



# **Report on Population Viability Analysis model investigations of threats to the Southern Resident Killer Whale population from Trans Mountain Expansion Project**

Prepared for the National Energy Board (NEB) hearings reviewing Kinder Morgan's proposed Trans Mountain Expansion project

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## Table of Contents

	Page
1.0. Introduction	1
2.0. PVA Methodology	3
2.1. The Population Viability Analysis (PVA) modeling approach	6
2.2. About the Vortex PVA software	6
2.3. Input variables used in developing the Vortex PVA model for the Southern Resident population	13
3.0 Results of modelling	13
3.1. Projections for the Southern Resident population under the status quo (baseline model)	17
3.2. Sensitivity testing of important model parameters	18
3.3. Examination of potential threats	18
4.0. Conclusions	36
5.0. Literature Cited	38
Appendix A	Review of Previous Southern Resident Population Viability Analyses
Appendix B	Curriculum vitae Dr. Robert C. Lacy, Ph.D.
Appendix B	Biography Kenneth C. Balcomb III
Appendix C	Curriculum vitae Laruen J.N. Brent, Ph.D.
Appendix D	Curriculum vitae Darren P. Croft, Ph.D.
Appendix E	Curriculum vitae Christopher W. Clark, Ph.D.
Appendix F	Curriculum vitae Paul Paquet, Ph.D.

## 1.0. Introduction

This report explains the methodology and results of a population viability analysis (PVA) of the risk associated with aspects of the proposed Trans Mountain Expansion Project (Project) on the endangered Southern Resident Killer Whales (“Southern Residents”). PVA uses quantitative methods to evaluate and predict the likely future status of a population. The Project will twin an existing pipeline from Alberta to Burnaby BC on the Pacific Coast. That pipeline will carry diluted bitumen from Alberta to Burnaby, British Columbia, to be shipped overseas. The Project will therefore result in the increased shipping of diluted bitumen by oil tanker through the shipping lane in the Salish Sea. This shipping lane transects the critical habitat of the Southern Residents.

A PVA is a risk management tool, which models the risk to a population over time. In this case the model was used to estimate the increased risk to the Southern Residents from three threats associated with the marine shipping component of the Project: an oil spill, increased acoustic and physical disturbance from ships, and ship strikes.

Projecting the impacts of changing and even new threats to a wildlife population can be difficult. Intuition, even by acknowledged experts, is usually not adequate because the factors influencing wildlife populations are numerous and interact in complex ways; new threats with which we have little prior experience are emerging; and even if the intuitive assessments are complete and correct, they cannot be documented in a way that allows understanding, review, and improvement by others. Standard demographic models used in wildlife ecology can be powerful methods for predicting population dynamics, although they often assume no or simple interactions among variables and necessarily omit much detail of the breeding system, spatial or social structure, and individual or group differences. Much uncertainty exists in any population projection, because any model is necessarily (and by design) a simplified representation of the system, some input variables will be known only approximately, future conditions cannot be known precisely, and some biological processes are inherently unpredictable (e.g., the sex of each newborn). This uncertainty cannot be eliminated, and it should not be ignored, but it can be explored through testing perturbations of the data and model (“sensitivity testing”) to determine which uncertain factors have the greatest influence on our projections for the future and what confidence we can place on the results. Overall, population models provide a framework not only for analyzing complex situations, but also for documenting assumptions and methods, reviewing and improving assessments, and integrating new potential threats to populations into our understanding.

We prepared this report using a PVA modeling approach. A PVA modelling approach uses demographic modeling to assess risks to wildlife populations and evaluate the likely efficacy of protection, recovery, or restoration options (Shaffer 1990; Boyce 1992; Burgman et al. 1993; Sjögren-Gulve and Ebenhard 2000; Beissinger and McCullough 2002; Morris and Doak 2002). Our goal was to evaluate the current population status of Southern Residents and future population dynamics, including the probability of recovery and risk of extinction under existing and future human caused threats. We assessed the likely response of population growth and viability to additional cumulative disturbances and threats, including increased ocean noise resulting from additional vessel traffic and oil spills from petroleum tankers

associated with the proposed Project.

