCESSING         @@@@@@@@@@@>>>
#<<<@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@>>>
#This section inputs demographic data of KW and estimates counts by year and
# stageaccording to the selection criteria from the age categories. See section
# 2.2 of the report for more information.

Cat2Names<-
c('calve','Juvenil','YoungRFem','OldRFem','PostRFem','YoungMale','OldMale')
#_____
#-----------------------------------------------------------------------------

KWdata<-
read.table(paste(getwd(),'/','R_Inputs','/',Population,'_R.csv',sep=""),header=T,
sep=",")
KWdata<-  subset(KWdata, Year >= Period[1] & Year <= Period[2])

#------ STAGES ------
Females<- subset(KWdata, Cat1=='Female')
Males  <- subset(KWdata, Cat1=='Male')

calvs<- subset(subset(KWdata, Cat1 == 'Juv')
                ,Age >= CalfAges[1] & Age <= CalfAges[2])
Cat2<- rep(Cat2Names[1],length(calvs[,1]))
calvs<- cbind(calvs,Cat2)

juvsC<- subset(subset(KWdata, Cat1 == 'Juv')
                ,Age >= JuvsAges[1] & Age <= JuvsAges[2])
Cat2<- rep(Cat2Names[2],length(juvsC[,1]))
juvsC<- cbind(juvsC,Cat2)

juvs<-  subset(KWdata, Cat1 == 'Juv')
Cat2<- rep(Cat2Names[2],length(juvs[,1]))
juvs<- cbind(juvs,Cat2)

YRFem<- subset(subset(KWdata, Cat1 == 'Female')
                ,Age >= YRFemAges[1] & Age <= YRFemAges[2])
Cat2<- rep(Cat2Names[3],length(YRFem[,1]))
YRFem<- cbind(YRFem,Cat2)
```

```r
ORFem<- subset(subset(KWdata, Cat1 == 'Female')
                ,Age >= ORFemAges[1] & Age <= ORFemAges[2])
Cat2<- rep(Cat2Names[4],length(ORFem[,1]))
ORFem<- cbind(ORFem,Cat2)

PRFem<- subset(subset(KWdata, Cat1 == 'Female')
                ,Age >= PRFemAges[1])
Cat2<- rep(Cat2Names[5],length(PRFem[,1]))
PRFem<- cbind(PRFem,Cat2)

YMMal<- subset(subset(KWdata, Cat1 == 'Male')
                ,Age >= YMMalAges[1] & Age <= YMMalAges[2])
Cat2<- rep(Cat2Names[6],length(YMMal[,1]))
YMMal<- cbind(YMMal,Cat2)

OMMal<- subset(subset(KWdata, Cat1 == 'Male')
                ,Age >= OMMalAges[1] & Age <= OMMalAges[2])
Cat2<- rep(Cat2Names[7],length(OMMal[,1]))
OMMal<- cbind(OMMal,Cat2)

Count_Calves <- CountFun(calvs$Count,calvs$Year)
Count_Juvs   <- CountFun(juvsC$Count,juvsC$Year)
Count_YRFem  <- CountFun(YRFem$Count,YRFem$Year)
Count_ORFem  <- CountFun(ORFem$Count,ORFem$Year)
Count_PRFem  <- CountFun(PRFem$Count,PRFem$Year)
Count_YMMal  <- CountFun(YMMal$Count,YMMal$Year)
Count_OMMal  <- CountFun(OMMal$Count,OMMal$Year)

df.abundances<- as.data.frame(cbind(seq(Period[1],Period[2],1),Count_Calves,
    Count_Juvs,Count_YRFem,Count_ORFem,Count_PRFem,Count_YMMal,Count_OMMal))
colnames(df.abundances)<- c("Year",Cat2Names)

Total_KW<- apply(df.abundances[-1],1,sum)
df.abundances<- cbind(df.abundances,Total_KW)

write.table(df.abundances, file = paste('Counts by
Year',Population[1],Period[1],"-",Period[2],'.csv'), sep=',', quote = FALSE,
row.names = FALSE)

#<<<@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@>>>
#<<<@@@@@@@@@@@@@@@@@  3.ESTIMATING SURVIVALS & FECUNDITIES   @@@@@@@@@@@@@@@>>>
#<<<@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@>>>
#This section estimates the KW survivals and fecundities (Vital rates) for the
#different age categories. See section 2.2 Killer Whale matrix population
# modeling of the report.

#_____
#--------------------------------------------------------------------------------

#************************         Juveniles   ******************************
SurtempJ<- 0.
for (j in 1:length(juvs$Year)){
    SurtempJ [j]<- (1/juvs$Count[j])*juvs$Count[j+YRFemAges[1]]
    }
SurtempJ <- c(NA,SurtempJ[-length(juvs$Year)])

Temp1     <- subset(rbind(YRFem,YMMal), Age == 10)
F_yearM_F <- factor(Temp1$Year)
factor.juvs <- tapply(Temp1$Count,F_yearM_F,sum)
Countjuvs= as.integer(factor.juvs)

Temp1df<- data.frame(Year= seq(min(Temp1$Year),max(Temp1$Year),1),
Age=rep(10,length(Countjuvs)),
        Count=Countjuvs, Offspring=rep(NA,length(Countjuvs)),
Cat1=rep('M+F',length(Countjuvs)),Cat2=rep('Juvs2',length(Countjuvs)))
```

```
Temp2df<- rbind(subset(juvs, Age == JuvsAges[2]),Temp1df)

Surtemp10s<- 0.
for (k in 1:length(Temp2df$Year)){
     Surtemp10s[k]<- (1/Temp2df$Count[k])*Temp2df$Count[k+length(Temp1df$Year)+1]
     }
Surtemp10s<-Surtemp10s[-seq((length(Females[Females$Age==YRFemAges[1],]$Year)+1),
                     (length(Females[Females$Age==YRFemAges[1],]$Year)*2),1)]

Dummy5<- cbind(juvs,SurtempJ) [cbind(juvs,SurtempJ) $Age ==1,]
Dummy5$SurtempJ<-Surtemp10s
Dummy6<- cbind(juvs,SurtempJ) [!(cbind(juvs,SurtempJ) $Age==1),]
Dummy7<-rbind(Dummy5,Dummy6)
Dummy7$Age<-ifelse(Dummy7$Age==1, 10,Dummy7$Age)
Dummy8 <- Dummy7[order(Dummy7$Year,Dummy7$Age),]
Dummy9<- subset(Dummy8, Age>=JuvsAges[1]+1 & Age <=JuvsAges[2]+1)
Dummy10<- subset(Dummy9, Dummy9$SurtempJ!= "NaN")
F_SurvJuvsYear <- factor(Dummy10$Year)
Juvenile_Survival <- as.numeric(tapply(Dummy10$SurtempJ,F_SurvJuvsYear, mean))


#*************************         Calves      *********************************

Dummy11<- subset(Dummy8, Age==JuvsAges[1])
Dummy11<- subset(Dummy11, Dummy11$SurtempJ!= "NA")
Calf_Survival<- Dummy11$SurtempJ

#*************************         Females     *********************************
#This procedure is different from the one above used to estimate the survival of
#juveniles.
#The main reason is that it uses a four loop plus a index (IND) which allows
# adding a year to the max age each year. For example, if in 1990 the max age of
# femaleswas 56, in 1991 the max age will be 57. The procedure also allows
# estimating all survivals of the different groups of females at once, rather
# than one at the time.

IND<- rep(0:(length(Females[Females$Age==YRFemAges[1],]$Year)-
1),length(Females[Females$Year==min(Females$Year),]$Year):length(Females[Females$
Year==max(Females$Year),]$Year))

SurFem<-0.
for (j in 1:length(Females$Year)){
    SurFem [j]<- (1/Females$Count[j])*Females$Count[j+(max(Females[Females$Year==
min(Females$Year),]$Age) -YRFemAges[1]+2+IND[j])]
    }

FemaleSurvs<- as.data.frame(cbind(Females,SurFem))
FemaleSurvs<- subset(FemaleSurvs, FemaleSurvs$SurFem!= "NaN")

YRFSurvs<- subset(FemaleSurvs, Age >= YRFemAges[1] & Age <=YRFemAges[2])
F_SurvYRFYear <- factor(YRFSurvs$Year)
F1_Survival <- as.numeric(tapply(YRFSurvs$SurFem,F_SurvYRFYear, mean))

ORFSurvs<- subset(FemaleSurvs, Age >= ORFemAges[1] & Age <=ORFemAges[2])
F_SurvORFYear <- factor(ORFSurvs$Year)
F2_Survival <- as.numeric(tapply(ORFSurvs$SurFem,F_SurvORFYear, mean))

PRFSurvs<- subset(FemaleSurvs, Age >= PRFemAges[1] & Age <=PRFemAges[2])
F_SurvPRFYear <- factor(PRFSurvs$Year)
F3_Survival <- as.numeric(tapply(PRFSurvs$SurFem,F_SurvPRFYear, mean))


#*************************         Males       *********************************
```

```
INDm<- rep(0:(length(Males[Males$Age==YMMalAges[1],]$Year)-
1),length(Males[Males$Year==min(Males$Year),]$Year):length(Males[Males$Year==max(
Males$Year),]$Year))

SurMal<-0.
for (j in 1:length(Males$Year)){
    SurMal [j]<- (1/Males$Count[j])*Males$Count[j+(max(Males[Males$Year==
min(Males$Year),]$Age)-YMMalAges[1]+2+INDm[j])]
    }

Malesurvs<- as.data.frame(cbind(Males,SurMal))
Malesurvs<- subset(Malesurvs, Malesurvs$SurMal!= "NaN")

YMMSurvs<- subset(Malesurvs, Age >= YMMalAges[1] & Age <=YMMalAges[2])
F_SurvYMMYear <- factor(YMMSurvs$Year)
M1_Survival <- as.numeric(tapply(YMMSurvs$SurMal,F_SurvYMMYear, mean))


OMMSurvs<- subset(Malesurvs, Age >= OMMalAges[1] & Age <=OMMalAges[2])
F_SurvOMMYear <- factor(OMMSurvs$Year)
M2_Survival <- as.numeric(tapply(OMMSurvs$SurMal,F_SurvOMMYear, mean))


Year<- seq(min(KWdata$Year),max(KWdata$Year)-1,1)
SurvTable<- cbind(Year, Calf_Survival,
Juvenile_Survival,F1_Survival,F2_Survival,F3_Survival,M1_Survival, M2_Survival)


F_yearYRFem <- factor(YRFem$Year)
Offs.YRFem <- as.numeric(tapply(YRFem$Offspring , F_yearYRFem, sum))
Count.YRFem <- as.numeric(tapply(YRFem$Count, F_yearYRFem, sum))
F1_Fecundity<- Offs.YRFem/Count.YRFem

F_yearORFem <- factor(ORFem$Year)
Offs.ORFem <- as.numeric(tapply(ORFem$Offspring , F_yearORFem, sum))
Count.ORFem <- as.numeric(tapply(ORFem$Count, F_yearORFem, sum))
F2_Fecundity<- Offs.ORFem/Count.ORFem

YearOff<- seq(min(KWdata$Year),max(KWdata$Year),1)
OffspringTable<- cbind(YearOff, F1_Fecundity,F2_Fecundity )

SurvTable
OffspringTable

SurvTable2<- rbind(SurvTable[,-1],rep(NA,7))
OffsprTable2<-OffspringTable[,-1]

VR_orig<- cbind(SurvTable2,OffsprTable2)
write.table(cbind(OffspringTable[,1],VR_orig), file = paste('Vital rates
estimates',Population[1],Period[1],"-",Period[2],'.csv'), sep=',', quote = FALSE,
row.names = FALSE)


#<<<@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@>>>
#<<<@@@@@@@   4.DETERMINISTIC MATRIX ELEMENTS AND MEAN MATRIX       @@@@@@@@@@>>>
#<<<@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@>>>
#This section produces a series of matrix elements constructed from the
#vital rates estimated previously. See section 2.2 Killer Whale matrix population
#modeling of the report.


SurvSigma<- as.numeric(colMeans(SurvTable, na.rm = TRUE, dims = 1))[-1]
MaxAge<-c(CalfAges[2],JuvsAges[2], YRFemAges[2],ORFemAges[2],
max(PRFem[PRFem$Count>0,]$Age),YMMalAges[2],max(OMMal[OMMal$Count>0,]$Age))
SurvGamma<-c(1, 1/(MaxAge[2]-MaxAge[1]), 1/(MaxAge[3]-MaxAge[2]),  1/(MaxAge[4]-
```

```r
MaxAge[3]),  1/(MaxAge[5]-MaxAge[4]), 1/(MaxAge[6]-MaxAge[2]),1/(MaxAge[7]-
MaxAge[6]) )

Temp1.Mal<-Temp1[Temp1$Cat1=='Male',]
Temp1.Fem<-Temp1[Temp1$Cat1=='Female',]
Perc.Mal<-Temp1.Mal[3]/(Temp1.Mal[3]+Temp1.Fem[3])
Perc.Fem<-Temp1.Fem[3]/(Temp1.Mal[3]+Temp1.Fem[3])
Mean.Perc.Mal<- colMeans(Perc.Mal,na.rm = TRUE);Var.Perc.Mal<- var(Perc.Mal,na.rm
= TRUE)
Mean.Perc.Fem<- colMeans(Perc.Fem,na.rm = TRUE);Var.Perc.Fem<- var(Perc.Fem,na.rm
= TRUE)

Mean.Ratio.Mal<- sum(Temp1.Mal[3])/sum(Temp1.Mal[3]+Temp1.Fem[3])
Mean.Ratio.Fem<- sum(Temp1.Fem[3])/sum(Temp1.Mal[3]+Temp1.Fem[3])

PercentPhi<- c(NaN,NaN,as.numeric(Mean.Ratio.Fem[1]),NaN,NaN,
as.numeric(Mean.Ratio.Mal[1]), NaN)
MuOffsp<- c(0,0,na.omit(mean(F1_Fecundity)),na.omit(mean(F2_Fecundity)),0,0,0)

VitalR<- rbind(SurvSigma,MaxAge,SurvGamma,PercentPhi,MuOffsp)

                          # <<< Matrix Elements>>>

P1=SurvSigma[1] *(1-SurvGamma[1])
P2=SurvSigma[2] *(1-SurvGamma[2])
P3=SurvSigma[3] *(1-SurvGamma[3])
P4=SurvSigma[4] *(1-SurvGamma[4])
P5=SurvSigma[5]
P6=SurvSigma[6] *(1-SurvGamma[6])
P7=SurvSigma[7]

G1<-SurvSigma[1]^0.5
G2f<-SurvSigma[2]*SurvGamma[2]*PercentPhi[3]
G3<-SurvSigma[3]*SurvGamma[3]
G4<-SurvSigma[4]*SurvGamma[4]
G2m<-SurvSigma[2]*SurvGamma[2]*PercentPhi[6]
G5<-SurvSigma[6]*SurvGamma[6]

#**************************     MEAN MATRIX        **************************

CalveMat<-c(0,G1,0,0,0,0,0)
JuvMat  <-c(G1*(((1+P2)*MuOffsp[2])+(G2f*MuOffsp[3]))/2, P2,G2f,0,0,G2m,0)
YoFemMat<-c(G1*(((1+P3)*MuOffsp[3])+(G3* MuOffsp[4]))/2, 0,P3,G3,0,0,0)
OlFemMat<-c(G1*(((1+P4)*MuOffsp[4])+(G4* MuOffsp[5]))/2, 0,0,P4,G4,0,0)
PRFemMat<-c(0,0,0,0,P5,0,0)
YoMalMat<-c(0,0,0,0,0,P6,G5)
OlMalMat<-c(0,0,0,0,0,0,P7)

MeanMat<-
as.matrix(cbind(CalveMat,JuvMat,YoFemMat,OlFemMat,PRFemMat,YoMalMat,OlMalMat))#,
dimnames = list(Cat2Names,Cat2Names),byrow = TRUE)
write.table(MeanMat, file = paste('MeanMatrix',Population[1],'.csv'), sep=',',
quote = FALSE, row.names = FALSE)
cat(paste('Mean Matrix',Population[1]),'(saved in working
folder)',"\n");print(MeanMat)

#<<<@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@>>>
#<<<@@@@@@@@@@@@@@@@@@         5.ALIVE IN LAST YEAR          @@@@@@@@@@@@@@@@>>>
#<<<@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@>>>

#This section estimates the percentage of individuals alive in a determined year
#(Year_Q) by year of birth. It determines how young or senile the population in
#a year is.

Year_Q <- Period[2]    # Year of the query, by default the last year in Period.
```

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```r
#It could be change e.g. 1987.

#_____
#--------------------------------------------------------------------------------
tempalive<- KWdata[KWdata$Year==Year_Q,]
F_Agetempalive<- factor(tempalive$Age)
tempalive2 <- as.numeric(tapply(tempalive$Count, F_Agetempalive, sum))
tempalive3<-tempalive2/sum(tempalive2)

Yearsback<- seq(Year_Q,Year_Q-length(tempalive3)+1,-1)
alive<- cbind(Yearsback,tempalive3*100)
colnames(alive)<-c('Year','Percentage')
write.table(alive, file =paste('Alive',Year_Q[1],Population[1],'.csv') , sep=',',
quote = FALSE, row.names = FALSE)

graphics.off()
pdf(paste('Alive',Year_Q[1],Population[1] ,'.pdf'),width=12,height=8)
plot(alive, type='h', lwd=2, main=paste('Percentage of individuals alive
in',Year_Q[1],'by year of birth'), ylim=c(0,10), ylab='percentage')
dev.off()


#<<<@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@>>>
#<<<@@@@@@@@@@@@@@@@@@@@@@@@@@  6.BASIC MATRIX ESTIMATES  @@@@@@@@@@@@@@@@@@@@@@@@>>>
#<<<@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@>>>
#This section estimates dominant lambda and other eigenvectors, the stable stage
#distribution (and population projection), and the damping ratio. See section
#2.5 of the report.

#<<<Prior Running the following modules, these R packages must be installed.
# Select "YES" from install all packages in settings. Every time a new R version
# is installed, packages need to be re-installed.>>>

Sims<- 1000              #Number of simulations  used for the population projection
#_____
#--------------------------------------------------------------------------------

if(install_pcks == "YES"){
install.packages("popbio")
install.packages("lattice")
install.packages("betareg")}

library(popbio)
library(lattice)
library(betareg)

#*********************     Estimating Eigen Vactors       ******************

eigenall (MeanMat)

#*********************        Population Projection        ******************

# Creating a projection Matrix

nlastYear<- c(
sum(calvs[calvs$Year==max(KWdata$Year),]$Count),
sum(juvs [ juvs$Year==max(KWdata$Year),]$Count)-
sum(calvs[calvs$Year==max(KWdata$Year),]$Count),
sum(YRFem[YRFem$Year==max(KWdata$Year),]$Count),
sum(ORFem[ORFem$Year==max(KWdata$Year),]$Count),
sum(PRFem[PRFem$Year==max(KWdata$Year),]$Count),
sum(YMMal[YMMal$Year==max(KWdata$Year),]$Count),
sum(OMMal[OMMal$Year==max(KWdata$Year),]$Count))

propLastYear<-nlastYear/sum(nlastYear)
```

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```
CountsLastyear<- data.frame(Cat2Names,nlastYear,propLastYear)

p.projection <- pop.projection(MeanMat, nlastYear, Sims)

CountsLastYearOrd <- CountsLastyear[order(CountsLastyear$nlastYear),]
StableStage<-p.projection$stage.vectors
Cat2Names->rownames(StableStage)

write.table(StableStage, file = paste('Stable State
Values',Population[1],Period[1],'-',Period[2],'.csv'), sep=',', quote = TRUE,
row.names = TRUE)
write.table(CountsLastYearOrd, file = paste('Counts and Proportions
T0',Population[1],Period[1],'-',Period[2],'.csv'), sep=',', quote = TRUE,
row.names = TRUE)

eigVals  <- eigen.analysis(MeanMat)
eigVals
Lambda1<- eigVals$lambda1

ResultsLambda<- eigenall (MeanMat)
DampTime10 <- log(10) / (log(Lambda1 / ResultsLambda$lambdas[2]))
DampTime10<- c("damping ratio'", round(DampTime10,0))

write.table(DampTime10, file = paste('Damping Time',Population[1],Period[1],'-
',Period[2],'.txt'), sep=',', quote = TRUE, col.names=FALSE, row.names = FALSE)
cat(paste('Damping time @ Z=10',Population[1]),'(Saved to
Folder)',"\n");print(DampTime10)

graphics.off()
pdf(paste('Stable Stage Projection',Population[1],Period[1],'-',Period[2]
,'.pdf'),width=8,height=8)
stage.vector.plot(StableStage,proportions=TRUE, legend.coords="topright",
        ylim=c(0,max(CountsLastYearOrd$propLastYear)+0.1), xlab="Years into the
future", xlim=c(-2, 50),
        ylab='proportion of total population', col=rainbow(7), main=paste("Stable
Stage Projection from",
        Population[1], Period[1],'-',Period[2]))
        text(5, y = CountsLastYearOrd$propLastYear, labels =
round(CountsLastYearOrd$nlastYear,0), col = 2, font = 2, cex=1)
        text(10, y = max(CountsLastYearOrd$propLastYear)+0.05, labels =
paste('Counts',Period[2]), col = 2, font = 2, cex=1)
dev.off()

#<<<@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@>>>
#<<<@@@@@     7. DETERMINISTIC VITAL RATE ELASTICITY AND SENSITIVITY     @@@@@>>>
#<<<@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@>>>
# This section estimates deterministic sensitivities of vital rates, and
# deterministic elasticities of vital rates. See section 2.5 Perturbation
# analysis of the report for more information.

#_____
#--------------------------------------------------------------------------------

#***************         Defining Vital Rates         ******************

MeansSigma<- as.numeric(colMeans(SurvTable, na.rm = TRUE, dims = 1))[-1]
VarsSigma<- as.numeric(apply(SurvTable, 2, var,na.rm = TRUE))[-1]

MeansMuOffsp<- c(0,0,mean(F1_Fecundity),mean(F2_Fecundity),0,0,0)
VarsMuOffsp<- c(0,0,var(F1_Fecundity),var(F2_Fecundity),0,0,0)

SummaryVrs<- data.frame(Cat2Names,MeansSigma,VarsSigma, MeansMuOffsp,
VarsMuOffsp)
names(SummaryVrs)<-  c('Category','Mean_Surv', 'Var_Surv', 'Mean_Offspr',
'Var_Offspr')
```

```r
write.table(SummaryVrs, file = paste('Stats by
Category',Population[1],Period[1],'-',Period[2],'.csv'), sep=',', quote = TRUE,
row.names = FALSE)

symsN<-
c('Ss1','Ss2','Ss3','Ss4','Ss5','Ss6','Ss7','Sg2','Sg3','Sg4','Sg6','Sp2','Sp3','
Sf3','Sf4')

Ss1 = SurvSigma[1]
Ss2 = SurvSigma[2]
Ss3 = SurvSigma[3]
Ss4 = SurvSigma[4]
Ss5 = SurvSigma[5]
Ss6 = SurvSigma[6]
Ss7 = SurvSigma[7]
Sg2 = SurvGamma [2]
Sg3 = SurvGamma [3]
Sg4 = SurvGamma [4]
Sg6 = SurvGamma [6]
Sp2 = PercentPhi[3]
Sp3 = PercentPhi[6]
Sf3 = MeansMuOffsp [3]
Sf4 = MeansMuOffsp [4]
MeanVR=c(Ss1,Ss2,Ss3,Ss4,Ss5,Ss6,Ss7,Sg2,Sg3,Sg4,Sg6,Sp2,Sp3,Sf3,Sf4)

#***********     Deterministic Elasticities of Vital Rates       *************

#Using POPbio fun vitalsens
KW.vr<- list(Ss1=Ss1 ,Ss2=Ss2 ,Ss3=Ss3 ,Ss4=Ss4 ,Ss5=Ss5 ,Ss6=Ss6, Ss7=Ss7
,Sg2=Sg2 ,Sg3=Sg3, Sg4=Sg4 ,Sg6=Sg6 ,Sp2=Sp2 ,Sp3=Sp3 ,Sf3=Sf3 ,Sf4=Sf4)

KW.el<- expression(
        0, (Ss1^0.5*(Ss2*Sg2*Sp2*Sf3))/2, (Ss1^0.5*(((1+(Ss3*(1-
Sg3)))*Sf3)+(Ss3*Sg3*Sf4)))/2,  (Ss1^0.5*((1+(Ss4*(1-Sg4)))*Sf4))/2, 0, 0, 0,
            Ss1^0.5, Ss2*(1-Sg2), 0, 0, 0, 0, 0,
        0, Ss2*Sg2*Sp2, Ss3*(1-Sg3), 0, 0, 0, 0,
        0, 0, Ss3*Sg3, Ss4*(1-Sg4), 0, 0, 0,
        0, 0, 0, Ss4*Sg4, Ss5, 0, 0,
        0, Ss2*Sg2*Sp3, 0, 0, 0, Ss6*(1-Sg6), 0,
        0, 0, 0, 0, 0, Ss6*Sg6, Ss7
        )

KW.mat<- matrix(c(
        0, (Ss1^0.5*(Ss2*Sg2*Sp2*Sf3))/2, (Ss1^0.5*(((1+(Ss3*(1-
Sg3)))*Sf3)+(Ss3*Sg3*Sf4)))/2,  (Ss1^0.5*((1+(Ss4*(1-Sg4)))*Sf4))/2, 0, 0, 0,
            Ss1^0.5, Ss2*(1-Sg2), 0, 0, 0, 0, 0,
        0, Ss2*Sg2*Sp2, Ss3*(1-Sg3), 0, 0, 0, 0,
        0, 0, Ss3*Sg3, Ss4*(1-Sg4), 0, 0, 0,
        0, 0, 0, Ss4*Sg4, Ss5, 0, 0,
        0, Ss2*Sg2*Sp3, 0, 0, 0, Ss6*(1-Sg6), 0,
        0, 0, 0, 0, 0, Ss6*Sg6, Ss7),
        nrow = 7, ncol = 7, byrow = TRUE
        )

KW.n<-length(KW.vr); vr<-seq(0,1,.1)
vrsen<-matrix(numeric(KW.n*length(vr)), ncol=KW.n, dimnames=list(vr,
names(KW.vr)))

for (h in 1:KW.n)
{
KW.vr2<-list(Ss1=Ss1 ,Ss2=Ss2 ,Ss3=Ss3  ,Ss4=Ss4 ,Ss5=Ss5 ,Ss6=Ss6 ,Ss7=Ss7
,Sg2=Sg2 ,Sg3=Sg3 ,Sg4=Sg4 ,Sg6=Sg6  ,Sp2=Sp2 ,Sp3=Sp3 ,Sf3=Sf3 ,Sf4=Sf4)
for (i in 1:length(vr)){
KW.vr2[[h]]<-vr[i]
A<-matrix(sapply(KW.el, eval,KW.vr2,NULL), nrow=sqrt(length(KW.el)), byrow=TRUE)
```

```r
vrsen[i,h] <- max(Re(eigen(A)$values))
}}

graphics.off()
pdf(paste('Effects of changing KW VRs ', Period[1],'-',Period[2],Population[1]
,'.pdf'),width=8,height=8)
matplot(rownames(vrsen), vrsen, type='l', lwd=2, las=1, col= rainbow(15),
lty=1:15,
ylab="KW population growth", xlab="Value of vital rate",
main=paste("Effects of changing KW vital rates ", Period[1],'-
',Period[2],Population[1]))
vrn<-
expression('Ss1','Ss2','Ss3','Ss4','Ss5','Ss6','Ss7','Sg2','Sg3','Sg4','Sg6','Sp2
','Sp3','Sf3','Sf4')
legend(.05, max(vrsen), vrn, lwd=2, lty=1:15, col= rainbow(15), cex=0.75,
border="gray100")
dev.off()

graphics.off()
pdf(paste('Det. VRs Sensitivity and Elasticity', Period[1],'-
',Period[2],Population[1],'.pdf'),width=12,height=8)
x.KW<-vitalsens(KW.el, KW.vr)
sum(x.KW$elasticity)
barplot(t(x.KW[,2:3]), beside=TRUE, legend=TRUE, las=1, xlab="Vital rate",
main=paste("KW vital rate sensitivity and elasticity",Period[1],'-
',Period[2],Population[1]))
abline(h=0, lwd=2, col=1)
dev.off()

#<<<@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@>>>
#<<<@@@@@@@     8.STOCHASTIC VITAL RATE ELASTICITY AND SENSITIVITY      @@@@@@>>>
#<<<@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@>>>
# This section estimates stochastic sensitivities of vital rates, and
# stochastic elasticities of vital rates as well as it produces a series of
# elasticity statistics. The procedure uses stochastic sampling of beta and
# lognormal distributions fit to the KW vital rate data. See section
# 2.5 Perturbation analysis of the report for more information.

reps=Sims                      # number of repetitions used in stochastic sampling

#_____
#-------------------------------------------------------------------------------

VDts1 =  'beta'
VDts2 =  'beta'
VDts3 =  'beta'
VDts4 =  'beta'
VDts5 =  'beta'
VDts6 =  'beta'
VDts7 =  'beta'
VDtg2 =  'lognorm'
VDtg3 =  'lognorm'
VDtg4 =  'lognorm'
VDtg6 =  'lognorm'
VDtp2 =  'lognorm'
VDtp3 =  'lognorm'
VDtf3 =  'lognorm'
VDtf4 =  'lognorm'
VDtVR=
c(VDts1,VDts2,VDts3,VDts4,VDts5,VDts6,VDts7,VDtg2,VDtg3,VDtg4,VDtg6,VDtp2,VDtp3,V
Dtf3,VDtf4)
VDtVR_T <- cbind(symsN,VDtVR)

#Variances
Vs1 = VarsSigma[1]
```

```
Vs2 = VarsSigma[2]
Vs3 = VarsSigma[3]
Vs4 = VarsSigma[4]
Vs5 = VarsSigma[5]
Vs6 = VarsSigma[6]
Vs7 = VarsSigma[7]
Vg2 = 0.00000
Vg3 = 0.00000
Vg4 = 0.00000
Vg6 = 0.00000
Vp2 = 0.00000
Vp3 = 0.00000
Vf3 = VarsMuOffsp [3]
Vf4 = VarsMuOffsp [4]
VarVR=c(Vs1,Vs2,Vs3,Vs4,Vs5,Vs6,Vs7,Vg2,Vg3,Vg4,Vg6,Vp2,Vp3,Vf3,Vf4)

numvrs <- length(KW.vr)
randvrsBeta <- matrix(NA, nrow=reps, ncol=numvrs)
randvrsLN <- matrix(NA, nrow=reps, ncol=numvrs)

beta.Ind <- which(VDtVR=="beta")
for (i in beta.Ind) {
    randvrsBeta[,i] <- betarv(m=MeanVR[i], v=VarVR[i], n=reps)
}

lognorm.Ind <- which(VDtVR=="lognorm")
for (i in lognorm.Ind) {
    randvrsLN[,i] <- rlnorm(reps, meanlog=log(MeanVR[i]), sdlog=sqrt(VarVR[i]))
    }

apply(randvrsBeta,2,function(x){!all(is.na(x))})
randvrsBeta<- randvrsBeta[,apply(randvrsBeta,2,function(x){!all(is.na(x))})]
colnames(randvrsBeta)<- subset(VDtVR_T, VDtVR=="beta")[,1]

apply(randvrsLN,2,function(x){!all(is.na(x))})
randvrsLN<- randvrsLN[,apply(randvrsLN,2,function(x){!all(is.na(x))})]
colnames(randvrsLN)<- subset(VDtVR_T, VDtVR=="lognorm")[,1]

StochRates<- cbind(randvrsBeta,randvrsLN)
StochRates<- StochRates[,symsN]
StochRates.df<- as.data.frame(StochRates)

graphics.off()
pdf(paste('Stochastic Vital rates',Population[1] ,'.pdf'),width=8,height=8)
par( mar=c(2,2,2,2), oma=c(2,2,2,2) )
par (mfrow=c(3,3),yaxt='n')
hist(StochRates.df$Ss1,main='Ss1', xlab="", ylab="")
hist(StochRates.df$Ss2,main='Ss2', xlab="", ylab="")
hist(StochRates.df$Ss3,main='Ss3', xlab="", ylab="")
hist(StochRates.df$Ss4,main='Ss4', xlab="", ylab="")
hist(StochRates.df$Ss5,main='Ss5', xlab="", ylab="")
hist(StochRates.df$Ss6,main='Ss6', xlab="", ylab="")
hist(StochRates.df$Ss7,main='Ss7', xlab="", ylab="")
hist(StochRates.df$Sf3,main='Sf3', xlab="", ylab="")
hist(StochRates.df$Sf4,main='Sf4', xlab="", ylab="" )
 mtext(paste('Stochastic Vital rates for',Population[1]),     side = 3, outer =
TRUE, col = "black", cex= 1.2, font = 2)
 mtext (text= "", side=1, outer=TRUE, cex=1., font = 2 )
 mtext (text= " ", side=2,outer=TRUE, cex=1., font = 2 )
dev.off()

dev.new(width=7, height=4)
plot(rep(0,10)~seq(1,10), ylim=c(0,1),type='l',xlab="", ylab="", col='white',
tck=0)
axis(1, NULL, col.axis = "white",tcl=0)
```

```
axis(2, NULL, col.axis = "white",tcl=0 )
text(5.3,0.6,  paste("Running Stochastic VR Elasticities
for",Population[1],'...'),cex=1.5, col=1)
text(5.3,0.3,  paste(reps,"Repetitions"),cex=1.5, col=1)

df.Elast<- as.data.frame(matrix(NA, nrow=reps, ncol=length(KW.vr)))
for (i in 1:reps){
stoch.KW <-vitalsens(KW.el, as.list(StochRates[i,]))
df.Elast[i,]<- stoch.KW$elasticity
}
colnames(df.Elast)<-names(KW.vr)

graphics.off()
pdf(paste('Stochastic Elasticity of VR',Population[1],'.pdf'),width=12,height=8)
boxplot(df.Elast, main=paste('Stochastic Elasticity of Vital rates
for',Population[1]), ylim=c(0,1), col=rainbow(length(KW.vr)))
legend(9,1, legend=names(KW.vr), lty=0 , lwd= 1.5, cex= 1, bty='n')
legend(10,1, legend= VDtVR,       lty=0 , lwd= 1.5, cex= 1, bty='n')
dev.off()


ElasMean.KW <-apply(df.Elast,2,mean)
ElasMed.KW <- apply(df.Elast,2,median)
ElasMin.KW <- apply(df.Elast,2,min)
ElasMax.KW <- apply(df.Elast,2,max)
ElasQuan.KW<- apply(df.Elast,2,quantile,probs = c(0.05, 0.95))
ElasStats.KW<- rbind(ElasMean.KW,ElasMed.KW,ElasMin.KW,ElasMax.KW,ElasQuan.KW)

write.table(ElasStats.KW, file = paste('Stoch. Elasticity
Stats',Population[1],'.csv'), sep=',')
cat(paste('Stoch. Elasticity Stats',Population[1]),'(saved in working
folder)',"\n");print(ElasStats.KW)


#<<<@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@>>>
#<<<@@@@@@@@@@@@@@@@@@@@    9. CHINOOK REGRESSION MODELS    @@@@@@@@@@@@@@@@@@@@@>>>
#<<<@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@>>>
# This section fits either simple beta or simple linear regression to all
possible
# combinations of chinook stock aggregates (abundance or standardized data) and
KW
# vital rates. The preference is the beta regression (using package betareg) as
# it considers the non-normal error structure present in the KW vital rates,
# particularly survivals. See section 2.4 Functional relationships between RKW
# vital rates and Chinook salmon abundance for more information.

Use_F.Impacts<- FALSE        # Use Fishery Impacts data and definitions (TRUE or
#FALSE?
BetaQ_SR<- "YES"             # BetaQ_SR defines if the simple regressions should
                            #be run with a Beta "YES" or Linear model "NO"
p_val=0.05                   # p- value for the regression
Standr_Data<- "NO"           # Use standarized data? "YES" or "NO"

#_____
#--------------------------------------------------------------------------------

Is.Beta<- ifelse(BetaQ_SR=="YES", '(Beta Regressions)','(Linear Regressions)')


if(Use_F.Impacts==FALSE){
ChinDefs<-
read.table(paste(getwd(),'/','R_Inputs','/','Chinook_Ab_Definitions_R.csv',sep=""
),header=T, sep=",")
```

```r
ChinData_raw<-
read.table(paste(getwd(),'/','R_Inputs','/','ChinookAbundance_Data_R.csv',sep="")
,header=T, sep=",")
}

if(Use_F.Impacts==TRUE) {
ChinDefs<-
read.table(paste(getwd(),'/','R_Inputs','/','Chinook_Ab_Defs_FI_R.csv',sep=""),he
ader=T, sep=",")
ChinData_raw<-
read.table(paste(getwd(),'/','R_Inputs','/','ChinookAbundance_FI_R.csv',sep=""),h
eader=T, sep=",")
}
ChinData<-  subset(ChinData_raw, Year >= Period[1] & Year <= Period[2])

if(Standr_Data== "NO"){
ChinData2   <- ChinData[,-1]
}
if(Standr_Data== "YES"){
ChinData2   <- apply(na.omit(ChinData[,-1]),2,Stdz_Fun)
}
Chindefs0.1.2 <- ChinDefs
Chindefs0.1   <- ChinDefs[!ChinDefs$lag==2,]
Chindefs0.2   <- ChinDefs[!ChinDefs$lag==1,]
Chindefs1.2   <- ChinDefs[!ChinDefs$lag==0,]
ChinData0.1<- subset(ChinData2,select=as.vector(Chindefs0.1$TimeSeries))
ChinData0.2<- subset(ChinData2,select=as.vector(Chindefs0.2$TimeSeries))
ChinData1.2<- subset(ChinData2,select=as.vector(Chindefs1.2$TimeSeries))

if(BetaQ_SR=="YES"){
dev.new(width=7, height=4)
plot(rep(0,10)~seq(1,10), ylim=c(0,1),type='l',xlab="", ylab="", col='white',
tck=0)
axis(1, NULL, col.axis = "white",tcl=0)
axis(2, NULL, col.axis = "white",tcl=0 )
text(5.3,0.5,  paste("Running Beta Regressions for",Population[1],'...'),cex=1.5,
col='red')
}

if(BetaQ_SR=="NO"){
dev.new(width=7, height=4)
plot(rep(0,10)~seq(1,10), ylim=c(0,1),type='l',xlab="",
ylab="",tck=0,col='white')
axis(1, NULL, col.axis = "white",tcl=0 )
axis(2, NULL, col.axis = "white",tcl=0 )
text(5.3,0.5,  paste("Running Linear Regressions
for",Population[1],'...'),cex=1.5, col='blue')
}

ifelse(BetaQ_SR== "YES",
SurvModsSim<-
SurvFunB(ChinD=ChinData0.1,SurvT=SurvTable2,Chindef=Chindefs0.1,p_val=p_val),
SurvModsSim<-
SurvFun(ChinD=ChinData0.1,SurvT=SurvTable2,Chindef=Chindefs0.1,p_val=p_val))

ifelse(BetaQ_SR== "YES",
FecModsSim <-
FecFunB(ChinD=ChinData2,OffsprT=OffsprTable2,Chindef=Chindefs0.1.2,p_val=p_val),
FecModsSim <-
FecFun(ChinD=ChinData2,OffsprT=OffsprTable2,Chindef=Chindefs0.1.2,p_val=p_val))

SimpleRegMods<- rbind(SurvModsSim,FecModsSim)
SimpleRegMods<- SimpleRegMods[SimpleRegMods$slope>0,]
#Filtering out negative slopes.
```

```r
write.table(SimpleRegMods, file =
paste('SimpleRegModels',Population[1],Is.Beta,'.csv'), sep=',', quote = TRUE,
row.names = FALSE)
cat(paste('Selected Simple Regression Models Chinook -
',Population[1],Is.Beta),'(Saved to Folder)',"\n");print(SimpleRegMods)
graphics.off()

#<<<@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@>>>
#<<<@@@@@@@@@@@@@@@@@@@      10. NORMAL STRUCTURE TESTS      @@@@@@@@@@@@@@@@@@@@>>>
#<<<@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@>>>
#This section performs graphical normality diagnostics using a Generalized Simple
#Linear Regression. It's not necessary to run it for subsequent analyses, it can
#be skipped using the command skipSection= TRUE or FALSE.

plot= TRUE                 # Plot section graphs ? TRUE or FALSE
ask = FALSE                # Press enter to switch between graphs?  TRUE or FALSE
skipSection= FALSE        # Skip section ?  TRUE or FALSE


#_____
#-------------------------------------------------------------------------------

if(skipSection==FALSE){
ChinD=ChinData0.1
SurvT=SurvTable2
Chindef=Chindefs0.1
storemVR<- matrix(NA, nrow=length(ChinD), ncol=5)
storem1<- list(storemVR,storemVR, storemVR,storemVR,storemVR,storemVR, storemVR)
storemREs<-matrix(NA, nrow=length(ChinD), ncol=length(ChinD[,1]))
storem1REs<-list(storemREs,storemREs, storemREs,storemREs,storemREs,storemREs,
storemREs)

for (i in 1:length(SurvT[1,])){
    for (j in 1:length(ChinD)){

        y <- SurvT[,i]
        x <- ChinD[,j]
     lmSimple    <- glm(y~x, family=gaussian, na.action=na.exclude)
     coefSimple <- coef(lmSimple)
     summSimple <- summary(lmSimple)
                 options(digits=5)
     Dev.Resid  <- summSimple$deviance.resid
     rsqr <-       summSimple[7]
     p_value     <- summSimple$coefficients[2,4]
storemVR[j,] <- c(i,j,coefSimple[1],coefSimple[2],p_value)
storem1[[i]] <- storemVR
storemREs[j,] <-  Dev.Resid
storem1REs [[i]] <- storemREs
   }
   }
storem1
SurvMods<- rbind(storem1[[1]],storem1[[2]], storem1[[3]],storem1[[4]],
storem1[[5]],storem1[[6]], storem1[[7]])
ResidMods<-rbind(storem1REs[[1]],storem1REs[[2]],
storem1REs[[3]],storem1REs[[4]], storem1REs[[5]],storem1REs[[6]],
storem1REs[[7]])
VRnamex<- rep(colnames(SurvT), each=length(ChinD))
Runnamex<- rep(colnames(ChinD),length(SurvT[1,]))
SurvModsnam<-
c('VitalRate','Chinook_Run','Lag','intercept','slope1','p_value',ifelse(Populatio
n[1]=='NRKW', paste('NR_Hyp'), paste('SR_Hyp')))
ifelse(Population[1]=='NRKW',
 SurvModsRes<-cbind(VRnamex, Runnamex, Chindef$lag,
as.data.frame(SurvMods),Chindef$NR_Hyp)[,-(4:5)]
,
```

```r
 SurvModsRes<-cbind(VRnamex, Runnamex, Chindef$lag,
as.data.frame(SurvMods),Chindef$SR_Hyp)[,-(4:5)]
 )
SurvModsRes
colnames(SurvModsRes)<-SurvModsnam

SurvModsResSel<- subset(SurvModsRes, p_value <= p_val)
SurvModsResSel

ResidMods_p<- as.data.frame(cbind(SurvModsRes,ResidMods))
ResidMods_p_sel<- subset(ResidMods_p,  p_value <= p_val, digits=3)

graphics.off()
par( oma=c(2,2,4,2), mar=c(4,2,4,2))
par(mfrow=c(4,2),ask=ask)
   for(i in 1:length(ResidMods_p_sel[,1])){
   hist(as.numeric(ResidMods_p_sel[i,][-(1:7)]), plot =
plot,main=paste(ResidMods_p_sel[i,]$VitalRate,'-
',ResidMods_p_sel[i,]$Chinook_Run),

   ylab="", xlab="")
   mtext(paste("p_value",round(ResidMods_p_sel[i,]$p_value,4)),cex=0.8,side=3)
   mtext(text=paste("Residuals of",Is.Beta), side=3, outer=TRUE)
   }

graphics.off()
par( oma=c(2,2,2,2), mar=c(1.5,2,3,2))
par(mfrow=c(4,2),ask=F)
   for(i in 1:length(ResidMods_p_sel[,1])){
   qqnorm(as.numeric(ResidMods_p_sel[i,][-(1:7)]), plot = plot,
main=paste(ResidMods_p_sel[i,]$VitalRate,'-',ResidMods_p_sel[i,]$Chinook_Run),
   ylab="", xlab="")
   qqline(as.numeric(ResidMods_p_sel[i,][-(1:7)]), col=2)
   mtext(paste("p_value",round(ResidMods_p_sel[i,]$p_value,4)),cex=0.8,side=3)
   mtext (text=paste("NORMAL QQ-PLot p_value < ",p_val), side = 3, outer = TRUE,
font=2)
   }
graphics.off()
}

if(skipSection==TRUE){
addSkip<- c(paste('No graphical tests of normality performed'))
print(addSkip)
}