Our baseline or status quo model, which reflects current population demographics, environmental conditions, and human caused threats, projects a mean population decline of 0.2% annually, with fluctuation of approximately  $\pm 4.5\%$  across 100 years, and no complete extinctions (i.e. either no males or no females remaining). There was however, a 9% chance of quasi-extinction<sup>1</sup>, where the population falls below 30 whales and is no longer viable. A 7% reduction in genetic diversity after 100 years is also projected. Birth rate (calves per adult female) dominated the variation in population growth, whereas, nonbreeding depression and mortality rates had moderate effects. The effects of inbreeding depression indicate that the population is small enough so that inbreeding is likely damaging to the future prospects for the population.

Reducing the abundance of Chinook salmon is projected to have a substantial negative impact on the Southern Residents population. Conversely, increasing Chinook abundance can lead to relatively robust population growth (up to 1.9% with 20% more prey) and protection from extinction or serious decline. The impact of oil spills on long-term population growth could be consequential. The probability of the population dropping to quasi-extinction (i.e. below 30 whales) due to an oil spill is more substantial, with a possibility of complete extinction within 100 years due to the potential of catastrophic decimation of the population to a small and unrecoverable number from which it could not recover. The modeled impact of noise and physical disturbance accompanying increased or added vessel traffic associated with the Project resulted in accelerated population decline, smaller mean population size, and increased probability of complete and quasi extinction. The cumulative impact of oil spills, increased noise, and incidental human caused deaths resulted in a population decline of more than 1% per year, resulting in a mean final population size of only 33 animals, a 8.6% probability of complete extinction of the Southern Residents, and more than 50% probability that the final population would be less than 30 animals and, therefore, probably on a course toward nearly inevitable extinction.

The Southern Resident population has experienced almost no population growth over the past 4 decades, and has declined in the last two decades. Based on status quo conditions, the population will most likely remain about at its current size or continue a very slow decline. It is abundantly clear that under status quo conditions the population cannot withstand additional negative pressures, recover from its current endangered status, and persist.

Our analysis shows that the Project will intensify existing threats, accelerating the rate of decline in the Southern Residents and possibly leading to a complete extinction. The factor projected to have the largest effect on depressing population size and possibly leading to extinction is a reduction of the Chinook prey base. In addition, occasional large or medium oil spills have the potential to depress long-

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<sup>1</sup> Quasi-extinction threshold is the minimum number below which extinction is very likely due to genetic or demographic risks. For this review, the quasi-extinction threshold is 30 killer whales, a level at which the Southern Residents are unlikely to persist.

term population stability and growth, leading to a considerable chance of the population declining below 30 animals. Cumulatively, the threats associated with the Project such as increased shipping of oil through critical habitat, the possibility of oil spills at the frequency estimated by Kinder Morgan, projected effects of noise from associated shipping traffic, and occasional additional mortalities due to boat strikes (one in 10 years) create the risk that the Southern Residents population becomes vulnerable to extinction (8.6% probability within 100 years), and increases the risk to more than 50% probability that the population will decline below 30 animals.

## **2.0. PVA Methodology**

### **2.1. The Population Viability Analysis (PVA) modeling approach**

PVA can extend standard demographic projections (Ricklefs 1979; Caswell 2001) in two important ways: (1) the impacts of forces external to the population (e.g., changing habitat quality, extent, and configuration; interactions with other species in the community; impacts of disease or contaminants; harvest, incidental killing, or other direct human impacts) on the demographic rates are explicitly considered and evaluated, and (2) uncertainty in the population trajectory caused by intrinsic (e.g., demographic stochasticity,<sup>2</sup> limitations in local mate availability or other density dependent feedbacks, inbreeding impacts) and extrinsic (e.g., environmental variation, occasional catastrophes) stochastic factors can be explicitly modeled, usually through the use of simulation modeling.

The outputs of PVA are any desired measure of population performance, but commonly assessed metrics include projected mean (i.e. average) population size ( $N$ ) over time, population growth rates ( $r$ ), expected annual fluctuations in both  $N$  and  $r$ , probability of population extinction, and probabilities of quasi-extinction (the likelihood of  $N$  falling below any specified number). These outputs are used to assess risk (e.g., for listing under Canada's Species at Risk Act and the U.S. Endangered Species Act or other protective regulations), assess vulnerability to possible threats, determine sustainable mortalities in the context of uncertainty, and determine the suites of actions that would be needed to achieve stated resource protection or restoration goals. PVA has become a cornerstone of conservation science and resource management.