#<<<@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@>>>
#<<<@@@@@@      11. ELASTICITIES OF INTERACTIONS- MATRIX PERT.       @@@@@@>>>
#<<<@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@>>>
# This section calculates the elasticity of KW vital rates using matrix
#perturbation.
# It considers the effect of chinook abundance on the vital rates in the simple
#regressions.
# There are two available approaches (variants):
# variant 1     Elasticity X = ((lambda_B/lambda_A)-1)/((x_B/x_A)-1)
# variant 2     Elasticity X = elast.median_VR((vr_B/vr_A)-1)/((x_B/x_A)-1)
# For more information see section 2.5.2 Quantification of Chinook salmon
abundance
# levels for RKW viability.
# Graphic output:  Hypothesis 1(a=blue)(b= green), 2(a,b) in gray.

percIncr <- 0.1        #(0.1 =10%) Percentage increment of chinook abundance
Variant<- 2            # or 1 . Use 2 as default because it includes 95% CI.
inputTable<-           SimpleRegMods
#_____
#------------------------------------------------------------------------------
```

```r
VRnames_SF<- c(colnames(SurvTable2),colnames(OffsprTable2))
MeanVR_SF<-c(Ss1,Ss2,Ss3,Ss4,Ss5,Ss6,Ss7,Sf3,Sf4)
MeanVR_SFnam<-c('Ss1_','Ss2_','Ss3_','Ss4_','Ss5_','Ss6_','Ss7_','Sf3_','Sf4_')
symsNVR<- c("Ss1","Ss2","Ss3","Ss4","Ss5","Ss6","Ss7","Sf3","Sf4")
Table_SF<- data.frame(VRnames_SF, MeanVR_SF, MeanVR_SFnam, symsNVR)

RegMod<- inputTable

RegMod$MatName  <-
Table_SF$MeanVR_SFnam[match(RegMod$VitalRate,Table_SF$VRnames_SF)]

RegMod$VR_Name <- Table_SF$symsNVR[match(RegMod$VitalRate ,Table_SF$VRnames_SF)]
TableStc.elas <- as.data.frame(t(ElasStats.KW))

colnames(TableStc.elas)<-
c('ElasMean.KW','ElasMed.KW','ElasMin.KW','ElasMax.KW','CI_5','CI_95')
TableStc.elas$Sx <- rownames(TableStc.elas)

RegMod$E.VR_Stc <-
TableStc.elas$ElasMed.KW[match(RegMod$VR_Name,TableStc.elas$Sx)]
RegMod$E.VR_95  <- TableStc.elas$CI_95[match(RegMod$VR_Name,TableStc.elas$Sx)]
#For the 95%

PerturbNames  <- data.frame(KW.matNames, MeanVR_SFnam)
RegMod$PerturbMat <-
PerturbNames$KW.matNames[match(RegMod$MatName,PerturbNames$MeanVR_SFnam)]

X_A<-colMeans(na.omit(ChinData))[-1]
RegMod$X_A <- X_A[match(RegMod$Chinook_Run,names(X_A))]

if (BetaQ_SR=="NO") {
VR_A<- 0.
for (e in 1:length(RegMod[,1])){
VR_A [e] <- RegMod$intercept[e]+ (RegMod$slope1[e] * RegMod$X_A[e])
}
RegMod$VR_A<-VR_A
}

if (BetaQ_SR=="YES") {
VR_A<- 0.
for (e in 1:length(RegMod[,1])){
VR_A [e] <-  1/(1+exp(-RegMod$intercept[e]-(RegMod$slope1[e] * RegMod$X_A[e])))
}
RegMod$VR_A<-VR_A
}

df.list <- vector("list", length(RegMod[,1]))
for(i in 1:length(RegMod[,1])){df.list[[i]] <- matrix(data = NA,
                                        nrow = 7,
                                        ncol = 7,
                                        byrow = FALSE,
                                        dimnames = NULL)}

for (f in 1:length(RegMod[,1])){

 if(RegMod$MatName[f]=='Ss1_') {df.list[[f]]<- FunTSs1(RegMod$VR_A[f])}
 if(RegMod$MatName[f]=='Ss2_') {df.list[[f]]<- FunTSs2(RegMod$VR_A[f])}
 if(RegMod$MatName[f]=='Ss3_') {df.list[[f]]<- FunTSs3(RegMod$VR_A[f])}
 if(RegMod$MatName[f]=='Ss4_') {df.list[[f]]<- FunTSs4(RegMod$VR_A[f])}
 if(RegMod$MatName[f]=='Ss5_') {df.list[[f]]<- FunTSs5(RegMod$VR_A[f])}
 if(RegMod$MatName[f]=='Ss6_') {df.list[[f]]<- FunTSs6(RegMod$VR_A[f])}
 if(RegMod$MatName[f]=='Ss7_') {df.list[[f]]<- FunTSs7(RegMod$VR_A[f])}
 if(RegMod$MatName[f]=='Sf3_') {df.list[[f]]<- FunTSf3(RegMod$VR_A[f])}
 if(RegMod$MatName[f]=='Sf4_') {df.list[[f]]<- FunTSf4(RegMod$VR_A[f])}
```

```r
 }
RegMod$LambdaA<- as.numeric(unlist(lapply(df.list,lambda)))
RegMod$X_B<- RegMod$X_A*(1+percIncr)

if (BetaQ_SR=="NO") {
VR_B<- 0.
for (e in 1:length(RegMod[,1])){
VR_B [e] <- RegMod$intercept[e]+ (RegMod$slope1[e] * RegMod$X_B[e])
}
RegMod$VR_B<-VR_B
}

if (BetaQ_SR=="YES") {
VR_B<- 0.
for (e in 1:length(RegMod[,1])){
VR_B [e] <-  1/(1+exp(-RegMod$intercept[e]-(RegMod$slope1[e] * RegMod$X_B[e])))
}
RegMod$VR_B<-VR_B
}

for (f in 1:length(RegMod[,1])){
 if(RegMod$MatName[f]=='Ss1_') {df.list[[f]]<- FunTSs1(RegMod$VR_B[f])}
 if(RegMod$MatName[f]=='Ss2_') {df.list[[f]]<- FunTSs2(RegMod$VR_B[f])}
 if(RegMod$MatName[f]=='Ss3_') {df.list[[f]]<- FunTSs3(RegMod$VR_B[f])}
 if(RegMod$MatName[f]=='Ss4_') {df.list[[f]]<- FunTSs4(RegMod$VR_B[f])}
 if(RegMod$MatName[f]=='Ss5_') {df.list[[f]]<- FunTSs5(RegMod$VR_B[f])}
 if(RegMod$MatName[f]=='Ss6_') {df.list[[f]]<- FunTSs6(RegMod$VR_B[f])}
 if(RegMod$MatName[f]=='Ss7_') {df.list[[f]]<- FunTSs7(RegMod$VR_B[f])}
 if(RegMod$MatName[f]=='Sf3_') {df.list[[f]]<- FunTSf3(RegMod$VR_B[f])}
 if(RegMod$MatName[f]=='Sf4_') {df.list[[f]]<- FunTSf4(RegMod$VR_B[f])}
 }
RegMod$LambdaB<- as.numeric(unlist(lapply(df.list,lambdaPop)))
ElX_V1<-  ((RegMod$LambdaB/RegMod$LambdaA)-1)/((RegMod$X_B/RegMod$X_A)-1)
ElX_V2    <-   (RegMod$E.VR_Stc*((RegMod$VR_B/RegMod$VR_A)-
1))/((RegMod$X_B/RegMod$X_A)-1)
ElX_V2_95 <-   (RegMod$E.VR_95* ((RegMod$VR_B/RegMod$VR_A)-
1))/((RegMod$X_B/RegMod$X_A)-1)

graphics.off()
pdf(paste('Comparison of Variant 1 and 2',Population[1],'.pdf'),width=8,height=8)
plot(ElX_V1,ElX_V2, xlab="Variant1", ylab="Variant2", main="Comparing Elasticity
Variants")
abline(coef=c(0,1),col='red', lwd=2)
dev.off()

ifelse(Variant==1,
RegMod$Elast.Inter <- ElX_V1 ,
RegMod$Elast.Inter <- ElX_V2)
RegMod$Elast.Inter95<- ElX_V2_95

RegModPos<- subset(RegMod, slope1>=0)
RegModPos<- RegModPos[order(RegModPos$Chinook_Run),]

RegModPos<- subset(RegModPos,MatName  != "Ss5_"& MatName  != "Ss6_"& MatName  !=
"Ss7_")

ifelse(Population[1]=='SRKW',
RegModPos <- subset(RegModPos, SR_Hyp != 'NA' & SR_Hyp !='Hybrid'),
RegModPos <- subset(RegModPos, NR_Hyp != 'NA' & NR_Hyp !='Hybrid'))

FreqVRs= as.data.frame(table(factor(RegModPos$VitalRate)) )
UniqDF<-  unique(factor(RegModPos$VitalRate))
NAsdm<- rep(NA,length(UniqDF))
```

```r
graphics.off()
pdf(paste('Elasticities of Interaction Method Matrix
Pert.',Population[1],Is.Beta[1],'.pdf'),width=12,height=8)
facVRT <- factor(RegModPos$VitalRate)
barchart(Elast.Inter~Chinook_Run | facVRT, data= RegModPos, horiz=F, layout =
c(1,length(UniqDF)), box.ratio=1,
 ylim=c(0,max(RegModPos$Elast.Inter)+0.005), xlab="Chinook Regressions",
cex=4,ylab=paste("Elasticity - Variant", Variant[1]),
col= ifelse(Population[1]=='NRKW','royalblue1','yellowgreen'), type="p",
main=paste('Elasticities of Interaction - Method Matrix
Pert.',Population[1],Is.Beta[1]), bg="white",
scales=list(x=list(rot=90, tck=c(-74,0), col='grey5',
labels=paste(unique(RegModPos$Chinook_Run)))))
dev.off()
Elast_Ss1  <-  funElastCI('Calf_Survival', RegModPos)
Elast_Ss2  <-  funElastCI('Juvenile_Survival', RegModPos)
Elast_Ss3  <-  funElastCI('F1_Survival', RegModPos)
Elast_Ss4  <-  funElastCI('F2_Survival', RegModPos)
Elast_Ss5  <-  funElastCI('F3_Survival', RegModPos)
Elast_Ss6  <-  funElastCI('M1_Survival', RegModPos)
Elast_Ss7  <-  funElastCI('M2_Survival', RegModPos)
Elast_Sf3  <-  funElastCI('F1_Fecundity', RegModPos)
Elast_Sf4  <-  funElastCI('F2_Fecundity', RegModPos)
write.table(RegModPos, file = paste('Elasticity of
Interactions',Population[1],'.csv'), sep=',', quote = FALSE, row.names = FALSE)
ListtoL<-RegModPos[1:2]
SignifR<-RegModPos[c('VitalRate','Chinook_Run', 'p_value')]

#<<<@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@>>>
#<<<@@@@@@@@@@@@@@@  12.PLOTTING BETA DIAGNOSTICS, AND AIC   @@@@@@@@@@@@@@@@@>>>
#<<<@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@>>>
# This optional section plots the linear and logit functions fit to the selected
# regressions and estimates the AIC for both linear and beta approaches.
# See <<<http://cran.r-project.org/web/packages/betareg/vignettes/betareg.pdf>>>
# for more info.

SkipBetaD = FALSE      # Skip this section ? "TRUE" or  "FALSE". This section has
                       # to be ran if conducting Chum multiple regressions
ask= FALSE             # Press enter to switch between graphs?  TRUE or FALSE
YLIM= c(0,1)           # Y limits for figures

#_____
#--------------------------------------------------------------------------------

allVR<- as.data.frame(cbind(SurvTable2,OffspringTable[,-1]))

df.AllVR<- matrix(NA,nrow=length(allVR[,1]), ncol=length(allVR[1,]))
for (i in 1:length(allVR[1,])){
   df.AllVR [,i] <- ifelse(allVR[,i]==1,0.99999,allVR[,i])
    }

df.AllVR2<- matrix(NA,nrow=length(allVR[,1]), ncol=length(allVR[1,]))
for (i in 1:length(allVR[1,])){
   df.AllVR2 [,i] <- ifelse(df.AllVR[,i]==0,0.000001,df.AllVR[,i])
    }

AllVR <- as.data.frame(df.AllVR2)
colnames(AllVR)<- names(allVR)

VR_Sel<-subset(AllVR, select = as.vector(unique(RegModPos$VitalRate)))
ChinSel <- subset(ChinData, select = as.vector(unique(RegModPos$Chinook_Run)))
AllVars<- cbind(VR_Sel,ChinSel)
AllVars<-na.omit(AllVars)

if(SkipBetaD==FALSE){
```

```r
#********************************************************************************

Slice.lt <- vector("list", length(ListtoL[,1]))
for(i in 1:length(ListtoL[,1])){Slice.lt[[i]] <- matrix(data = NA,
                                                  nrow = length(AllVars[,1]) ,
                                                  ncol = 2,
                                                  byrow = FALSE,
                                                  dimnames = NULL)}

AIC_storem<-  matrix(NA,nrow =length(ListtoL[,1]),ncol = 2)

par(oma=c(2,2,2,2), mar=c(1.5,2,3,2))
par(mfrow=c(1,1) ,ask=ask)

for (i in 1:length(ListtoL[,1])){

        y <- subset(AllVars, select=as.vector(ListtoL[i,1]))#
        x <- subset(AllVars, select=as.vector(ListtoL[i,2]))#

        Slice.lt[[i]] <- cbind(x,y)

        LSimple  <- lm(unlist(Slice.lt[[i]][2])~unlist(Slice.lt[[i]][1]),
na.action=na.omit)
        coefSimpleL <- coef(LSimple)
        AIC_L<- AIC(LSimple)

        BSimple  <-
betareg(as.numeric(unlist(Slice.lt[[i]][2]))~as.numeric(unlist(Slice.lt[[i]][1]))
, na.action=na.omit)
        coefSimpleB <- coef(BSimple)
        AIC_B<-  AIC(BSimple)

        AIC_storem[i,]<- c(AIC_B,AIC_L)

par(mfrow=c(1,1))
plot(unlist(Slice.lt[[i]][2])~unlist(Slice.lt[[i]][1]), ylim=YLIM, xlab="Chinook
Abundance", ylab="Vital Rate",
main=paste(colnames(Slice.lt[[i]][2]),"~",colnames(Slice.lt[[i]][1]) ))
par(new=T)
responseB<-1/(1+exp(-coefSimpleB[1]-(coefSimpleB[2] * unlist(Slice.lt[[i]][1])
)))
plot(unlist(Slice.lt[[i]][1]),responseB,type="b",lwd=2,col=2,lty= 1, axes=F,
ylim=YLIM, ylab="",xlab="" )
par(new=T)
responseL<-coefSimpleL[1]+(coefSimpleL[2] *unlist(Slice.lt[[i]][1]))
plot(unlist(Slice.lt[[i]][1]),responseL,type="b",lwd=2,col=3,lty= 1, axes=F,
ylim=YLIM, ylab="" ,xlab="")

mtext (text= paste('Selected Regressions',Population[1]), side=3, outer=TRUE,
cex=1., font = 2 )
}

colnames(AIC_storem)<- c("AIC_Beta","AIC_Linear" );as.data.frame(AIC_storem)
AIC_Comp<- cbind(ListtoL,round(AIC_storem,2))
write.table(AIC_Comp, file = paste('AIC Comparison Beta vs.
Linear',Population[1],'.csv'), sep=',', quote = TRUE, row.names = FALSE)

graphics.off()
}

if(SkipBetaD==TRUE){
   Skipadd<- c(paste('Section PLOTTING BETA DIAGNOSTICS, AND AIC has been
skipped'))
   print(Skipadd)
   }
```

```r
#<<<@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@>>>
#<<<@@@@@@@@@@@@@@@@@@@     13. RETROSPECTIVE ANALYSES    @@@@@@@@@@@@@@@@@@@@@@@>>>
#<<<@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@>>>
# This section breaks the study period in user-defined matrix for each period
# in an independently and the identically distributed (IID)
# environment (see section 2.6 PVA for more information) and performs
retrospective
# analysis for vital rates (first sub-section) and for Chinook interactions
# (second sub-section)


#*******************************************************************************
#***********          Contribution of VR to the CV of Lambda        ***********
#*******************************************************************************

AutoDiv<- "NO"              #if "YES" It divides the period of analyses
# automatically in an EQUAL number of periods specified in Auto_brakes
Auto_brakes=4               #Because of the number of periods are EQUAL,
Autobreakes
#is sensitive to the number of years available. Verify automatic division.

#If AutoDiv="NO" Set the sets for the study period manually .
Set1<- c(1987,1990)
Set2<- c(1991,1994)
Set3<- c(1995,1998)
Set4<- c(1999,2002)
Set5<- c(2003,2006)
Set6<- c(2007,2011)
Set7<- c(0,0)
Set8<- c(0,0)

#_____
#-----------------------------------------------------------------------------

if(Set1[1]<Period[1]){
 cat('WARNING !!!!!!!!: The period of analyses is:',Period,"\n") }
if(AutoDiv=="NO"){
Set1=Set1
Set2=Set2
Set3=Set3
Set4=Set4
Set5=Set5
Set6=Set6
Set7=Set7
Set8=Set8
}

if(AutoDiv=="YES"){
Inter_Y<- (floor((Period[2]-Period[1])/Auto_brakes))-1
Set1<-  c(Period[1],Period[1]+Inter_Y)
Set2<-  c(Set1[2]+1,Set1[2]+1+Inter_Y)
Set3<-  c(Set2[2]+1,Set2[2]+1+Inter_Y)
Set4<-  c(Set3[2]+1,Set3[2]+1+Inter_Y)
Set5<-  c(Set4[2]+1,Set4[2]+1+Inter_Y)
Set6<-  c(Set5[2]+1,Set5[2]+1+Inter_Y)
Set7<-  c(Set6[2]+1,Set6[2]+1+Inter_Y)
Set8<-  c(Set7[2]+1,Set7[2]+1+Inter_Y)
}

DataIID<- cbind(SurvTable2,OffsprTable2)

Std_DT<- as.numeric(apply(DataIID, 2, sd,na.rm = TRUE))
Var_DT<- as.numeric(apply(DataIID, 2, var,na.rm = TRUE))
Mea_DT<- as.numeric(apply(DataIID, 2, mean,na.rm = TRUE))
```

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```r
symsNIID<-symsNVR

meanElastIID<- ElasStats.KW[,symsNIID][2,]
CV_DT<-Std_DT/Mea_DT
CV_Elast <- meanElastIID*CV_DT
CV_to_Lambda  <-CV_Elast/sum(CV_Elast)
Var_to_Lambda  <-Var_Elast/sum(Var_Elast)

write.table(CV_to_Lambda, file = paste('Contribution of VR to the CV of
Lambda',Population[1],'.csv'), sep=',', quote = TRUE, col.names = FALSE,
row.names=TRUE)

graphics.off()
pdf(paste('Contribution of VR to the CV of
Lambda',Population[1],'.pdf'),width=12,height=8)
barplot(CV_to_Lambda, col=rainbow(length(CV_to_Lambda)), main= "Contribution of
VR to the CV of Lambda", ylim=c(0,max(CV_to_Lambda)+0.02))
dev.off()

IIDModelSumm<-
data.frame(meanElastIID,CV_DT,CV_Elast,CV_to_Lambda,Var_Elast,Var_to_Lambda)
IIDModelSumm

DataT_IID<- as.data.frame(cbind(year=seq(Period[1],Period[2]),DataIID))


SetIID1<-  subset(DataT_IID, year>=Set1[1] & year<=Set1[2])[-1]
SetIID2<-  subset(DataT_IID, year>=Set2[1] & year<=Set2[2])[-1]
SetIID3<-  subset(DataT_IID, year>=Set3[1] & year<=Set3[2])[-1]
SetIID4<-  subset(DataT_IID, year>=Set4[1] & year<=Set4[2])[-1]
SetIID5<-  subset(DataT_IID, year>=Set5[1] & year<=Set5[2])[-1]
SetIID6<-  subset(DataT_IID, year>=Set6[1] & year<=Set6[2])[-1]
SetIID7<-  subset(DataT_IID, year>=Set7[1] & year<=Set7[2])[-1]
SetIID8<-  subset(DataT_IID, year>=Set8[1] & year<=Set8[2])[-1]

Mat_IID1<-FunMat(SetIID1, Set1)
Mat_IID2<-FunMat(SetIID2, Set2)
Mat_IID3<-FunMat(SetIID3, Set3)
Mat_IID4<-FunMat(SetIID4, Set4)
Mat_IID5<-FunMat(SetIID5, Set5)
Mat_IID6<-FunMat(SetIID6, Set6)
Mat_IID7<-FunMat(SetIID7, Set7)
Mat_IID8<-FunMat(SetIID8, Set8)

RetroMats_pre<- list(Mat_IID1, Mat_IID2, Mat_IID3, Mat_IID4, Mat_IID5, Mat_IID6,
Mat_IID7, Mat_IID8 )
RetroMats<- RetroMats_pre[1:length(na.omit(unlist(lapply(RetroMats_pre,sum))))]
write.table(RetroMats, file = paste('IID Matrices',Population[1],'.csv'),
sep=',', quote = F, col.names=TRUE, row.names = FALSE)
LambdasIID<- as.numeric(unlist(lapply(RetroMats,lambda)))
Avg_Lambda_IID<- mean(LambdasIID)
cat('Average IID Lambda',Period,'=',Avg_Lambda_IID,'. Number of IID
Matrices=',length(RetroMats),'. Automatic Division=', AutoDiv ,"\n")

#**********************************************************************************
#**********    CONTRIBUTION OF THE INTERACTION TO THE CV of LAMBDA     **********
#**********************************************************************************
# This section estimates the contribution of the interaction of Chinook - KW
# vital rates to the CV of lambda. Graphic output:  Hypothesis 1(a,b) in blue,
# 2(a,b) in gray.

#_____
#--------------------------------------------------------------------------------
```

```r
CV_Chin<- apply(ChinSel,2,sd,na.rm = TRUE)/apply(ChinSel,2,mean,na.rm = TRUE)
CV_Chin<- as.data.frame(CV_Chin)
RegModPos$CV_Chin <- CV_Chin$CV_Chin[match(RegModPos$Chinook_Run,
row.names(CV_Chin))]
RegModPos$ContCV_lambda<-   RegModPos$Elast.Inter*RegModPos$CV_Chin
F_ChinR <- factor(RegModPos$Chinook_Run)
factor.ChinR <- tapply(RegModPos$ContCV_lambda,F_ChinR,sum)
CV_Chin_lambda = as.data.frame(factor.ChinR)
write.table(CV_Chin_lambda, file = paste('Contribution of Interacion CV to
Lambda',Population[1],'.csv'), sep=',', quote = T, row.names = TRUE)
graphics.off()

Table_SF$MeanVR_SFnam[match(RegMod$VitalRate,Table_SF$VRnames_SF)]
pdf(paste('Contribution of Interaction to the CV of
Lambda',Population[1],'.pdf'),width=12,height=8)

if(Population=="SRKW"){
colHy<-
ifelse(RegModPos$SR_Hyp[match(row.names(CV_Chin_lambda),RegModPos$Chinook_Run)]==
'1a','blue','gray')
}

if(Population=="NRKW"){
colHy<-
ifelse(RegModPos$NR_Hyp[match(row.names(CV_Chin_lambda),RegModPos$Chinook_Run)]==
'1b','blue','gray')
}

par(mai=c(1.4,0.8,0.8,0.4))
barplot(CV_Chin_lambda$factor.ChinR,col= colHy, main= paste("Contribution of
Interaction to the CV of Lambda",Population[1]),las=2,cex.names=0.8)
dev.off()

#<<<@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@>>>
#<<<@@@@@@@@@@@@@@@@   14. STOCHASTIC POPULATION GROWTH     @@@@@@@@@@@@@@@@@@@@>>>
#<<<@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@>>>
# This section estimates the stochastic population growth using either vital
rates
# as random variables or the IID matrices using the Tuljapurkar's approximation
# Output:
# sim: log stochastic growth rate by simulation
# sim.CI:confindence interval for simulation

#_____
#-----------------------------------------------------------------------------


mats.lt <- vector("list", length(StochRates[,1])) # create list
for(z in 1:length(StochRates[,1])){
Ss1[z]<-StochRates[,1][z]
Ss2[z]<-StochRates[,2][z]
Ss3[z]<-StochRates[,3][z]
Ss4[z]<-StochRates[,4][z]
Ss5[z]<-StochRates[,5][z]
Ss6[z]<-StochRates[,6][z]
Ss7[z]<-StochRates[,7][z]
Sg2[z]<-StochRates[,8][z]
Sg3[z]<-StochRates[,9][z]
Sg4[z]<-StochRates[,10][z]
Sg6[z]<-StochRates[,11][z]
Sp2[z]<-StochRates[,12][z]
Sp3[z]<-StochRates[,13][z]
Sf3[z]<-StochRates[,14][z]
Sf4[z]<-StochRates[,15][z]
```

```
mats.lt[[z]]<- matrix(c(
        0, (Ss1[z]^0.5*(Ss2[z]*Sg2[z]*Sp2[z]*Sf3[z]))/2,
(Ss1[z]^0.5*(((1+(Ss3[z]*(1-Sg3[z])))*Sf3[z])+(Ss3[z]*Sg3[z]*Sf4[z])))/2,
(Ss1[z]^0.5*((1+(Ss4[z]*(1-Sg4[z])))*Sf4[z]))/2, 0, 0, 0,
            Ss1[z]^0.5, Ss2[z]*(1-Sg2[z]), 0, 0, 0, 0, 0,
        0, Ss2[z]*Sg2[z]*Sp2[z], Ss3[z]*(1-Sg3[z]), 0, 0, 0, 0,
        0, 0, Ss3[z]*Sg3[z], Ss4[z]*(1-Sg4[z]), 0, 0, 0,
        0, 0, 0, Ss4[z]*Sg4[z], Ss5[z], 0, 0,
        0, Ss2[z]*Sg2[z]*Sp3[z], 0, 0, 0, Ss6[z]*(1-Sg6[z]), 0,
        0, 0, 0, 0, 0, Ss6[z]*Sg6[z], Ss7[z]),
        nrow = 7, ncol = 7, byrow = TRUE
        )
}

Stch_GR_Dem<- stoch.growth.rate(mats.lt, prob = NULL, maxt = 50000, verbose=TRUE)
stoch_lambda_Dem<-exp(Stch_GR_Dem$approx)
stoch_CI_Dem<-exp(Stch_GR_Dem$sim.CI)
lamda_VR_Random<- c(stoch_lambda_Dem,stoch_CI_Dem)

#**********        POP GROWTH (Lambda) USING IID MATRICES        **********

GR_Retro<- stoch.growth.rate(RetroMats, prob = NULL, maxt = 50000, verbose=TRUE)
lambda_Retro<-exp(GR_Retro$approx)
lambda_Retro_CI<-exp(GR_Retro$sim.CI)
lambda_stoch <- c(lambda_Retro,lambda_Retro_CI)

lamda_Envir<- data.frame(lambda_stoch,lamda_VR_Random)
rownames(lamda_Envir)<-c('Lamda','CI5','CI95')
write.table(lamda_Envir, file = paste('lamda from IID and VR
random',Population[1],'.csv'), sep=',', quote = F, row.names = TRUE)

#<<<@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@>>>
#<<<@@@@@@@@@@@@@@@@@   15. PROJECTING POPULATION SIZE      @@@@@@@@@@@@@@@@@@>>>
#<<<@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@>>>
# This section projects the population size using either vital rates
# as random variables or random sampling of IID matrices set in 'Envir'.
# In addition it creates a demographic projection.

tmax=DampTime10[2] # number of time steps or projection intervals to predict
# future population size
nreps=5000          # number of iterations
Envir<-"IID"       #"IID"  or "VR_Random".  If desired the user can run this
# section using either IID matrices (IDD) OR the VR as random variables
# (VR_Random)
tmaxes<- c(10,20,30,DampTime10[2])    # Time horizons; number of years to project
#into the future.

# Colour for IID analyses output. It can be changed according to user
# preferences. See ?palette
IID_col<- rainbow(20)
VRR_col<- terrain.colors(20)

#_____
#-----------------------------------------------------------------------------

if(Envir=="IID")      {colh<-IID_col}
if(Envir=="VR_Random"){colh<-VRR_col}
if(Envir=="IID")      {SelMats<-RetroMats}
if(Envir=="VR_Random"){SelMats<-mats.lt   }
Project.lt <- vector("list", length(tmaxes)) # creates list
for(i in 1:length(tmaxes)){Project.lt [[i]] <- matrix(data = NA,
                                nrow = nreps ,
                                ncol = 7,
                                byrow = FALSE,
                                dimnames = NULL)}
```

```r
for(t in 1:length(tmaxes)){
Project.lt [[t]]<- stoch.projection(SelMats, n0=CountsLastyear$nlastYear, tmax =
tmaxes[t], nreps = nreps, prob = NULL,
nmax = NULL, sumweight = rep(1, length(n0)), verbose=FALSE)
}

graphics.off()
pdf(paste('Projections of Pop Size',Population[1],Period[1],'-
',Period[2],Envir,'.pdf'),width=10,height=8)
par( oma=c(2,2,2,2), mar=c(1.5,2,3,2),mai=c(0.4,0.8,0.8,0.4))
par (mfrow=c(2,2))
hist(apply(Project.lt[[1]],1,sum),col = colh, ylab="", xlab="", main=
paste(tmaxes[1],'years'));legend('topleft',bty='n', paste('Mean Pop',
round(mean(apply(Project.lt[[1]],1,sum)),0)))
hist(apply(Project.lt[[2]],1,sum),col = colh, ylab="", xlab="", main=
paste(tmaxes[2],'years'));legend('topleft',bty='n', paste('Mean Pop',
round(mean(apply(Project.lt[[2]],1,sum)),0)))
hist(apply(Project.lt[[3]],1,sum),col = colh, ylab="", xlab="", main=
paste(tmaxes[3],'years'));legend('topleft',bty='n', paste('Mean Pop',
round(mean(apply(Project.lt[[3]],1,sum)),0)))
hist(apply(Project.lt[[4]],1,sum),col = colh, ylab="", xlab="", main=
paste(tmaxes[4],'years'));legend('topleft',bty='n', paste('Mean Pop',
round(mean(apply(Project.lt[[4]],1,sum)),0)))
 mtext(paste('Projections of Pop Size',Envir,Population[1]),side = 3, outer =
TRUE, col = "black", cex= 1.2)
 mtext (text= "Population Numbers", side=1, outer=TRUE, cex=1., font = 2 )
 mtext (text= "Frequency", side=2,outer=TRUE, cex=1., font = 2 )
dev.off()


#************************* Demographic Projection  **************************

Dem_project<- stoch.projection(SelMats, n0=CountsLastyear$nlastYear, tmax = tmax,
nreps = nreps, prob = NULL,
nmax = NULL, sumweight = rep(1, length(n0)), verbose=FALSE)

graphics.off()
pdf(paste('Projection',Envir ,Population[1],Period[1],'-',Period[2]
,'.pdf'),width=8,height=8)
colnames(Dem_project)<-Cat2Names
matplot(Dem_project,type = "l", lty = 1:7, lwd = 1.5, lend = par("lend"),pch =
NULL, col = rainbow(7), xlim=c(-10,nreps),
ylim=c(-9.5,max(Dem_project)*3/2), ylab="KW Abundances", xlab="Reps",
main=paste('Projection',Envir, nreps , 'reps', Population[1]))
legend(-10, max(Dem_project)*3/2, Cat2Names, lwd=2, lty=1:7, col= colh, cex=1,
bty='n')
dev.off()

#<<<@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@>>>
#<<<@@@@@@@@@@@@@@@@@   16. FISHING SCENARIOS – TERMINAL RUN   @@@@@@@@@@@@@@@@@@>>>
#<<<@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@>>>
# This section simulates fishing scenarios for chinook terminal run. The user
# controls a multiplier for the harvest rate (HR) that affects the indicator
# stocks.  The stock aggregate is user defined from the list of significant
stocks
# from the multiple regressions (SignifR). See section 2.7 Fishing scenarios for
# more information.
# Note: if HR_new > 1, the HR is automatically set to 1.

Mult<-1.5  # User defined multiplier of Ocean HR affecting TR;
# Mult = 0.00 for closing fisheries
print(SignifR)   # List of significant stock aggregates
cat('Fishing Scenario for Population', Population ,"\n")
# Make sure the stock is selected from the right population
StockAggr<- "FEPS_TR_1" # Set stock aggregate FROM SignifR  e.g.: "FE_TR_1"
```

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```r
colhS<- topo.colors(20) # Colour for output. It can be changed according to user
#preferences. See ?palette

#_____
#----------------------------------------------------------------------------

if(Use_F.Impacts==FALSE){

if(length(subset(SignifR,Chinook_Run==StockAggr)[,1])==0){
addNoRun1<- paste('Error: Stock Aggregate',StockAggr,'not found in Significant TR
Chinook Run')
stop(print(addNoRun1))
}

TR        <-
read.table(paste(getwd(),'/','R_Inputs','/','Term_Run_R.csv',sep=""),header=T,
sep=",")
TRE       <-
read.table(paste(getwd(),'/','R_Inputs','/','TRE_R.csv',sep=""),header=T,
sep=",")
TRE_HR    <-
read.table(paste(getwd(),'/','R_Inputs','/','TRE_HR_R.csv',sep=""),header=T,
sep=",")
ER_Stock <-
read.table(paste(getwd(),'/','R_Inputs','/','ER_Indicators_R.csv',sep=""),header=
T, sep=",")

TR        <-  subset(TR   , Year >= Period[1] & Year <= Period[2])
TRE       <-  subset(TRE  , Year >= Period[1] & Year <= Period[2])
TRE_HR    <-  subset(TRE_HR, Year >= Period[1] & Year <= Period[2])

TR_ChinStocks<- subset(ChinData,
select=as.character(ChinDefs[ChinDefs$Ab_ID==1,]$TimeSeries))

IndStock_HR <- subset(TRE_HR, select=
unlist(strsplit(as.character(ER_Stock[ER_Stock$Time.series==StockAggr,]$ER.Indica
tor.Stocks), ",", fixed = TRUE)))
IndStock_HR

IndStock_HRMod <- Mult*IndStock_HR

new.HR <- matrix(NA,nrow =length(IndStock_HRMod[,1]),ncol =
length(IndStock_HRMod[1,]))
for(i in 1:length(IndStock_HRMod)){
new.HR[,i]<- ifelse(IndStock_HRMod[,i]>1,1,IndStock_HRMod[,i])
options(warn=-1)
}

for(i in 1:length(IndStock_HRMod)){
ifelse(na.omit(IndStock_HRMod[,i])>=1, print(paste("Antention: At least one
harvest
rate is greater than 1 and have been adjusted to 1
in",colnames(IndStock_HRMod[i]))), print(paste("values ok")))
}

colnames(new.HR)<- names(IndStock_HRMod)

TRE_sel<- subset(TRE[row.names(IndStock_HRMod),], select=colnames(new.HR))
TR_sel <- subset(TR [row.names(IndStock_HRMod),], select=colnames(new.HR))
as.data.frame(new.HR)

N_y <- (new.HR*(TRE_sel+TR_sel))- TRE_sel
N_y

TR_scalar <- apply((TR_sel - N_y),1,sum) / apply(TR_sel,1,sum)
```

```r
TR_scalar[is.na(TR_scalar)]<- mean(na.omit(TR_scalar))
TR_scalar_aggr <- cbind(TR$Year,TR_scalar)
TR_scalar_aggr <-as.data.frame(TR_scalar_aggr)

Orig_TR_Stock <- subset(ChinData,select=c('Year',StockAggr))
New_TR_Stock<- (Orig_TR_Stock* TR_scalar_aggr)[2]
New_TR_Stock

identRun  <- subset(RegModPos, Chinook_Run==StockAggr)

New_VR <- matrix(NA, ncol=length(identRun[,1]),nrow=length(New_TR_Stock[,1]))
for(f in 1:length(identRun[,1])){
New_VR[,f]  <-
beta_backtr(identRun$intercept[f],identRun$slope1[f],New_TR_Stock[,1])
colnames(New_VR)<- as.character(identRun$VitalRate)
}
New_VR<-ifelse(New_VR>1,stop(paste('Warning, scenario produced VR > 1')),New_VR)

New_VR<-ifelse(colnames(New_VR)== "F1_Fecundity" & New_VR >
max(F1_Fecundity),max(F1_Fecundity),New_VR)
New_VR<-ifelse(colnames(New_VR)== "F2_Fecundity" & New_VR >
max(F2_Fecundity),max(F2_Fecundity),New_VR)
New_VR

Old_VR<-  subset(allVR, select= as.character(identRun$VitalRate))
Old_VR

if(Mult<=1){
  Sce_VR<- matrix(NA,ncol=length(New_VR[1,]) ,nrow=length(New_VR[,1]))
  for(v in 1: length(New_VR[1,])){
     Sce_VR[,v] <-ifelse(Old_VR[,v]>New_VR[,v],Old_VR[,v],New_VR[,v])
     }}

if(Mult>1){
  Sce_VR<- matrix(NA,ncol=length(New_VR[1,]) ,nrow=length(New_VR[,1]))
  for(v in 1: length(New_VR[1,])){
     Sce_VR[,v] <-ifelse(Old_VR[,v]<New_VR[,v],Old_VR[,v],New_VR[,v])
     }}
colnames(Sce_VR)<- as.character(identRun$VitalRate)

TestVR_Sc <- cbind(Old_VR[,1], New_VR[,1], Sce_VR[,1])
colnames(TestVR_Sc) <- c('Old_VR','New_VR','Sce_VR')
cat(paste("Multiplier=",Mult),"VR=",as.character(identRun$VitalRate)[1]   ,"\n")
TestVR_Sc

DataT_IID_S  <- allVR
DataT_IID_S[as.character(identRun$VitalRate)]<- Sce_VR

DataT_IID_S – allVR

DataT_IID_S<- cbind(year=DataT_IID$year,DataT_IID_S)

SetIID_S1<-  subset(DataT_IID_S, year>=Set1[1] & year<=Set1[2])[-1]
SetIID_S2<-  subset(DataT_IID_S, year>=Set2[1] & year<=Set2[2])[-1]
SetIID_S3<-  subset(DataT_IID_S, year>=Set3[1] & year<=Set3[2])[-1]
SetIID_S4<-  subset(DataT_IID_S, year>=Set4[1] & year<=Set4[2])[-1]
SetIID_S5<-  subset(DataT_IID_S, year>=Set5[1] & year<=Set5[2])[-1]
SetIID_S6<-  subset(DataT_IID_S, year>=Set6[1] & year<=Set6[2])[-1]
SetIID_S7<-  subset(DataT_IID_S, year>=Set7[1] & year<=Set7[2])[-1]
SetIID_S8<-  subset(DataT_IID_S, year>=Set8[1] & year<=Set8[2])[-1]

Mat_IID_S1<-FunMat(SetIID_S1, Set1)
Mat_IID_S2<-FunMat(SetIID_S2, Set2)
Mat_IID_S3<-FunMat(SetIID_S3, Set3)
Mat_IID_S4<-FunMat(SetIID_S4, Set4)
```

```r
Mat_IID_S5<-FunMat(SetIID_S5, Set5)
Mat_IID_S6<-FunMat(SetIID_S6, Set6)
Mat_IID_S7<-FunMat(SetIID_S7, Set7)
Mat_IID_S8<-FunMat(SetIID_S8, Set8)

RetroMats_pre_S<- list(Mat_IID_S1, Mat_IID_S2, Mat_IID_S3, Mat_IID_S4,
Mat_IID_S5, Mat_IID_S6, Mat_IID_S7, Mat_IID_S8 )
RetroMats_S<-
RetroMats_pre_S[1:length(na.omit(unlist(lapply(RetroMats_pre_S,sum))))]
write.table(RetroMats_S, file = paste('IID_S
Matrices',StockAggr,Population[1],'.csv'), sep=',', quote = F, col.names=TRUE,
row.names = FALSE)
LambdasIID_S<- as.numeric(unlist(lapply(RetroMats_S,lambda)))

Avg_Lambda_IID_S<- mean(LambdasIID_S)
cat('Average IID_S Lambda TR',Period,'=',Avg_Lambda_IID_S,'. Number of IID_S
Matrices=',length(RetroMats_S),"\n")
MeanMat_S <- FunMat(DataT_IID_S[-1],Period)

SdMat_S  <- matrix(NA, ncol= length(RetroMats_S[[1]][,1]),nrow=
length(RetroMats_S[[1]][1,]))
for(i in 1:length(RetroMats_S[[1]][,1])){
  for(j in 1:length(RetroMats_S[[1]][1,])){
    SdMat_S [i,j] = sd(sapply(RetroMats_S,function(x)x[i,j]))
    }}
SdMat_S

write.table(MeanMat_S, file = paste('Mean Matrix
Scenario',StockAggr,Population[1],'.csv'), sep=',', quote = F, col.names=F,
row.names = F)
write.table(SdMat_S,   file = paste('SD Matrix Scenario',
StockAggr,Population[1],'.csv'), sep=',', quote = F, col.names=F, row.names = F)

#**************  Stochastic Growth Rate  Scenarios   IID only   *****************

GR_Retro_S<- stoch.growth.rate(RetroMats_S, prob = NULL, maxt = 50000,
verbose=TRUE)
lambda_Retro_S<-exp(GR_Retro_S$approx)
lambda_Retro_S_CI<-exp(GR_Retro_S$sim.CI)
lambda_stoch_S <- c(lambda_Retro_S,lambda_Retro_S_CI)


#************** Stochastic Projected Population Size Scenarios *****************

Project_S.lt <- vector("list", length(tmaxes)) # create list
for(i in 1:length(tmaxes)){Project_S.lt [[i]] <- matrix(data = NA,
                                      nrow = nreps ,
                                      ncol = 7,
                                      byrow = FALSE,
                                      dimnames = NULL)}
for(t in 1:length(tmaxes)){
Project_S.lt [[t]]<- stoch.projection(RetroMats_S, n0=CountsLastyear$nlastYear,
tmax = tmaxes[t], nreps = nreps, prob = NULL,
nmax = NULL, sumweight = rep(1, length(n0)), verbose=FALSE)
}

graphics.off()
pdf(paste('Projections of Pop Size',Population[1],Period[1],'-
',Period[2],StockAggr, "IID",'.pdf'),width=10,height=8)
par( oma=c(2,2,2,2), mar=c(1.5,2,3,2),mai=c(0.4,0.8,0.8,0.4))
par (mfrow=c(2,2))
hist(apply(Project_S.lt[[1]],1,sum),col = colhS, ylab="", xlab="", main=
paste(tmaxes[1],'years'));legend('topleft',bty='n', paste('Mean Pop',
round(mean(apply(Project_S.lt[[1]],1,sum)),0)))
```

```
hist(apply(Project_S.lt[[2]],1,sum),col = colhS, ylab="", xlab="", main=
paste(tmaxes[2],'years'));legend('topleft',bty='n', paste('Mean Pop',
round(mean(apply(Project_S.lt[[2]],1,sum)),0)))
hist(apply(Project_S.lt[[3]],1,sum),col = colhS, ylab="", xlab="", main=
paste(tmaxes[3],'years'));legend('topleft',bty='n', paste('Mean Pop',
round(mean(apply(Project_S.lt[[3]],1,sum)),0)))
hist(apply(Project_S.lt[[4]],1,sum),col = colhS, ylab="", xlab="", main=
paste(tmaxes[4],'years'));legend('topleft',bty='n', paste('Mean Pop',
round(mean(apply(Project_S.lt[[4]],1,sum)),0)))
 mtext(paste('Projections of Pop Size',StockAggr, "IID",Population[1], "mult of
HR=",Mult),side = 3, outer = TRUE, col = "black", cex= 1.2)
 mtext (text= "Population Numbers", side=1, outer=TRUE, cex=1., font = 2 )
 mtext (text= "Frequency", side=2,outer=TRUE, cex=1., font = 2 )
 mtext(paste('Stoch. Lambda Demographic=',round(lambda_stoch[1],5),'.
Scenario=',round(lambda_stoch_S[1],5)),side=4,outer=TRUE, cex=1., font = 2)
dev.off()
}

if(Use_F.Impacts==TRUE){
addFI<- paste('Fishing scenarios TR is disabled. Fishery impacts=',Use_F.Impacts)
print(addFI)
}


#<<<@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@>>>
#<<<@@@@@@@@@@@@   17. FISHING SCENARIOS – OCEAN ABUNDANCE    @@@@@@@@@@@@@@@@@>>>
#<<<@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@>>>

           # <<< NOTE: THIS SECTION ALSO RUNS FISHERY IMPACTS >>>#

# This section simulates fishing scenarios for chinook Ocean Abundance. The user
# controls an inverse multiplier for the harvest rate (HR) that affects the stock
# aggregates directly. The stock aggregate is user defined from the list of
#significant stocks
# from the multiple regressions (SignifR). See section 2.7 Fishing scenarios for
# more information.
# Note: The multiplier MLT can take values from 0.0 to 2.0, with the latter value
#impling HR=0.


MLT <- 1.64     # Multiplier. In OA is directly proportional to VR; Between 1 and
2
#only for increases in OA. FI  is an alternative measure of OA and is also
directly #proportional to VR
# MLT = 0.0 to maximize HR
print(SignifR)  # List of significant stock aggregates
cat('OA or FI Scenario for Population', Population ,"\n")  # Make sure the stock
is #selected from the right population
StockAggrOA= "CW_OA_2"   # Set stock aggregate FROM SignifR. Test: "FE_OA_5YA"
"ALL2a_FI_0"
colhOA<- terrain.colors(20) # Colour for output. It can be changed according to
user #preferences. See ?palette


#_____
#-------------------------------------------------------------------------------

if(length(subset(SignifR,Chinook_Run==StockAggrOA)[,1])==0){
addNoRun<- paste('Error: Stock Aggregate',StockAggrOA,'not found in Significant
OA or FI  Chinook Run')
print(addNoRun)
stop(paste('Fishery Impacts=',Use_F.Impacts))
}

OA_Stock  <- subset(ChinData,select=StockAggrOA)
```

```r
OA_Stock_New <- OA_Stock*MLT

identRunOA  <- subset(RegModPos, Chinook_Run==StockAggrOA)

New_VR_OA <- matrix(NA, ncol=length(identRunOA[,1]),nrow=length(OA_Stock_New
[,1]))
for(f in 1:length(identRunOA[,1])){
New_VR_OA[,f]  <-
beta_backtr(identRunOA$intercept[f],identRunOA$slope1[f],OA_Stock_New [,1])
colnames(New_VR_OA)<- as.character(identRunOA$VitalRate)
}
New_VR_OA

New_VR_OA<-ifelse(colnames(New_VR_OA)== "F1_Fecundity" & New_VR_OA >
max(F1_Fecundity),max(F1_Fecundity),New_VR_OA)
New_VR_OA<-ifelse(colnames(New_VR_OA)== "F2_Fecundity" & New_VR_OA >
max(F2_Fecundity),max(F2_Fecundity),New_VR_OA)
New_VR_OA

Old_VR_OA<-  subset(allVR, select= as.character(identRunOA$VitalRate))
Old_VR_OA

if(MLT<1){   #
  Sce_VR_OA<- matrix(NA,ncol=length(New_VR_OA[1,]) ,nrow=length(New_VR_OA[,1]))
  for(v in 1: length(New_VR_OA[1,])){
     Sce_VR_OA[,v] <-
ifelse(Old_VR_OA[,v]>New_VR_OA[,v],New_VR_OA[,v],Old_VR_OA[,v])
     }}

if(MLT>1){
  Sce_VR_OA<- matrix(NA,ncol=length(New_VR_OA[1,]) ,nrow=length(New_VR_OA[,1]))
  for(v in 1: length(New_VR_OA[1,])){
     Sce_VR_OA[,v] <-
ifelse(Old_VR_OA[,v]>New_VR_OA[,v],Old_VR_OA[,v],New_VR_OA[,v])
     }}

colnames(Sce_VR_OA)<- as.character(identRunOA$VitalRate)

TestVR_OA_Sc <- cbind(Old_VR_OA[,1], New_VR_OA[,1], Sce_VR_OA[,1])
colnames(TestVR_OA_Sc) <- c('Old_VR_OA','New_VR_OA','Sce_VR_OA')
cat(paste("MLT OA=",MLT),"VR_OA=",as.character(identRunOA$VitalRate)[1]   ,"\n");
print(TestVR_OA_Sc)

DataT_IID_OA  <- allVR
DataT_IID_OA[as.character(identRunOA$VitalRate)]<-Sce_VR_OA

DataT_IID_OA – allVR
DataT_IID_OA<- cbind(year=DataT_IID$year,DataT_IID_OA)

SetIID_OA1<-  subset(DataT_IID_OA, year>=Set1[1] & year<=Set1[2])[-1]
SetIID_OA2<-  subset(DataT_IID_OA, year>=Set2[1] & year<=Set2[2])[-1]
SetIID_OA3<-  subset(DataT_IID_OA, year>=Set3[1] & year<=Set3[2])[-1]
SetIID_OA4<-  subset(DataT_IID_OA, year>=Set4[1] & year<=Set4[2])[-1]
SetIID_OA5<-  subset(DataT_IID_OA, year>=Set5[1] & year<=Set5[2])[-1]
SetIID_OA6<-  subset(DataT_IID_OA, year>=Set6[1] & year<=Set6[2])[-1]
SetIID_OA7<-  subset(DataT_IID_OA, year>=Set7[1] & year<=Set7[2])[-1]
SetIID_OA8<-  subset(DataT_IID_OA, year>=Set8[1] & year<=Set8[2])[-1]

Mat_IID_OA1<-FunMat(SetIID_OA1, Set1)
Mat_IID_OA2<-FunMat(SetIID_OA2, Set2)
Mat_IID_OA3<-FunMat(SetIID_OA3, Set3)
Mat_IID_OA4<-FunMat(SetIID_OA4, Set4)
Mat_IID_OA5<-FunMat(SetIID_OA5, Set5)
Mat_IID_OA6<-FunMat(SetIID_OA6, Set6)
Mat_IID_OA7<-FunMat(SetIID_OA7, Set7)
```

```r
Mat_IID_OA8<-FunMat(SetIID_OA8, Set8)

RetroMats_pre_OA<- list(Mat_IID_OA1, Mat_IID_OA2, Mat_IID_OA3, Mat_IID_OA4,
Mat_IID_OA5, Mat_IID_OA6, Mat_IID_OA7, Mat_IID_OA8 )
RetroMats_OA<-
RetroMats_pre_OA[1:length(na.omit(unlist(lapply(RetroMats_pre_OA,sum))))]
write.table(RetroMats_OA, file = paste('IID_OA Matrices',StockAggrOA,
Population[1],'.csv'), sep=',', quote = F, col.names=TRUE, row.names = FALSE)
LambdasIID_OA<- as.numeric(unlist(lapply(RetroMats_OA,lambda)))

Avg_Lambda_IID_OA<- mean(LambdasIID_OA)
cat('Average IID_OA Lambda OA',Period,'=',Avg_Lambda_IID_OA,'. Number of IID_OA
Matrices=',length(RetroMats_OA),"\n")

MeanMat_OA <- FunMat(DataT_IID_OA[-1],Period)
SdMat_OA  <- matrix(NA, ncol= length(RetroMats_OA[[1]][,1]),nrow=
length(RetroMats_OA[[1]][1,]))
for(i in 1:length(RetroMats_OA[[1]][,1])){
  for(j in 1:length(RetroMats_OA[[1]][1,])){
    SdMat_OA [i,j] = sd(sapply(RetroMats_OA,function(x)x[i,j]))
    }}
SdMat_OA

write.table(MeanMat_OA, file = paste('Mean Matrix
Scenario',StockAggrOA,Population[1],'.csv'), sep=',', quote = F, col.names=F,
row.names = F)
write.table(SdMat_OA,   file = paste('SD Matrix Scenario',
StockAggrOA,Population[1],'.csv'), sep=',', quote = F, col.names=F, row.names =
F)

#*************    Stochastic Growth Rate  Scenarios IID only     **************
GR_RetroS_OA<- stoch.growth.rate(RetroMats_OA, prob = NULL, maxt = 50000,
verbose=TRUE)
lambda_Retro_OA<-exp(GR_RetroS_OA$approx)
lambda_Retro_OA_CI<-exp(GR_RetroS_OA$sim.CI)
lambda_stoch_OA <- c(lambda_Retro_OA,lambda_Retro_OA_CI)

#************** Stochastic Projected Population Size Scenarios *****************
Project_OA.lt <- vector("list", length(tmaxes))
for(i in 1:length(tmaxes)){Project_OA.lt [[i]] <- matrix(data = NA,
                                        nrow = nreps ,
                                        ncol = 7,
                                        byrow = FALSE,
                                        dimnames = NULL)}
for(t in 1:length(tmaxes)){
Project_OA.lt [[t]]<- stoch.projection(RetroMats_OA, n0=CountsLastyear$nlastYear,
tmax = tmaxes[t], nreps = nreps, prob = NULL,
nmax = NULL, sumweight = rep(1, length(n0)), verbose=FALSE)
}

graphics.off()
pdf(paste('Projections of Pop Size',Population[1],Period[1],'-
',Period[2],StockAggrOA, "IID",'.pdf'),width=10,height=8)
par( oma=c(2,2,2,2), mar=c(1.5,2,3,2),mai=c(0.4,0.8,0.8,0.4))
par (mfrow=c(2,2))
hist(apply(Project_OA.lt[[1]],1,sum),col = colhOA, ylab="", xlab="", main=
paste(tmaxes[1],'years'));legend('topleft',bty='n', paste('Mean Pop',
round(mean(apply(Project_OA.lt[[1]],1,sum)),0)))
hist(apply(Project_OA.lt[[2]],1,sum),col = colhOA, ylab="", xlab="", main=
paste(tmaxes[2],'years'));legend('topleft',bty='n', paste('Mean Pop',
round(mean(apply(Project_OA.lt[[2]],1,sum)),0)))
hist(apply(Project_OA.lt[[3]],1,sum),col = colhOA, ylab="", xlab="", main=
paste(tmaxes[3],'years'));legend('topleft',bty='n', paste('Mean Pop',
round(mean(apply(Project_OA.lt[[3]],1,sum)),0)))
```

```
hist(apply(Project_OA.lt[[4]],1,sum),col = colhOA, ylab="", xlab="", main=
paste(tmaxes[4],'years'));legend('topleft',bty='n', paste('Mean Pop',
round(mean(apply(Project_OA.lt[[4]],1,sum)),0)))
 mtext(paste('Projections of Pop Size',StockAggrOA, "IID",Population[1], "mult
of", ifelse(Use_F.Impacts==TRUE,paste('FI'),paste('OA')),'=',MLT),side = 3, outer
= TRUE, col = "black", cex= 1.2)
 mtext (text= "Population Numbers", side=1, outer=TRUE, cex=1., font = 2 )
 mtext (text= "Frequency", side=2,outer=TRUE, cex=1., font = 2 )
 mtext(paste('Stoch. Lambda Demographic=',round(lambda_stoch[1],5),'.
Scenario=',round(lambda_stoch_OA[1],5)),side=4,outer=TRUE, cex=1., font = 2)
dev.off()

#<<<@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@>>>
#<<<@@@@@@@@@@@ 18. REGRESSIONS KW ABUNDANCE ~ CHINOOK ABUNDANCE  @@@@@@@@@@@@@>>>
#<<<@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@>>>
# This section performs simple linear regressions with abundance data.
#_____
#-------------------------------------------------------------------------------
CountModsSim<- AbundFun(ChinD=ChinData0.1,SurvT=df.abundances[-
1],Chindef=Chindefs0.1,p_val=p_val)

CountModsSim<- subset(CountModsSim,slope1>=0)

ifelse(Population[1]=='SRKW',
CountModsSim <- subset(CountModsSim, SR_Hyp != 'NA' & SR_Hyp !='Hybrid'),
CountModsSim <- subset(CountModsSim, NR_Hyp != 'NA' & NR_Hyp !='Hybrid'))

colnames(CountModsSim)[1]<- 'Stage'
write.table(CountModsSim, file = paste('Abundance
Regressions',Population[1],Period[1],"-",Period[2],'.csv'), sep=',', quote =
FALSE, row.names = FALSE)

#<<<@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@>>>
#<<<@@@@@@@@@@@@@           19. CHUM MULTIPLE REGRESSIONS          @@@@@@@@@@@@@>>>
#<<<@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@>>>
# This section runs analyses using chum data and performs a multiple regeression
the
# it is then compared to the simple regression used in chinook models.
# NOTE: The outputs of this section may overwrite previous outputs, therefore
# this section must be ran at the end of analyses with Chinook.

#<<<requires running BetaDiagniostics Section>>>

Hyp_Ind=2        # Hypothesis 1 or 2.  Used for the SELECTION OF VR for CHUM MR

#_____
#-------------------------------------------------------------------------------
if(SkipBetaD == TRUE){stop(paste('ERROR, Beta Diagnostics Section is not
enabled'))}


ChumDefs<-
read.table(paste(getwd(),'/','R_Inputs','/','Chum_Ab_Definitions_R.csv',sep=""),h
eader=T, sep=",")
ChumData<-
read.table(paste(getwd(),'/','R_Inputs','/','ChumAbundance_Data_R.csv',sep=""),he
ader=T, sep=",")
ChumModsSim <- AllFunB(chumD=ChumData[-
1],AllvrT=AllVR,ChumDef=ChumDefs,p_val=p_val)
ChumModsSim <- subset(ChumModsSim,slope1>=0)
Chum_sel<-ChumModsSim[ChumModsSim$p_value %in%
as.vector(tapply(ChumModsSim$p_value,factor(ChumModsSim$VitalRate),min)),]

if(Population=='NRKW'){Chum_sel$NR_Hyp<- NULL}
if(Population=='SRKW'){Chum_sel$SR_Hyp<- NULL}
```

```r
ifelse(Population=="NRKW",
SignifRcm<-RegModPos[c('VitalRate','Chinook_Run', 'NR_Hyp' ,'p_value',
'slope1')],
SignifRcm<-RegModPos[c('VitalRate','Chinook_Run', 'SR_Hyp' ,'p_value',
'slope1')])

if(Population=="SRKW"){
SignifRcm1<- subset(SignifRcm,  SR_Hyp=='1a');SignifRcm2<- subset(SignifRcm,
SR_Hyp=='2a')}

if(Population=="NRKW"){
SignifRcm1<- subset(SignifRcm,  NR_Hyp=='1b');SignifRcm2<- subset(SignifRcm,
NR_Hyp=='2b')}

Sel_Hyp1<-SignifRcm1[SignifRcm1$p_value %in%
as.vector(tapply(SignifRcm1$p_value,factor(SignifRcm1$VitalRate),min)),]
Sel_Hyp2<-SignifRcm2[SignifRcm2$p_value %in%
as.vector(tapply(SignifRcm2$p_value,factor(SignifRcm2$VitalRate),min)),]

df.AllVR<- matrix(NA,nrow=length(allVR[,1]), ncol=length(allVR[1,]))
for (i in 1:length(allVR[1,])){
   df.AllVR [,i] <- ifelse(allVR[,i]==1,0.99999,allVR[,i])
     }

df.AllVR2<- matrix(NA,nrow=length(allVR[,1]), ncol=length(allVR[1,]))
for (i in 1:length(allVR[1,])){
    df.AllVR2 [,i] <- ifelse(df.AllVR[,i]==0,0.000001,df.AllVR[,i])
     }

AllVR <- as.data.frame(df.AllVR2)
colnames(AllVR)<- names(allVR)

if(Hyp_Ind==1){Hyp=Sel_Hyp1}
if(Hyp_Ind==2){Hyp=Sel_Hyp2}


Sel_VR<- subset(AllVR, select=as.character(factor(unique(Hyp$VitalRate))))

factor(unique(Hyp$VitalRate));factor(unique(Chum_sel$VitalRate))
Overlap_VR<-  factor(unique(Chum_sel$VitalRate))[
factor(unique(Chum_sel$VitalRate)) %in% factor(unique(Hyp$VitalRate)) ]
print(Overlap_VR)

#*********************************************************************************
#**********                 SELECTION OF VR for CHUM MR             **********
#*********************************************************************************
VR= "F1_Fecundity"

if(length(Overlap_VR[Overlap_VR==VR]) ==0){stop(paste('VR is not found in
Overlap_VR'))}

Y= as.vector(subset(Sel_VR, select=VR))
X1<- as.vector(subset(ChinData,select=as.character(factor(subset(Hyp,
VitalRate==VR)$Chinook_Run))))
X2<- as.vector(subset(ChumData,select=as.character(factor(subset(Chum_sel,
VitalRate==VR)$Chum_Run))))

MR_CC<- betareg(Y[,1]~X1[,1]+X2[,1])
coefMR_CC <- coef(MR_CC)

options(scipen=8)
SlopeSR= Hyp[Hyp$VitalRate==VR,]$slope1
SlopeMR= round(as.vector(coefMR_CC[2]),8)
InterMR= round(as.vector(coefMR_CC[1]),8)
```

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```r
rsqrMR <- summary(MR_CC)$pseudo.r.squared
p_valueMR  <- summary(MR_CC)$coefficients$precision[4]

AIC_SR= subset(AIC_Comp,VitalRate==VR &
Chinook_Run==Hyp[Hyp$VitalRate==VR,]$Chinook_Run)$AIC_Beta
AIC_MR= AIC(MR_CC)

Table_chum<-
data.frame(chin.stk=names(X1),chum.stk=names(X2),VR,SlopeSR,SlopeMR,AIC_SR,AIC_MR
)
Table_chum
write.table(Table_chum, file = paste('Simple-
Mult.Chum',VR,"H=",Hyp_Ind,Population[1],Period[1],"-",Period[2],'.csv'),
sep=',', quote = FALSE, row.names = FALSE)

options(scipen=0)

if(SlopeMR>SlopeSR){
RegSel<- subset(SimpleRegMods, VitalRate==VR & Chinook_Run==
Hyp[Hyp$VitalRate==VR,]$Chinook_Run & p_value== Hyp[Hyp$VitalRate==VR,]$p_value)
RegWin<-RegSel
RegWin$slope1<-SlopeMR
RegWin$intercept<-InterMR
RegWin$R_squared<- rsqrMR
RegWin$p_value<-  p_valueMR
}

if(SlopeMR < SlopeSR){
stop(print(paste('For hypothesis',Hyp_Ind,'and',VR,"no regression meets the
conditions specified for slope and AIC")))
}

#<<<@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@>>>
#<<<@@@@@@@@@     20. ELASTICITY OF INTERACTION FOR CHUM MR        @@@@@@@@@>>>
#<<<@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@>>>

percIncr <- 0.1          #(0.1 =10%) Percentage increment of chinnok abundance
Variant<- 2              # or 1 . Use 2 as default because it includes 95% CI.

#_____
#--------------------------------------------------------------------------------

if(SlopeMR > SlopeSR){

chum.stock=c(names(X2),"NA")
Hypothesis= c(Hyp_Ind,Hyp_Ind)
ResultChum<- funElastMR(RegWin)
ResultChin<- funElastMR(RegSel)

Compar_CC<- cbind(chum.stock,Hypothesis,rbind(ResultChum,ResultChin))

Compar_CC<-
Compar_CC[c('VitalRate','Chinook_Run','chum.stock','R_squared','intercept','slope
1','p_value','Elast.Inter','Elast.Inter95','Hypothesis')]
Compar_CC
write.table(Compar_CC, file = paste('Elasticity of Interactions MR
Chum',VR,'H=',Hyp_Ind,Population[1],'.csv'), sep=',', quote = FALSE, row.names =
FALSE)
}

if(SlopeMR < SlopeSR){
stop(print(paste('For hypothesis',Hyp_Ind,'and',VR,"no regression meets the
conditions specified for slope and AIC")))
}
```

```
#<<<@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@>>>
#    @@@@@@@@@@@@                    ##<<< END >>>##                  @@@@@@@@@@@@
#<<<@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@>>>
```

R-Code written by Andres Araujo, February 2013.

A 8.2. R-code functions

```
#*************************  FUNCTIONS   *********************************
```

```r
set.seed=pi*pi
CountFun<-function(counts, factor){
Count<- as.integer(tapply(counts,factor(factor),sum))
}

# Function modified from RPA code to estimate all Eigen (does not use popbio)
eigenall <- function(A) {
    EV <- eigen(A, symmetric=F)
         EigenVecs <- EV$vectors
         lambdas <- EV$values
    V  <- Conj(solve(EigenVecs ))

    lambda1_dominant <- as.numeric(lambdas[1])
    w <- as.numeric(EigenVecs [,1])
    w <- w/sum(w)
    v <- Re(V[1,])
    v <- v/v[1]

    list(lambdas=lambdas, lambda1_dominant =lambda1_dominant, EigenVecs=EigenVecs
, w=w, V=V, v=v)
}

lnorms <- function(means, vars, rawelems) {


nmeans <- log(means) - 0.5*log(vars/means^2+1)
nvars <- log(vars/means^2+1)
normals <- rawelems*sqrt(nvars) + nmeans;
lns <- exp(normals)
lns
}


# GammaRV: See G.S. Fishman, 1973, Concepts and Methods in Discrete Event
# Digital Simulation, Wiley, New York, pp. 208-209.

gammarv <- function(Alpha, Beta, n){
Gamm <- matrix(NA, 1, n)
for(i in 1:n){
    X <- 0
    k <- floor(Alpha)
    g <- Alpha - k
    if(k > 0){
        X <- -log( prod( runif(k) ) )
    }
    if(g == 0){
        Gamm[i] <- Beta*X
    }
    else{
        a <- g
        b <- 1 - g
        y <- 1
        z <- 1
        while(y + z > 1){
            y=runif(1)^(1/a)
            z=runif(1)^(1/b)
        }
        Y <- y/(y+z)
        Z <- -log( runif(1) )
        Gamm[i] <- Beta*(X+Y*Z)
    }
}
Gamm
}
```

```r
# betarv(m,v,n) generates a row vector of length n, the elements of which
# are Beta random variables with mean m and variance v;
# see G.S. Fishman, 1973, Concepts and Methods in Discrete Event
# Digital Simulation, Wiley, New York, pp. 204-208.

betarv <- function(m,v,n) {

if (v==0) {
   Beta <- matrix(m,1,n)
}
else if (v >= m*(1-m) ) {
    print("Variance of Beta too large given the mean")
}
else {
    a <- m*(m*(1-m)/v - 1)
    b <- (1-m)*(m*(1-m)/v - 1)
    Beta <- matrix(NA, 1,n)
    for (i in 1:n) {
        k1 <- floor(a)
        k2 <- floor(b)
        if (k1==0 & k2==0) {
            Y <- 1
            Z <- 1
            while (Y+Z > 1) {
                Y <- runif(1)^(1/a)
                Z <- runif(1)^(1/b)
            }
        }
        else {
            Y <- gammarv(a,1,1)
            Z <- gammarv(b,1,1)
        }
        Beta[i] <- Y/(Y+Z)
    }
}
Beta

}


# Scaled BetaRV
# betarv(m,v,n) generates a row vector of length n, the elements of which
# are Beta random variables with mean m and variance v;
# see G.S. Fishman, 1973, Concepts and Methods in Discrete Event
# Digital Simulation, Wiley, New York, pp. 204-208.

betarv <- function(m,v,n, bmin=0, bmax=1) {

mbeta <- (m-bmin)/(bmax-bmin)
vbeta <- v/(bmax-bmin)^2

if (v==0) {
   Beta <- matrix(m, 1,n)
}
else if (vbeta >= mbeta*(1-mbeta) ) {
    print("Variance of Beta too large given the mean")
}
else {
    a <- mbeta*(mbeta*(1-mbeta)/vbeta - 1)
    b <- (1-mbeta)*(mbeta*(1-mbeta)/vbeta - 1)
    Beta <- matrix(NA, 1,n)
    for (i in 1:n) {
        k1 <- floor(a)
        k2 <- floor(b)
```

```
        if (k1==0 & k2==0) {
            Y <- 1
            Z <- 1
            while (Y+Z > 1) {
                Y <- runif(1)^(1/a)
                Z <- runif(1)^(1/b)
            }
        }
        else {
            Y <- gammarv(a,1,1)
            Z <- gammarv(b,1,1)
        }
        Beta[i] <- Y/(Y+Z)
    }
    Beta <- Beta*(bmax-bmin)+bmin
}

Beta

}



SampFun<- function(a){
sample(Vrtable, size=1, replace = TRUE, prob = NULL)
}


#Standarizing Function
Stdz_Fun <- function(x){
out<- x/mean(x) ; out
}

#Survivals Function, Simple Regression
#Produces a data.frame containing the vital rates, run name, lag, r-squared,
#regressions coefficients based on a > specified p-value of models based on
#Survivals.


SurvFun<- function(ChinD, SurvT, Chindef, p_val){
storemVR<- matrix(NA, nrow=length(ChinD), ncol=6)
storem1<- list(storemVR,storemVR, storemVR,storemVR,storemVR,storemVR, storemVR)

for (i in 1:length(SurvT[1,])){
    for (j in 1:length(ChinD)){

        y <- SurvT[,i]
        x <- ChinD[,j]

    lmSimple    <- lm( y~x)
    coefSimple <- coef(lmSimple)

    summSimple <- summary(lmSimple)
                  options(digits=5)
    rsqr <- summSimple$adj.r.squared
    p_value    <- summSimple$coefficients[8]



storemVR[j,] <- c(i,j,rsqr,coefSimple[1],coefSimple[2],p_value)
storem1[[i]] <- storemVR
   }
   }
SurvMods<- rbind(storem1[[1]],storem1[[2]], storem1[[3]],storem1[[4]],
storem1[[5]],storem1[[6]], storem1[[7]])
```

```
VRnamex<- rep(colnames(SurvT), each=length(ChinD))
Runnamex<- rep(colnames(ChinD),length(SurvT[1,]))
SurvModsnam<-
c('VitalRate','Chinook_Run','Lag','R_squared','intercept','slope1','p_value',
ifelse(Population[1]=='NRKW', paste('NR_Hyp'), paste('SR_Hyp')))

ifelse(Population[1]=='NRKW',
 SurvModsRes<-cbind(VRnamex, Runnamex, Chindef$lag,
as.data.frame(SurvMods),Chindef$NR_Hyp)[,-(4:5)]
,
 SurvModsRes<-cbind(VRnamex, Runnamex, Chindef$lag,
as.data.frame(SurvMods),Chindef$SR_Hyp)[,-(4:5)]
 )
SurvModsRes
colnames(SurvModsRes)<-SurvModsnam


SurvModsResSel<- subset(SurvModsRes, p_value <= p_val)
}


#Function modified to estimate regressions with abundance
AbundFun<- function(ChinD, SurvT, Chindef, p_val){

storemVR<- matrix(NA, nrow=length(ChinD), ncol=6)
storem1<- list(storemVR,storemVR, storemVR,storemVR,storemVR,storemVR, storemVR,
storemVR)

for (i in 1:length(SurvT[1,])){


    for (j in 1:length(ChinD)){

        y <- SurvT[,i]
        x <- ChinD[,j]

     lmSimple    <- lm( y~x)
     coefSimple <- coef(lmSimple)

     summSimple <- summary(lmSimple)
                 options(digits=5)
     rsqr <- summSimple$adj.r.squared
     p_value    <- summSimple$coefficients[8]

storemVR[j,] <- c(i,j,rsqr,coefSimple[1],coefSimple[2],p_value)
storem1[[i]] <- storemVR
    }
    }
SurvMods<- rbind(storem1[[1]],storem1[[2]], storem1[[3]],storem1[[4]],
storem1[[5]],storem1[[6]], storem1[[7]],storem1[[8]] )

VRnamex<- rep(colnames(SurvT), each=length(ChinD))
Runnamex<- rep(colnames(ChinD),length(SurvT[1,]))
SurvModsnam<-
c('VitalRate','Chinook_Run','Lag','R_squared','intercept','slope1','p_value',
ifelse(Population[1]=='NRKW', paste('NR_Hyp'), paste('SR_Hyp')))


ifelse(Population[1]=='NRKW',
 SurvModsRes<-cbind(VRnamex, Runnamex, Chindef$lag,
as.data.frame(SurvMods),Chindef$NR_Hyp)[,-(4:5)]
,
```

```r
 SurvModsRes<-cbind(VRnamex, Runnamex, Chindef$lag,
as.data.frame(SurvMods),Chindef$SR_Hyp)[,-(4:5)]
 )
SurvModsRes
colnames(SurvModsRes)<-SurvModsnam

SurvModsResSel<- subset(SurvModsRes, p_value <= p_val)
}


#Fecundities Function, Simple Regression
#Produces a data.frame containing the vital rates, run name, lag, r-squared,
#regressions coefficients based on a > specified p-value of models based on
#Fecundities


FecFun<- function(ChinD, OffsprT, Chindef, p_val){
#For loop
storemVR<- matrix(NA, nrow=length(ChinD), ncol=6)
storem1<- list(storemVR,storemVR)

for (i in 1:length(OffsprT[1,])){
    for (j in 1:length(ChinD)){

        y <- OffsprT[,i]
        x <- ChinD[,j]

     lmSimple   <- lm( y~x)
     coefSimple <- coef(lmSimple)

     summSimple <- summary(lmSimple)
                   options(digits=5)
     rsqr <- summSimple$adj.r.squared
     p_value     <- summSimple$coefficients[8]

storemVR[j,] <- c(i,j,rsqr,coefSimple[1],coefSimple[2],p_value)
storem1[[i]] <- storemVR
   }
   }
FecMods<- rbind(storem1[[1]],storem1[[2]])

VRnamex<- rep(colnames(OffsprT), each=length(ChinD))
Runnamex<- rep(colnames(ChinD),length(OffsprT[1,]))
FecModsnam<-
c('VitalRate','Chinook_Run','Lag','R_squared','intercept','slope1','p_value',
ifelse(Population[1]=='NRKW', paste('NR_Hyp'), paste('SR_Hyp')))


ifelse(Population[1]=='NRKW',
 FecModsRes<-cbind(VRnamex, Runnamex, Chindef$lag,
as.data.frame(FecMods),Chindef$NR_Hyp)[,-(4:5)]
,
 FecModsRes<-cbind(VRnamex, Runnamex, Chindef$lag,
as.data.frame(FecMods),Chindef$SR_Hyp)[,-(4:5)]
 )
FecModsRes
colnames(FecModsRes)<-FecModsnam

FecModsResSel<- subset(FecModsRes, p_value <= p_val)

}

#Fecundities Function, Multiple Regression 2 Independent Variables
#Produces a data.frame containing the vital rates, run name, lag, r-squared,
```

```r
#regressions coefficients based on a > specified p-value of models based on
#Fecundities


FecFunMR<- function(ChinD, VRateT, Chindef, p_val){
storemVR<- matrix(NA, nrow=max(Chindef$ChinMR2), ncol=7)
storem1<- list(storemVR,storemVR)

for (i in 1:length(VRateT[1,])){
    for (j in 1:max(Chindef$ChinMR2)){
        y <- VRateT[,i]
        x1 <- subset(ChinD,select=as.vector(subset(Chindef,
ChinMR2==j)$TimeSeries)[1])
        x2 <- subset(ChinD,select=as.vector(subset(Chindef,
ChinMR2==j)$TimeSeries)[2])
x1<-as.vector(x1[,1])
x2<-as.vector(x2[,1])


    lmMR    <- lm( y~x1+x2)
    coefMR <- coef(lmMR)

    summMR <- summary(lmMR)
                options(digits=5)
    rsqr <- summMR$adj.r.squared
    p_value    <-
pf(summMR$fstatistic[1],summMR$fstatistic[2],summMR$fstatistic[3],lower.tail=FALS
E)

storemVR[j,] <- c(i,j,rsqr,coefMR[1],coefMR[2],coefMR[3],p_value)
storem1[[i]] <- storemVR
    }
    }
FecMods<- rbind(storem1[[1]],storem1[[2]])

VRnamex<- rep(colnames(VRateT), each=max(Chindef$ChinMR2))

storeVec<- matrix(NA, nrow=max(Chindef$ChinMR2), ncol=1)
Chindef$TimeSeries
F_Chindef <- factor(Chindef$ChinMR2)
haha<- apply(as.data.frame(tapply(Chindef$TimeSeries, F_Chindef, list) ),2,paste)
for (i in 1:length(haha)/2){
storeVec[i,]<-paste(haha[,i][1],"+",haha[,i][2])
}
storeVec<-as.vector(storeVec[,1])

Runnamex<- rep(storeVec,length(VRateT[1,]))
FecModsnam<-
c('VitalRate','Chinook_Run','Lag','R_squared','intercept','slope1','slope2','p_va
lue', ifelse(Population[1]=='NRKW', paste('NR_Hyp'), paste('SR_Hyp')))


ifelse(Population[1]=='NRKW',
 FecModsRes<-cbind(VRnamex, Runnamex, Chindef$lag,
as.data.frame(FecMods),Chindef$NR_Hyp)[,-(4:5)]
,
 FecModsRes<-cbind(VRnamex, Runnamex, Chindef$lag,
as.data.frame(FecMods),Chindef$SR_Hyp)[,-(4:5)]
 )
FecModsRes
colnames(FecModsRes)<-FecModsnam


FecModsResSel<- subset(FecModsRes, p_value <= p_val)
```

```r
}

#Survivals Function, Multiple Regression 2 Independent Variables
#Produces a data.frame containing the vital rates, run name, lag, r-squared,
#regressions coefficients based on a > specified p-value of models based on
#Survivals


SurFunMR<- function(ChinD, VRateT, Chindef, p_val){
storemVR<- matrix(NA, nrow=max(Chindef$ChinMR2), ncol=7)
storem1<- list(storemVR,storemVR)

for (i in 1:length(VRateT[1,])){
    for (j in 1:max(Chindef$ChinMR2)){

        y <- VRateT[,i]
        x1 <- subset(ChinD,select=as.vector(subset(Chindef,
ChinMR2==j)$TimeSeries)[1])
        x2 <- subset(ChinD,select=as.vector(subset(Chindef,
ChinMR2==j)$TimeSeries)[2])
x1<-as.vector(x1[,1])
x2<-as.vector(x2[,1])


    lmMR    <- lm( y~x1+x2)
    coefMR <- coef(lmMR)

    summMR <- summary(lmMR)
                options(digits=5)
    rsqr <- summMR$adj.r.squared
    p_value     <-
pf(summMR$fstatistic[1],summMR$fstatistic[2],summMR$fstatistic[3],lower.tail=FALS
E)



storemVR[j,] <- c(i,j,rsqr,coefMR[1],coefMR[2],coefMR[3],p_value)
storem1[[i]] <- storemVR
    }
    }
storem1
SurMods<-
rbind(storem1[[1]],storem1[[2]],storem1[[3]],storem1[[4]],storem1[[5]],storem1[[6
]],storem1[[7]])


VRnamex<- rep(colnames(VRateT), each=max(Chindef$ChinMR2))


storeVec<- matrix(NA, nrow=max(Chindef$ChinMR2), ncol=1)
Chindef$TimeSeries
F_Chindef <- factor(Chindef$ChinMR2)
haha<- apply(as.data.frame(tapply(Chindef$TimeSeries, F_Chindef, list) ),2,paste)
for (i in 1:length(haha)/2){
storeVec[i,]<-paste(haha[,i][1],"+",haha[,i][2])
}
storeVec<-as.vector(storeVec[,1])

Runnamex<- rep(storeVec,length(VRateT[1,]))
SurModsnam<-
c('VitalRate','Chinook_Run','Lag','R_squared','intercept','slope1','slope2','p_va
lue', ifelse(Population[1]=='NRKW', paste('NR_Hyp'), paste('SR_Hyp')))


ifelse(Population[1]=='NRKW',
```

```
 SurModsRes<-cbind(VRnamex, Runnamex,
rep(Chindef$lag[Chindef$lag==0],length(VRateT[1,])),
as.data.frame(SurMods),rep(Chindef$NR_Hyp[Chindef$lag==0],length(VRateT[1,])))[,-
(4:5)]
,
 SurModsRes<-cbind(VRnamex, Runnamex,
rep(Chindef$lag[Chindef$lag==0],length(VRateT[1,])),
as.data.frame(SurMods),rep(Chindef$SR_Hyp[Chindef$lag==0],length(VRateT[1,])))[,-
(4:5)]
 )
SurModsRes
colnames(SurModsRes)<-SurModsnam

SurModsResSel<- subset(SurModsRes, p_value <= p_val)


}


#Fecundities Function, Multiple Regression 3 Independent Variables
#Produces a data.frame containing the vital rates, run name, lag, r-squared,
#regressions coefficients based on a > specified p-value of models based on
#Fecundities


FecFunMR3<- function(ChinD, VRateT, Chindef, p_val, pop){

storemVR<- matrix(NA, nrow=max(Chindef$ChinMR3), ncol=8)
storem1<- list(storemVR,storemVR)

for (i in 1:length(VRateT[1,])){
    for (j in 1:max(Chindef$ChinMR3)){

        y <- VRateT[,i]
        x1 <- subset(ChinD,select=as.vector(subset(Chindef,
ChinMR3==j)$TimeSeries)[1])
        x2 <- subset(ChinD,select=as.vector(subset(Chindef,
ChinMR3==j)$TimeSeries)[2])
        x3 <- subset(ChinD,select=as.vector(subset(Chindef,
ChinMR3==j)$TimeSeries)[3])
x1<-as.vector(x1[,1])
x2<-as.vector(x2[,1])
x3<-as.vector(x3[,1])

    lmMR    <- lm( y~x1+x2+x3)
    coefMR <- coef(lmMR)

    summMR <- summary(lmMR)
                options(digits=5)
    rsqr <- summMR$adj.r.squared
    p_value      <-
pf(summMR$fstatistic[1],summMR$fstatistic[2],summMR$fstatistic[3],lower.tail=FALS
E)


storemVR[j,] <- c(i,j,rsqr,coefMR[1],coefMR[2],coefMR[3],coefMR[4],p_value)
storem1[[i]] <- storemVR
    }
    }
storem1
SurMods<- rbind(storem1[[1]],storem1[[2]])


VRnamex<- rep(colnames(VRateT), each=max(Chindef$ChinMR3))
```

```
storeVec<- matrix(NA, nrow=max(Chindef$ChinMR3), ncol=1)
Chindef$TimeSeries
F_Chindef <- factor(Chindef$ChinMR3)
haha<- apply(as.data.frame(tapply(Chindef$TimeSeries, F_Chindef, list) ),2,paste)
for (i in 1:length(haha)/3){
storeVec[i,]<-paste(haha[,i][1],"+",haha[,i][2],"+",haha[,i][3])
}
storeVec<-as.vector(storeVec[,1])

Runnamex<- rep(storeVec,length(VRateT[1,]))
SurModsnam<-
c('VitalRate','Chinook_Run','Lag','R_squared','intercept','slope1','slope2','slop
e3','p_value', ifelse(Population[1]=="NRKW", paste('NR_Hyp'), paste('SR_Hyp')))

ifelse(Population[1]=='NRKW',
 SurModsRes<-cbind(VRnamex, Runnamex,
rep(Chindef$lag[Chindef$lag==0],length(VRateT[1,])),
as.data.frame(SurMods),rep(Chindef$NR_Hyp[Chindef$lag==0],length(VRateT[1,])))[,-
(4:5)]
,
 SurModsRes<-cbind(VRnamex, Runnamex,
rep(Chindef$lag[Chindef$lag==0],length(VRateT[1,])),
as.data.frame(SurMods),rep(Chindef$SR_Hyp[Chindef$lag==0],length(VRateT[1,])))[,-
(4:5)]
 )
SurModsRes
colnames(SurModsRes)<-SurModsnam


SurModsResSel<- subset(SurModsRes, p_value <= p_val)

}


#Beta Regressions betareg


SurvFunB<- function(ChinD, SurvT, Chindef, p_val){


storemVR<- matrix(NA, nrow=length(ChinD), ncol=6)
storem1<- list(storemVR,storemVR, storemVR,storemVR,storemVR,storemVR, storemVR)

for (i in 1:length(SurvT[1,])){
    for (j in 1:length(ChinD)){
         y <- SurvT[,i]
         x <- ChinD[,j]
        y= ifelse(y==1,0.9999,y)
        y= ifelse(y==0,0.0001,y)
     lmSimple    <- betareg( y~x, na.action=na.omit)

     coefSimple <- coef(lmSimple)
     summSimple <- summary(lmSimple)
                 options(digits=5)
     summSimple$residuals
     rsqr <- summSimple$pseudo.r.squared
     p_value    <- summSimple$coefficients$mean[8]

storemVR[j,] <- c(i,j,rsqr,coefSimple[1],coefSimple[2],p_value)
storem1[[i]] <- storemVR
    }
    }
storem1
SurvMods<- rbind(storem1[[1]],storem1[[2]], storem1[[3]],storem1[[4]],
storem1[[5]],storem1[[6]], storem1[[7]])
```

```r
VRnamex<- rep(colnames(SurvT), each=length(ChinD))
Runnamex<- rep(colnames(ChinD),length(SurvT[1,]))
SurvModsnam<-
c('VitalRate','Chinook_Run','Lag','R_squared','intercept','slope1','p_value',
ifelse(Population[1]=='NRKW', paste('NR_Hyp'), paste('SR_Hyp')))


ifelse(Population[1]=='NRKW',
 SurvModsRes<-cbind(VRnamex, Runnamex, Chindef$lag,
as.data.frame(SurvMods),Chindef$NR_Hyp)[,-(4:5)]
,
 SurvModsRes<-cbind(VRnamex, Runnamex, Chindef$lag,
as.data.frame(SurvMods),Chindef$SR_Hyp)[,-(4:5)]
 )
SurvModsRes
colnames(SurvModsRes)<-SurvModsnam

SurvModsResSel<- subset(SurvModsRes, p_value <= p_val)
}

#Beta FecFun
FecFunB<- function(ChinD, OffsprT, Chindef, p_val){
storemVR<- matrix(NA, nrow=length(ChinD), ncol=6)
storem1<- list(storemVR,storemVR)

for (i in 1:length(OffsprT[1,])){
    for (j in 1:length(ChinD)){

        y <- OffsprT[,i]
        x <- ChinD[,j]
        y= ifelse(y==1,0.9999,y)
        y= ifelse(y==0,0.0001,y)
    lmSimple    <- betareg( y~x, na.action=na.omit)
    coefSimple <- coef(lmSimple)

    summSimple <- summary(lmSimple)
                options(digits=5)
    rsqr <- summSimple$pseudo.r.squared
    p_value    <- summSimple$coefficients$mean[8]


storemVR[j,] <- c(i,j,rsqr,coefSimple[1],coefSimple[2],p_value)
storem1[[i]] <- storemVR
    }
    }
storem1
FecMods<- rbind(storem1[[1]],storem1[[2]])


VRnamex<- rep(colnames(OffsprT), each=length(ChinD))
Runnamex<- rep(colnames(ChinD),length(OffsprT[1,]))
FecModsnam<-
c('VitalRate','Chinook_Run','Lag','R_squared','intercept','slope1','p_value',
ifelse(Population[1]=='NRKW', paste('NR_Hyp'), paste('SR_Hyp')))

ifelse(Population[1]=='NRKW',
 FecModsRes<-cbind(VRnamex, Runnamex, Chindef$lag,
as.data.frame(FecMods),Chindef$NR_Hyp)[,-(4:5)]
,
 FecModsRes<-cbind(VRnamex, Runnamex, Chindef$lag,
as.data.frame(FecMods),Chindef$SR_Hyp)[,-(4:5)]
 )
FecModsRes
```

```r
colnames(FecModsRes)<-FecModsnam

FecModsResSel<- subset(FecModsRes, p_value <= p_val)
}


# Beta Fecundities Function, Multiple Regression 2 Independent Variables
FecFunMRB<- function(ChinD, VRateT, Chindef, p_val){
storemVR<- matrix(NA, nrow=max(Chindef$ChinMR2), ncol=7)
storem1<- list(storemVR,storemVR)

for (i in 1:length(VRateT[1,])){
    for (j in 1:max(Chindef$ChinMR2)){
         y <- VRateT[,i]
         x1 <- subset(ChinD,select=as.vector(subset(Chindef,
ChinMR2==j)$TimeSeries)[1])
         x2 <- subset(ChinD,select=as.vector(subset(Chindef,
ChinMR2==j)$TimeSeries)[2])
x1<-as.vector(x1[,1])
x2<-as.vector(x2[,1])
         y= ifelse(y==1,0.9999,y)
         y= ifelse(y==0,0.0001,y)


     lmMR    <- betareg( y~x1+x2, na.action=na.omit)
     coefMR <- coef(lmMR)

     summMR <- summary(lmMR)
                  options(digits=5)
     rsqr <- summMR$pseudo.r.squared
     p_value    <- summSimple$coefficients$precision[4]


storemVR[j,] <- c(i,j,rsqr,coefMR[1],coefMR[2],coefMR[3],p_value)
storem1[[i]] <- storemVR
    }
    }
storem1
FecMods<- rbind(storem1[[1]],storem1[[2]])


VRnamex<- rep(colnames(VRateT), each=max(Chindef$ChinMR2))


storeVec<- matrix(NA, nrow=max(Chindef$ChinMR2), ncol=1)
Chindef$TimeSeries
F_Chindef <- factor(Chindef$ChinMR2)
haha<- apply(as.data.frame(tapply(Chindef$TimeSeries, F_Chindef, list) ),2,paste)
for (i in 1:length(haha)/2){
storeVec[i,]<-paste(haha[,i][1],"+",haha[,i][2])
}
storeVec<-as.vector(storeVec[,1])

Runnamex<- rep(storeVec,length(VRateT[1,]))
FecModsnam<-
c('VitalRate','Chinook_Run','Lag','R_squared','intercept','slope1','slope2','p_va
lue', ifelse(Population[1]=='NRKW', paste('NR_Hyp'), paste('SR_Hyp')))


ifelse(Population[1]=='NRKW',
 FecModsRes<-cbind(VRnamex, Runnamex, Chindef$lag,
as.data.frame(FecMods),Chindef$NR_Hyp)[,-(4:5)]
,
```

```
 FecModsRes<-cbind(VRnamex, Runnamex, Chindef$lag,
as.data.frame(FecMods),Chindef$SR_Hyp)[,-(4:5)]
 )
FecModsRes
colnames(FecModsRes)<-FecModsnam


FecModsResSel<- subset(FecModsRes, p_value <= p_val)


}


# Beta Survivals Function, Multiple Regression 2 Independent Variables
SurFunMRB<- function(ChinD, VRateT, Chindef, p_val){
storemVR<- matrix(NA, nrow=max(Chindef$ChinMR2), ncol=7)
storem1<- list(storemVR,storemVR)

for (i in 1:length(VRateT[1,])){
    for (j in 1:max(Chindef$ChinMR2)){

        y <- VRateT[,i]
        x1 <- subset(ChinD,select=as.vector(subset(Chindef,
ChinMR2==j)$TimeSeries)[1])
        x2 <- subset(ChinD,select=as.vector(subset(Chindef,
ChinMR2==j)$TimeSeries)[2])
x1<-as.vector(x1[,1])
x2<-as.vector(x2[,1])
     y= ifelse(y==1,0.9999,y)
     y= ifelse(y==0,0.0001,y)

    lmMR   <- betareg( y~x1+x2, na.action=na.omit)
    coefMR <- coef(lmMR)

    summMR <- summary(lmMR)
               options(digits=5)
    rsqr <- summMR$pseudo.r.squared
    p_value     <- summSimple$coefficients$precision[4]


storemVR[j,] <- c(i,j,rsqr,coefMR[1],coefMR[2],coefMR[3],p_value)
storem1[[i]] <- storemVR
    }
    }

SurMods<-
rbind(storem1[[1]],storem1[[2]],storem1[[3]],storem1[[4]],storem1[[5]],storem1[[6
]],storem1[[7]])

VRnamex<- rep(colnames(VRateT), each=max(Chindef$ChinMR2))

storeVec<- matrix(NA, nrow=max(Chindef$ChinMR2), ncol=1)
Chindef$TimeSeries
F_Chindef <- factor(Chindef$ChinMR2)
haha<- apply(as.data.frame(tapply(Chindef$TimeSeries, F_Chindef, list) ),2,paste)
for (i in 1:length(haha)/2){
storeVec[i,]<-paste(haha[,i][1],"+",haha[,i][2])
}
storeVec<-as.vector(storeVec[,1])

Runnamex<- rep(storeVec,length(VRateT[1,]))
SurModsnam<-
c('VitalRate','Chinook_Run','Lag','R_squared','intercept','slope1','slope2','p_va
lue', ifelse(Population[1]=='NRKW', paste('NR_Hyp'), paste('SR_Hyp')))

ifelse(Population[1]=='NRKW',
```

```
 SurModsRes<-cbind(VRnamex, Runnamex,
rep(Chindef$lag[Chindef$lag==0],length(VRateT[1,])),
as.data.frame(SurMods),rep(Chindef$NR_Hyp[Chindef$lag==0],length(VRateT[1,])))[,-
(4:5)]
,
 SurModsRes<-cbind(VRnamex, Runnamex,
rep(Chindef$lag[Chindef$lag==0],length(VRateT[1,])),
as.data.frame(SurMods),rep(Chindef$SR_Hyp[Chindef$lag==0],length(VRateT[1,])))[,-
(4:5)]
 )
SurModsRes
colnames(SurModsRes)<-SurModsnam

SurModsResSel<- subset(SurModsRes, p_value <= p_val)
}

# Beta Fecundities Function, Multiple Regression 3 Independent Variables
FecFunMR3B<- function(ChinD, VRateT, Chindef, p_val, pop){

storemVR<- matrix(NA, nrow=max(Chindef$ChinMR3), ncol=8)
storem1<- list(storemVR,storemVR)

for (i in 1:length(VRateT[1,])){
    for (j in 1:max(Chindef$ChinMR3)){

        y <- VRateT[,i]
        x1 <- subset(ChinD,select=as.vector(subset(Chindef,
ChinMR3==j)$TimeSeries)[1])
        x2 <- subset(ChinD,select=as.vector(subset(Chindef,
ChinMR3==j)$TimeSeries)[2])
        x3 <- subset(ChinD,select=as.vector(subset(Chindef,
ChinMR3==j)$TimeSeries)[3])
x1<-as.vector(x1[,1])
x2<-as.vector(x2[,1])
x3<-as.vector(x3[,1])
        y= ifelse(y==1,0.9999,y)
        y= ifelse(y==0,0.0001,y)

    lmMR    <- betareg( y~x1+x2+x3, na.action=na.omit)
    coefMR <- coef(lmMR)

    summMR <- summary(lmMR)
                options(digits=5)
    rsqr <- summMR$pseudo.r.squared
    p_value    <- summSimple$coefficients$precision[4]

storemVR[j,] <- c(i,j,rsqr,coefMR[1],coefMR[2],coefMR[3],coefMR[4],p_value)
storem1[[i]] <- storemVR
    }
    }

SurMods<- rbind(storem1[[1]],storem1[[2]])

VRnamex<- rep(colnames(VRateT), each=max(Chindef$ChinMR3))

storeVec<- matrix(NA, nrow=max(Chindef$ChinMR3), ncol=1)
Chindef$TimeSeries
F_Chindef <- factor(Chindef$ChinMR3)
haha<- apply(as.data.frame(tapply(Chindef$TimeSeries, F_Chindef, list) ),2,paste)
for (i in 1:length(haha)/3){
storeVec[i,]<-paste(haha[,i][1],"+",haha[,i][2],"+",haha[,i][3])
}
storeVec<-as.vector(storeVec[,1])

Runnamex<- rep(storeVec,length(VRateT[1,]))
```

```r
SurModsnam<-
c('VitalRate','Chinook_Run','Lag','R_squared','intercept','slope1','slope2','slop
e3','p_value', ifelse(Population[1]=="NRKW", paste('NR_Hyp'), paste('SR_Hyp')))

ifelse(Population[1]=='NRKW',
 SurModsRes<-cbind(VRnamex, Runnamex,
rep(Chindef$lag[Chindef$lag==0],length(VRateT[1,])),
as.data.frame(SurMods),rep(Chindef$NR_Hyp[Chindef$lag==0],length(VRateT[1,])))[,-
(4:5)]
,
 SurModsRes<-cbind(VRnamex, Runnamex,
rep(Chindef$lag[Chindef$lag==0],length(VRateT[1,])),
as.data.frame(SurMods),rep(Chindef$SR_Hyp[Chindef$lag==0],length(VRateT[1,])))[,-
(4:5)]
 )
SurModsRes
colnames(SurModsRes)<-SurModsnam

SurModsResSel<- subset(SurModsRes, p_value <= p_val)
}

#Mean Matrices for direct perturbation. This section contains a several matrices
#as a function of a new vital rate estimated from perturbations #of chinook
#abundances. There is one function for each vital rate.

KW.matNames<-
c('KW.matSs1','KW.matSs2','KW.matSs3','KW.matSs4','KW.matSs5','KW.matSs6','KW.mat
Ss7','KW.matSf3','KW.matSf4')
FunTSs1<- function(Ss1_){
KW.matSs1_<- matrix(c(
        0, (Ss1_^0.5*(Ss2*Sg2*Sp2*Sf3))/2, (Ss1_^0.5*(((1+(Ss3*(1-
Sg3)))*Sf3)+(Ss3*Sg3*Sf4)))/2,  (Ss1_^0.5*((1+(Ss4*(1-Sg4)))*Sf4))/2, 0, 0, 0,
            Ss1_^0.5, Ss2*(1-Sg2), 0, 0, 0, 0, 0,
        0, Ss2*Sg2*Sp2, Ss3*(1-Sg3), 0, 0, 0, 0,
        0, 0, Ss3*Sg3, Ss4*(1-Sg4), 0, 0, 0,
        0, 0, 0, Ss4*Sg4, Ss5, 0, 0,
        0, Ss2*Sg2*Sp3, 0, 0, 0, Ss6*(1-Sg6), 0,
        0, 0, 0, 0, 0, Ss6*Sg6, Ss7),
        nrow = 7, ncol = 7, byrow = TRUE
        )
        }


FunTSs2<- function(Ss2_){
KW.matSs2<- matrix(c(
        0, (Ss1^0.5*(Ss2_*Sg2*Sp2*Sf3))/2, (Ss1^0.5*(((1+(Ss3*(1-
Sg3)))*Sf3)+(Ss3*Sg3*Sf4)))/2,  (Ss1^0.5*((1+(Ss4*(1-Sg4)))*Sf4))/2, 0, 0, 0,
            Ss1^0.5, Ss2_*(1-Sg2), 0, 0, 0, 0, 0,
        0, Ss2_*Sg2*Sp2, Ss3*(1-Sg3), 0, 0, 0, 0,
        0, 0, Ss3*Sg3, Ss4*(1-Sg4), 0, 0, 0,
        0, 0, 0, Ss4*Sg4, Ss5, 0, 0,
        0, Ss2_*Sg2*Sp3, 0, 0, 0, Ss6*(1-Sg6), 0,
        0, 0, 0, 0, 0, Ss6*Sg6, Ss7),
        nrow = 7, ncol = 7, byrow = TRUE
        )
        }

FunTSs3<- function(Ss3_){
KW.matSs3<- matrix(c(
        0, (Ss1^0.5*(Ss2*Sg2*Sp2*Sf3))/2, (Ss1^0.5*(((1+(Ss3_*(1-
Sg3)))*Sf3)+(Ss3_*Sg3*Sf4)))/2,  (Ss1^0.5*((1+(Ss4*(1-Sg4)))*Sf4))/2, 0, 0, 0,
            Ss1^0.5, Ss2*(1-Sg2), 0, 0, 0, 0, 0,
        0, Ss2*Sg2*Sp2, Ss3_*(1-Sg3), 0, 0, 0, 0,
        0, 0, Ss3_*Sg3, Ss4*(1-Sg4), 0, 0, 0,
        0, 0, 0, Ss4*Sg4, Ss5, 0, 0,
```

```r
        0, Ss2*Sg2*Sp3, 0, 0, 0, Ss6*(1-Sg6), 0,
        0, 0, 0, 0, 0, Ss6*Sg6, Ss7),
        nrow = 7, ncol = 7, byrow = TRUE
        )
        }

FunTSs4<- function(Ss4_){
KW.matSs4_<- matrix(c(
        0, (Ss1^0.5*(Ss2*Sg2*Sp2*Sf3))/2, (Ss1^0.5*(((1+(Ss3*(1-
Sg3)))*Sf3)+(Ss3*Sg3*Sf4)))/2,  (Ss1^0.5*((1+(Ss4_*(1-Sg4)))*Sf4))/2, 0, 0, 0,
             Ss1^0.5, Ss2*(1-Sg2), 0, 0, 0, 0, 0,
        0, Ss2*Sg2*Sp2, Ss3*(1-Sg3), 0, 0, 0, 0,
        0, 0, Ss3*Sg3, Ss4_*(1-Sg4), 0, 0, 0,
        0, 0, 0, Ss4_*Sg4, Ss5, 0, 0,
        0, Ss2*Sg2*Sp3, 0, 0, 0, Ss6*(1-Sg6), 0,
        0, 0, 0, 0, 0, Ss6*Sg6, Ss7),
        nrow = 7, ncol = 7, byrow = TRUE
        )
        }

FunTSs5<- function(Ss5_){
KW.matSs5<- matrix(c(
        0, (Ss1^0.5*(Ss2*Sg2*Sp2*Sf3))/2, (Ss1^0.5*(((1+(Ss3*(1-
Sg3)))*Sf3)+(Ss3*Sg3*Sf4)))/2,  (Ss1^0.5*((1+(Ss4*(1-Sg4)))*Sf4))/2, 0, 0, 0,
             Ss1^0.5, Ss2*(1-Sg2), 0, 0, 0, 0, 0,
        0, Ss2*Sg2*Sp2, Ss3*(1-Sg3), 0, 0, 0, 0,
        0, 0, Ss3*Sg3, Ss4*(1-Sg4), 0, 0, 0,
        0, 0, 0, Ss4*Sg4, Ss5_, 0, 0,
        0, Ss2*Sg2*Sp3, 0, 0, 0, Ss6*(1-Sg6), 0,
        0, 0, 0, 0, 0, Ss6*Sg6, Ss7),
        nrow = 7, ncol = 7, byrow = TRUE
        )
        }

FunTSs6<- function(Ss6_){
KW.matSs6_<- matrix(c(
        0, (Ss1^0.5*(Ss2*Sg2*Sp2*Sf3))/2, (Ss1^0.5*(((1+(Ss3*(1-
Sg3)))*Sf3)+(Ss3*Sg3*Sf4)))/2,  (Ss1^0.5*((1+(Ss4*(1-Sg4)))*Sf4))/2, 0, 0, 0,
             Ss1^0.5, Ss2*(1-Sg2), 0, 0, 0, 0, 0,
        0, Ss2*Sg2*Sp2, Ss3*(1-Sg3), 0, 0, 0, 0,
        0, 0, Ss3*Sg3, Ss4*(1-Sg4), 0, 0, 0,
        0, 0, 0, Ss4*Sg4, Ss5, 0, 0,
        0, Ss2*Sg2*Sp3, 0, 0, 0, Ss6_*(1-Sg6), 0,
        0, 0, 0, 0, 0, Ss6_*Sg6, Ss7),
        nrow = 7, ncol = 7, byrow = TRUE
        )
        }

FunTSs7<- function(Ss7_){
KW.matSs7<- matrix(c(
        0, (Ss1^0.5*(Ss2*Sg2*Sp2*Sf3))/2, (Ss1^0.5*(((1+(Ss3*(1-
Sg3)))*Sf3)+(Ss3*Sg3*Sf4)))/2,  (Ss1^0.5*((1+(Ss4*(1-Sg4)))*Sf4))/2, 0, 0, 0,
             Ss1^0.5, Ss2*(1-Sg2), 0, 0, 0, 0, 0,
        0, Ss2*Sg2*Sp2, Ss3*(1-Sg3), 0, 0, 0, 0,
        0, 0, Ss3*Sg3, Ss4*(1-Sg4), 0, 0, 0,
        0, 0, 0, Ss4*Sg4, Ss5, 0, 0,
        0, Ss2*Sg2*Sp3, 0, 0, 0, Ss6*(1-Sg6), 0,
        0, 0, 0, 0, 0, Ss6*Sg6, Ss7_),
        nrow = 7, ncol = 7, byrow = TRUE
        )
        }

FunTSf3<- function(Sf3_){
KW.matSf3<- matrix(c(
```

```r
        0, (Ss1^0.5*(Ss2*Sg2*Sp2*Sf3_))/2, (Ss1^0.5*(((1+(Ss3*(1-
Sg3)))*Sf3_)+(Ss3*Sg3*Sf4)))/2,  (Ss1^0.5*((1+(Ss4*(1-Sg4)))*Sf4))/2, 0, 0, 0,
            Ss1^0.5, Ss2*(1-Sg2), 0, 0, 0, 0, 0,
        0, Ss2*Sg2*Sp2, Ss3*(1-Sg3), 0, 0, 0, 0,
        0, 0, Ss3*Sg3, Ss4*(1-Sg4), 0, 0, 0,
        0, 0, 0, Ss4*Sg4, Ss5, 0, 0,
        0, Ss2*Sg2*Sp3, 0, 0, 0, Ss6*(1-Sg6), 0,
        0, 0, 0, 0, 0, Ss6*Sg6, Ss7),
        nrow = 7, ncol = 7, byrow = TRUE
        )
        }

FunTSf4<- function(Sf4_){
KW.matSf4<- matrix(c(
        0, (Ss1^0.5*(Ss2*Sg2*Sp2*Sf3))/2, (Ss1^0.5*(((1+(Ss3*(1-
Sg3)))*Sf3)+(Ss3*Sg3*Sf4_)))/2,  (Ss1^0.5*((1+(Ss4*(1-Sg4)))*Sf4_))/2, 0, 0, 0,
            Ss1^0.5, Ss2*(1-Sg2), 0, 0, 0, 0, 0,
        0, Ss2*Sg2*Sp2, Ss3*(1-Sg3), 0, 0, 0, 0,
        0, 0, Ss3*Sg3, Ss4*(1-Sg4), 0, 0, 0,
        0, 0, 0, Ss4*Sg4, Ss5, 0, 0,
        0, Ss2*Sg2*Sp3, 0, 0, 0, Ss6*(1-Sg6), 0,
        0, 0, 0, 0, 0, Ss6*Sg6, Ss7),
        nrow = 7, ncol = 7, byrow = TRUE
        )
        }


#Testing Chinook Runs affecting Several VRs
FunSs3_Ss4<- function(VR_o1,VR_ch1,VR_o2,VR_ch2){

KW.vr_Ss3_Ss4<- list(Ss1=Ss1, Ss2=Ss2 ,Ss3_1=VR_o1, Ss3_2=VR_ch1 ,Ss4_1=VR_o2,
Ss4_2=VR_ch2,Ss5=Ss5 ,Ss6=Ss6, Ss7=Ss7 ,Sg2=Sg2 ,Sg3=Sg3, Sg4=Sg4 ,Sg6=Sg6
,Sp2=Sp2 ,Sp3=Sp3 ,Sf3=Sf3 ,Sf4=Sf4)
KW.EC_Ss3_Ss4<- expression(
        0, (Ss1^0.5*(Ss2*Sg2*Sp2*Sf3))/2, (Ss1^0.5*(((1+((Ss3_1+Ss3_2)*(1-
Sg3)))*Sf3)+((Ss3_1+Ss3_2)*Sg3*Sf4)))/2,  (Ss1^0.5*((1+((Ss4_1+Ss4_2)*(1-
Sg4)))*Sf4))/2, 0, 0, 0,
            Ss1^0.5, Ss2*(1-Sg2), 0, 0, 0, 0, 0,
        0, Ss2*Sg2*Sp2, (Ss3_1+Ss3_2)*(1-Sg3), 0, 0, 0, 0,
        0, 0, (Ss3_1+Ss3_2)*Sg3, (Ss4_1+Ss4_2)*(1-Sg4), 0, 0, 0,
        0, 0, 0, (Ss4_1+Ss4_2)*Sg4, Ss5, 0, 0,
        0, Ss2*Sg2*Sp3, 0, 0, 0, Ss6*(1-Sg6), 0,
        0, 0, 0, 0, 0, Ss6*Sg6, Ss7
        )
KW2_Ss3_Ss4  <- vitalsens(KW.EC_Ss3_Ss4,KW.vr_Ss3_Ss4)
ElasVR_3_4<- c(
as.numeric(KW2_Ss3_Ss4["Ss3_2",][3]),as.numeric(KW2_Ss3_Ss4["Ss4_2",][3]))
        }

#Function modified from PopBio to estimate lambda only.
lambdaPop<- function (A, zero = TRUE){
    ev <- eigen(A)
    lmax <- which.max(Re(ev$values))
    lambda <- Re(ev$values[lmax])
    dr <- rle(round(Mod(ev$values), 5))$values
    dr <- dr[1]/dr[2]
    W <- ev$vectors
    w <- abs(Re(W[, lmax]))
    V <- try(Conj(solve(W)), silent = TRUE)
    if (class(V) == "try-error") {
        eigen.analysis <- list(lambda1 = lambda, stable.stage = w/sum(w),
            sensitivities = A * NA, elasticities = A * NA, repro.value = w *
                NA, damping.ratio = dr)
    }
    else {
```

```r
        v <- abs(Re(V[lmax, ]))
        s <- v %o% w
        if (zero) {
            s[A == 0] <- 0
        }
        e <- s * A/lambda
        x <- dimnames(A)
        dimnames(s) <- x
        names(w) <- x[[1]]
        names(v) <- x[[1]]
        lambdaPop <- list(lambda1 = lambda)
    }
    lambdaPop
}


#Function creates a set of truncated matrixes
FunTrunc<- function(DataTrunc,Set){

SurvDeltaTR<- as.numeric(colMeans(DataTrunc[,1:5], na.rm = TRUE, dims = 1))
MaxAgeTR<-c(CalfAges[2],JuvsAges[2], YRFemAges[2],ORFemAges[2], NA)
SurvGammaTR<-c(1, 1/(MaxAge[2]-MaxAge[1]), 1/(MaxAge[3]-MaxAge[2]),
1/(MaxAge[4]-MaxAge[3]), NA)
MuOffspTR<- c(0,0,mean(DataTrunc[,6]),mean(DataTrunc[,7]) ,0)

VitalR_TR<- rbind(SurvDeltaTR,MaxAgeTR,SurvGammaTR,MuOffspTR)

Mean.Ratio.Fem

Ss1tr = SurvDeltaTR[1]
Ss2tr = SurvDeltaTR[2]
Ss3tr = SurvDeltaTR[3]
Ss4tr = SurvDeltaTR[4]
Ss5tr = SurvDeltaTR[5]
Sg2tr = SurvGammaTR[2]
Sg3tr = SurvGammaTR[3]
Sg4tr = SurvGammaTR[4]
Sp2tr = Mean.Ratio.Fem
Sf3tr = MuOffspTR [3]
Sf4tr = MuOffspTR [4]
MeanVRtr=c(Ss1tr,Ss2tr,Ss3tr,Ss4tr,Ss5tr,Sg2tr,Sg3tr,Sg4tr,Sp2tr,Sf3tr,Sf4tr)

KW.TR.ep<- expression(
        0, (Ss1tr^0.5*(Ss2tr*Sg2tr*Sp2tr*Sf3tr))/2, (Ss1tr^0.5*(((1+(Ss3tr*(1-
Sg3tr)))*Sp2tr*Sf3tr)+(Ss3tr*Sg3tr*Sp2tr*Sf4tr)))/2,  (Ss1tr^0.5*((1+(Ss4tr*(1-
Sg4tr)))*Sp2tr*Sf4tr))/2,
             Ss1tr^0.5, Ss2tr*(1-Sg2tr), 0, 0,
        0, Ss2tr*Sg2tr, Ss3tr*(1-Sg3tr), 0,
        0, 0, Ss3tr*Sg3tr, Ss4tr*(1-Sg4tr)
        )

KW.mat.TR<- matrix(c(
         0, (Ss1tr^0.5*(Ss2tr*Sg2tr*Sp2tr*Sf3tr))/2,
(Ss1tr^0.5*(((1+(Ss3tr*(1-Sg3tr)))*Sp2tr*Sf3tr)+(Ss3tr*Sg3tr*Sp2tr*Sf4tr)))/2,
(Ss1tr^0.5*((1+(Ss4tr*(1-Sg4tr)))*Sp2tr*Sf4tr))/2,
             Ss1tr^0.5, Ss2tr*(1-Sg2tr), 0, 0,
        0, Ss2tr*Sg2tr, Ss3tr*(1-Sg3tr), 0,
        0, 0, Ss3tr*Sg3tr, Ss4tr*(1-Sg4tr)),
        nrow = 4, ncol = 4, byrow = TRUE
        )

cat(paste('Mean Matrix Period',Set[1],'-
',Set[2],Population[1]),"\n");print(KW.mat.TR)
}
```

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```r
#Function creates a set of non-truncated matrixes
FunMat<- function(VRData,Set){
SurvSigmaF<- as.numeric(colMeans(VRData, na.rm = TRUE, dims = 1))

MaxAge<-c(CalfAges[2],JuvsAges[2], YRFemAges[2],ORFemAges[2],
max(PRFem[PRFem$Count>0,]$Age),YMMalAges[2],max(OMMal[OMMal$Count>0,]$Age))

SurvGamma<-c(1, 1/(MaxAge[2]-MaxAge[1]), 1/(MaxAge[3]-MaxAge[2]),  1/(MaxAge[4]-
MaxAge[3]),  1/(MaxAge[5]-MaxAge[4]), 1/(MaxAge[6]-MaxAge[2]),1/(MaxAge[7]-
MaxAge[6]) )


Temp1.Mal<-Temp1[Temp1$Cat1=='Male',]
Temp1.Fem<-Temp1[Temp1$Cat1=='Female',]
Perc.Mal<-Temp1.Mal[3]/(Temp1.Mal[3]+Temp1.Fem[3])
Perc.Fem<-Temp1.Fem[3]/(Temp1.Mal[3]+Temp1.Fem[3])

Mean.Perc.Mal<- colMeans(Perc.Mal,na.rm = TRUE);Var.Perc.Mal<- var(Perc.Mal,na.rm
= TRUE)
Mean.Perc.Fem<- colMeans(Perc.Fem,na.rm = TRUE);Var.Perc.Fem<- var(Perc.Fem,na.rm
= TRUE)

Mean.Ratio.Mal<- sum(Temp1.Mal[3])/sum(Temp1.Mal[3]+Temp1.Fem[3])
Mean.Ratio.Fem<- sum(Temp1.Fem[3])/sum(Temp1.Mal[3]+Temp1.Fem[3])

PercentPhi<- c(NaN,NaN,as.numeric(Mean.Ratio.Fem[1]),NaN,NaN,
as.numeric(Mean.Ratio.Mal[1]), NaN)
MuOffspF<- c(0,0,mean(na.omit(VRData[,8])),mean(na.omit(VRData[,9])),0,0,0)

FSs1 = SurvSigmaF[1]
FSs2 = SurvSigmaF[2]
FSs3 = SurvSigmaF[3]
FSs4 = SurvSigmaF[4]
FSs5 = SurvSigmaF[5]
FSs6 = SurvSigmaF[6]
FSs7 = SurvSigmaF[7]
Sg2 = SurvGamma [2]
Sg3 = SurvGamma [3]
Sg4 = SurvGamma [4]
Sg6 = SurvGamma [6]
Sp2 = Mean.Ratio.Fem
Sp3 = PercentPhi[6]
FSf3 = MuOffspF [3]
FSf4 = MuOffspF [4]
FMeanVR=c(FSs1,FSs2,FSs3,FSs4,FSs5,FSs6,FSs7,Sg2,Sg3,Sg4,Sg6,Sp2,Sp3,FSf3,FSf4)


KW.matF<- matrix(c(
      0, (FSs1^0.5*(FSs2*Sg2*Sp2*FSf3))/2, (FSs1^0.5*(((1+(FSs3*(1-
Sg3)))*FSf3)+(FSs3*Sg3*FSf4)))/2,  (FSs1^0.5*((1+(FSs4*(1-Sg4)))*FSf4))/2, 0, 0,
0,
          FSs1^0.5, FSs2*(1-Sg2), 0, 0, 0, 0, 0,
      0, FSs2*Sg2*Sp2, FSs3*(1-Sg3), 0, 0, 0, 0,
      0, 0, FSs3*Sg3, FSs4*(1-Sg4), 0, 0, 0,
      0, 0, 0, FSs4*Sg4, FSs5, 0, 0,
      0, FSs2*Sg2*Sp3, 0, 0, 0, FSs6*(1-Sg6), 0,
      0, 0, 0, 0, 0, FSs6*Sg6, FSs7),
      nrow = 7, ncol = 7, byrow = TRUE
      )

cat(paste('Mean Matrix',Set[1],'-',Set[2],Population[1]),"\n");print(KW.matF)
}
```

```r
#Functions to estimate vital rates from either a Beta or Linear regression
coefficients

#Logit
LogitApl<- function(intercept, slope, x){
VR_Y <-  1/(1+exp(-intercept-(slope*x)))
VR_Y
}

#Linear
LinearApl<- function(intercept, slope, x){
VR_Y <- intercept+ (slope*x)
VR_Y
}

# Function to estimate dependent variable based on the betareg coefficients
beta_backtr<- function(intercept,slope,data){
     1 /(1+exp(-intercept-(slope*data)))
     }

#Function to plot CI elasticities
funElastCI<- function(VR, table){
Elast_VRa  <-  subset(table, VitalRate==VR); options(warn=-1)
graphics.off()

if(length(Elast_VRa[,1])<1){
addNoVR<- paste('No significant regressions with',VR)
print(addNoVR)
}

if(Population=="SRKW"){
colbars<-   ifelse(Elast_VRa$SR_Hyp=='1a','blue','gray')}
if(Population=="NRKW"){
colbars<-   ifelse(Elast_VRa$NR_Hyp=='1b','green','gray')}


if(length(Elast_VRa[,1])>1){
pdf(paste('Elasticity with upper CI',Population[1],VR,'.pdf'),width=8,height=8)
par(mai=c(1.7,0.8,0.8,0.4))
dum<- barplot(Elast_VRa$Elast.Inter, col=colbars,
names.arg=Elast_VRa$Chinook_Run, las=3, main=unique(Elast_VRa$VitalRate),
ylim=c(0,max(Elast_VRa$Elast.Inter95)+0.005))
points(x=dum, y=Elast_VRa$Elast.Inter95, pch=16)
lines(x=dum,y=Elast_VRa$Elast.Inter95,type='h',lty=2,col=colbars)
dev.off()
}}


#Beta Function for Chum, all KW VRs

AllFunB<- function(chumD, AllvrT, ChumDef, p_val){

storemVR<- matrix(NA, nrow=length(chumD), ncol=7)
storem1<- list(storemVR,storemVR,  storemVR,storemVR,storemVR,storemVR,
storemVR,storemVR,  storemVR)


for (i in 1:length(AllvrT[1,])){
    for (j in 1:length(chumD)){
         y <- AllvrT[,i]
         x <- chumD[,j]
       y= ifelse(y==1,0.9999,y)
       y= ifelse(y==0,0.0001,y)
     BSimple   <- betareg( y~x, na.action=na.omit)
     coefSimple <- coef(BSimple)
```

```
        summSimple <- summary(BSimple)
                    options(digits=5)
        summSimple$residuals
        rsqr <- summSimple$pseudo.r.squared
        p_value     <- summSimple$coefficients$mean[8]

        AIC_B<-  AIC(BSimple)

AIC_storem[i,]<- c(AIC_B,AIC_L)

storemVR[j,] <- c(i,j,rsqr,coefSimple[1],coefSimple[2],p_value, AIC_B)
storem1[[i]] <- storemVR
    }
    }
storem1
SurvMods<- rbind(storem1[[1]],storem1[[2]], storem1[[3]],storem1[[4]],
storem1[[5]],storem1[[6]], storem1[[7]],storem1[[8]], storem1[[9]])

VRnamex<- rep(colnames(AllvrT), each=length(chumD))
Runnamex<- rep(colnames(chumD),length(AllvrT[1,]))
SurvModsnam<-
c('VitalRate','Chum_Run','Lag','R_squared','intercept','slope1','p_value', 'AIC',
ifelse(Population[1]=='NRKW', paste('NR_Hyp'), paste('SR_Hyp')))


ifelse(Population[1]=='NRKW',
 SurvModsRes<-cbind(VRnamex, Runnamex, ChumDef$lag,
as.data.frame(SurvMods),ChumDef$NR_Hyp)[,-(4:5)]
,
 SurvModsRes<-cbind(VRnamex, Runnamex, ChumDef$lag,
as.data.frame(SurvMods),ChumDef$SR_Hyp)[,-(4:5)]
 )
SurvModsRes
colnames(SurvModsRes)<-SurvModsnam


SurvModsResSel<- subset(SurvModsRes, p_value <= p_val)
 }


funElastMR<- function(inputTable){

percIncr <- 0.1
Variant<- 2


VRnames_SF<- c(colnames(SurvTable2),colnames(OffsprTable2))
MeanVR_SF<-c(Ss1,Ss2,Ss3,Ss4,Ss5,Ss6,Ss7,Sf3,Sf4)
MeanVR_SFnam<-c('Ss1_','Ss2_','Ss3_','Ss4_','Ss5_','Ss6_','Ss7_','Sf3_','Sf4_')
symsNVR<- c("Ss1","Ss2","Ss3","Ss4","Ss5","Ss6","Ss7","Sf3","Sf4")
Table_SF<- data.frame(VRnames_SF, MeanVR_SF, MeanVR_SFnam, symsNVR)

RegMod<- inputTable

RegMod$MatName  <-
Table_SF$MeanVR_SFnam[match(RegMod$VitalRate,Table_SF$VRnames_SF)]


RegMod$VR_Name <- Table_SF$symsNVR[match(RegMod$VitalRate ,Table_SF$VRnames_SF)]
TableStc.elas <- as.data.frame(t(ElasStats.KW))

colnames(TableStc.elas)<-
c('ElasMean.KW','ElasMed.KW','ElasMin.KW','ElasMax.KW','CI_5','CI_95')
TableStc.elas$Sx <- rownames(TableStc.elas)
```

```
RegMod$E.VR_Stc <-
TableStc.elas$ElasMed.KW[match(RegMod$VR_Name,TableStc.elas$Sx)]
RegMod$E.VR_95  <- TableStc.elas$CI_95[match(RegMod$VR_Name,TableStc.elas$Sx)]

PerturbNames  <- data.frame(KW.matNames, MeanVR_SFnam)
RegMod$PerturbMat <-
PerturbNames$KW.matNames[match(RegMod$MatName,PerturbNames$MeanVR_SFnam)]

X_A<-colMeans(na.omit(ChinData))[-1]
RegMod$X_A <- X_A[match(RegMod$Chinook_Run,names(X_A))]
if (BetaQ_SR=="NO") {
VR_A<- 0.
for (e in 1:length(RegMod[,1])){
VR_A [e] <- RegMod$intercept[e]+ (RegMod$slope1[e] * RegMod$X_A[e])
}
RegMod$VR_A<-VR_A
}

if (BetaQ_SR=="YES") {
VR_A<- 0.
for (e in 1:length(RegMod[,1])){
VR_A [e] <-  1/(1+exp(-RegMod$intercept[e]-(RegMod$slope1[e] * RegMod$X_A[e])))
}
RegMod$VR_A<-VR_A
}


df.list <- vector("list", length(RegMod[,1]))
for(i in 1:length(RegMod[,1])){df.list[[i]] <- matrix(data = NA,
                                      nrow = 7,
                                      ncol = 7,
                                      byrow = FALSE,
                                      dimnames = NULL)}
for (f in 1:length(RegMod[,1])){

 if(RegMod$MatName[f]=='Ss1_') {df.list[[f]]<- FunTSs1(RegMod$VR_A[f])}
 if(RegMod$MatName[f]=='Ss2_') {df.list[[f]]<- FunTSs2(RegMod$VR_A[f])}
 if(RegMod$MatName[f]=='Ss3_') {df.list[[f]]<- FunTSs3(RegMod$VR_A[f])}
 if(RegMod$MatName[f]=='Ss4_') {df.list[[f]]<- FunTSs4(RegMod$VR_A[f])}
 if(RegMod$MatName[f]=='Ss5_') {df.list[[f]]<- FunTSs5(RegMod$VR_A[f])}
 if(RegMod$MatName[f]=='Ss6_') {df.list[[f]]<- FunTSs6(RegMod$VR_A[f])}
 if(RegMod$MatName[f]=='Ss7_') {df.list[[f]]<- FunTSs7(RegMod$VR_A[f])}
 if(RegMod$MatName[f]=='Sf3_') {df.list[[f]]<- FunTSf3(RegMod$VR_A[f])}
 if(RegMod$MatName[f]=='Sf4_') {df.list[[f]]<- FunTSf4(RegMod$VR_A[f])}
 }

RegMod$LambdaA<- as.numeric(unlist(lapply(df.list,lambda)))
RegMod$X_B<- RegMod$X_A*(1+percIncr)

if (BetaQ_SR=="NO") {
VR_B<- 0.
for (e in 1:length(RegMod[,1])){
VR_B [e] <- RegMod$intercept[e]+ (RegMod$slope1[e] * RegMod$X_B[e])
}
RegMod$VR_B<-VR_B
}

if (BetaQ_SR=="YES") {
VR_B<- 0.
for (e in 1:length(RegMod[,1])){
VR_B [e] <-  1/(1+exp(-RegMod$intercept[e]-(RegMod$slope1[e] * RegMod$X_B[e])))
}
RegMod$VR_B<-VR_B
}
```

```r
for (f in 1:length(RegMod[,1])){

 if(RegMod$MatName[f]=='Ss1_') {df.list[[f]]<- FunTSs1(RegMod$VR_B[f])}
 if(RegMod$MatName[f]=='Ss2_') {df.list[[f]]<- FunTSs2(RegMod$VR_B[f])}
 if(RegMod$MatName[f]=='Ss3_') {df.list[[f]]<- FunTSs3(RegMod$VR_B[f])}
 if(RegMod$MatName[f]=='Ss4_') {df.list[[f]]<- FunTSs4(RegMod$VR_B[f])}
 if(RegMod$MatName[f]=='Ss5_') {df.list[[f]]<- FunTSs5(RegMod$VR_B[f])}
 if(RegMod$MatName[f]=='Ss6_') {df.list[[f]]<- FunTSs6(RegMod$VR_B[f])}
 if(RegMod$MatName[f]=='Ss7_') {df.list[[f]]<- FunTSs7(RegMod$VR_B[f])}
 if(RegMod$MatName[f]=='Sf3_') {df.list[[f]]<- FunTSf3(RegMod$VR_B[f])}
 if(RegMod$MatName[f]=='Sf4_') {df.list[[f]]<- FunTSf4(RegMod$VR_B[f])}
 }

RegMod$LambdaB<- as.numeric(unlist(lapply(df.list,lambdaPop)))

ElX_V1<-  ((RegMod$LambdaB/RegMod$LambdaA)-1)/((RegMod$X_B/RegMod$X_A)-1)

ElX_V2   <-   (RegMod$E.VR_Stc*((RegMod$VR_B/RegMod$VR_A)-
1))/((RegMod$X_B/RegMod$X_A)-1)
ElX_V2_95 <-   (RegMod$E.VR_95* ((RegMod$VR_B/RegMod$VR_A)-
1))/((RegMod$X_B/RegMod$X_A)-1)

ifelse(Variant==1,
RegMod$Elast.Inter <- ElX_V1 ,
RegMod$Elast.Inter <- ElX_V2)

RegMod$Elast.Inter95<- ElX_V2_95

RegModPos<- subset(RegMod, slope1>=0)
RegModPos<- RegModPos[order(RegModPos$Chinook_Run),]

RegModPos<- subset(RegModPos,MatName  != "Ss5_"& MatName  != "Ss6_"& MatName  !=
"Ss7_")

ifelse(Population[1]=='SRKW',
RegModPos <- subset(RegModPos, SR_Hyp != 'NA' & SR_Hyp !='Hybrid'),
RegModPos <- subset(RegModPos, NR_Hyp != 'NA' & NR_Hyp !='Hybrid'))

FreqVRs= as.data.frame(table(factor(RegModPos$VitalRate)) )
UniqDF<-  unique(factor(RegModPos$VitalRate))
NAsdm<- rep(NA,length(UniqDF))

RegModPos
}
```

R-Code written by Andres Araujo, February 2013.

A 8.3. Examples of input data

KW Abundance Data

Year	Age	Count	Offspring	Cat1
1973	1	6	NA	Juv
1973	2	5	NA	Juv
1973	3	9	NA	Juv
1973	4	2	NA	Juv
1973	5	3	NA	Juv
1973	6	2	NA	Juv
1973	7	3	NA	Juv
1973	8	4	NA	Juv
1973	9	5.5	NA	Juv
1973	10	4	NA	Male
1973	10	0.5	0	Female
1973	11	1	NA	Male
1973	11	0.5	0	Female
1973	12	2	NA	Male
1974	1	8.5	NA	Juv
1974	2	5	NA	Juv
1974	3	5	NA	Juv
1974	4	9	NA	Juv
1974	5	2	NA	Juv
1974	6	3	NA	Juv
1974	7	2	NA	Juv
1974	8	2	NA	Juv
1974	9	4	NA	Juv
1974	10	4	NA	Male
1974	10	1.5	0	Female
1974	11	4	NA	Male
1974	11	0.5	0	Female
1974	12	1	NA	Male
1974	12	0.5	0	Female
1974	13	1	NA	Male
1974	13	0.5	0	Female

Chinook/Chum Abundance Data

Stock Group_Run Type_Lag

Year	FE_TR_0	FE_TR_1	FE_TR_2	FE_TR_5YA
1983	82641	90670	73741	89780
1984	112697	82641	90670	89484
1985	136405	112697	82641	99231
1986	160271	136405	112697	116537
1987	144071	160271	136405	127217
1988	149717	144071	160271	140632
1989	117553	149717	144071	141603
1990	152585	117553	149717	144839
1991	128548	152585	117553	138495
1992	143685	128548	152585	138418
1993	120905	143685	128548	132655
1994	161964	120905	143685	141537
1995	157329	161964	120905	142486
1996	216402	157329	161964	160057
1997	233918	216402	157329	178104
1998	204364	233918	216402	194795
1999	154677	204364	233918	193338
2000	169405	154677	204364	195753
2001	223299	169405	154677	197133
2002	262677	223299	169405	202884
2003	283475	262677	223299	218707
2004	234716	283475	262677	234714
2005	197047	234716	283475	240243
2006	285212	197047	234716	252625
2007	151099	285212	197047	230310
2008	223888	151099	285212	218392
2009	207228	223888	151099	212895
2010	263036	207228	223888	226093
2011	NA	NA	NA	NA

Definitions Files

KW Demographics

TimeSeries	Stock	Ab.Type	lag	SR_Hyp	NR_Hyp	Ab_ID
FE_TR_0	Fraser Early (Spring and Summer)	Terminal run	0	1a	2b	1
FE_TR_1	Fraser Early (Spring and Summer)	Terminal run	1	1a	2b	1
FE_TR_2	Fraser Early (Spring and Summer)	Terminal run	2	1a	2b	1
FE_TR_5YA	Fraser Early (Spring and Summer)	Terminal run	5YA	1a	2b	1

Fishing Scenarios

Time series	Stock or stock aggregate	Lag	ER Indicator Stocks
FE_TR_0	Fraser Early (Spring and Summer)	0	DOM,NIC,SHU
FE_TR_1	Fraser Early (Spring and Summer)	1	DOM,NIC,SHU
FE_TR_2	Fraser Early (Spring and Summer)	2	DOM,NIC,SHU
FE_TR_5YA	Fraser Early (Spring and Summer)	5YA	DOM,NIC,SHU

TRE_Harvest Rates (same format for TR and TRE)

Indicator Stock

Year	KLM	ATN	PPS	QUI
1982	0.4442	NA	0.4332	0.347306
1983	0.0043	NA	0.4746	0.4831385
1984	0.1066	NA	0.2827	0.3294556
1985	0.2148	NA	0.4779	0.3020232
1986	0.149	NA	0.483	0.3268915
1987	0.1931	NA	0.3647	0.3057604
1988	0.1046	NA	0.3585	0.2241371
1989	0.1941	NA	0.3235	0.2980182
1990	0.1747	0.0244	0.2335	0.3325402
1991	0.2525	0.0551	0.4201	0.3735121
1992	0.2524	0.1074	0.4327	0.4009146
1993	0.1945	0.1349	0.6162	0.338489
1994	0.1717	0.0883	0.5143	0.2763701
1995	0.1151	0.0618	0.3701	0.2554541
1996	0.0802	0.0402	0.2624	0.1383983
1997	0.195	0.0796	0.1466	0.3123559
1998	0.0944	0.0872	0.1906	0.2268675
1999	0.3144	0.0821	0.0932	0.2617231
2000	0.1575	0.0862	0.0286	0.1675622
2001	0.1689	0.0822	0.0815	0.1243823
2002	0.2907	0.1382	0.2539	0.2661888
2003	0.2126	0.2613	0.1002	0.3214712
2004	0.2212	0.2019	0.1354	0.2369916
2005	0.2272	0.2511	0.2609	0.300341
2006	0.1971	0.1859	0.1702	0.2617753
2007	0.218	0.2616	0.2991	0.3789272
2008	0.1935	0.0096	0.1901	0.1392628
2009	0.0951	0.075	0.149	0.236773
2010	NA	0.1678	NA	NA
2011	NA	NA	NA	NA