Most PVA models can be classified into three general types that span top-down to bottom-up approaches:

(1) Deterministic (analytical) models calculate average population trajectories based on equations describing population growth, usually evaluated from matrix representations of the "life table" of fecundity and survival rates.

(2) Population-based simulation models add temporal and spatial variability to the demographic rates and then project a distribution of possible population trajectories based on simulations that sample

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<sup>2</sup> Demographic stochasticity is the random change in population size over time due to random variation in individual survival and reproductive success.

from those distributions. Thus, they use simulation of stochastic (probabilistic) population processes to generate population trends as emergent properties.

(3) Individual-based (also termed “agent-based”) simulation models use the probabilities of demographic events (including temporal, spatial, and individual variability) to simulate the life cycle of each individual and then project population level outcomes as the aggregate fates of the individuals in the population.

Any of these three kinds of PVA can be used to integrate impacts on individual animals (with respect to mortality, reproduction, and dispersal) into projections of the cumulative consequences at the level of the population, *if* the effects on individuals can be described adequately in the parameters at the level used in the model. However, deterministic analytical and population-based simulation approaches require that impacts on individuals be accurately captured in consequent changes to a few population-level rates, while individual-based simulations let the population-level effects emerge from more detailed descriptions of individual processes.

Deterministic models are most useful for describing dynamics of generalized populations with the typical species characteristics. Their output is usually in the form of calculated exponential rates of population growth and the stable age structure that will develop if all demographic rates remain constant. Because deterministic models assume constancy of demographic rates, they will over-estimate population growth and stability if rates fluctuate over time or space, if there is individual variation in rates, or if population sizes are small (on the order of 100s rather than 1000s).

Population-based and individual-based models provide the same mean outputs as do deterministic models (usually with lower estimates, due to the non-linear effects of fluctuations), but also add estimates of variation in population trajectories. To obtain these estimates of variation, the simulation models are repeated many times (500 iterations are usually considered sufficient to provide acceptably precise results) to generate a distribution of results, thereby allowing calculation of the probability that an outcome (a performance measure) will fall outside of an acceptable range.

Population-based simulations are most useful when individual characteristics and impacts can be averaged across the population without loss of ability to model key processes of interest, and populations are large enough so that chance variation among individuals is not a significant contributor to uncertainty.

Individual-based models are most useful for assessment of populations with a relatively small number of individuals in a specific and well-described environmental and management setting. Accordingly, the Vortex PVA model that we used is an individual-based model, with the fate of each animal tracked through its lifetime. In contrast to “population-based” models or analytical calculations of average population growth, individual-based models allow for determination of matriline, individual variation in reproductive success, loss of genetic diversity, inbreeding, inbreeding avoidance, and any demographic consequences of these processes.

It is important to note that deterministic models, population-based models, and individual-based models all yield the same population predictions when the assumptions of the higher level models are met. Thus, the three kinds of models sequentially add accuracy, ability to capture more details of dynamic processes, and consideration of more sources of uncertainty, and they often represent the same demographic rates in different terms, but they are not generally conflicting approaches. However, some measures of viability cannot be assessed from the simpler deterministic or population-based models, because these measures describe specific individual or group statistics (such as the number of pods with more than two breeding adults) that are not represented at the higher population level. For example, deterministic models and population-based models almost always omit consideration of males, because reproduction in a polygamous species only requires sufficient availability of adult males to inseminate all potentially breeding females, and the models simplistically assume that there will always be enough males to ensure maximal reproduction. However, in reality, if social groups are so small that there is a lack of suitable males for breeding, the population size will decrease and perhaps crash.

A requirement for any PVA model to provide sufficiently accurate and robust projections to allow estimation of population performance (rather than simply to provide a modeling tool that allows exploration of a wide range of uncertainty) is the availability of detailed demographic data. Model input is required from the focal population or comparable reference populations for mortality rates, aspects of reproduction (e.g., age of breeding, inter-birth intervals, infant survival, or composite measures such as overall fecundity), population size, and habitat carrying capacity<sup>3</sup> – as well as the natural fluctuations in these rates. The difficulty in obtaining sufficient demographic data on endangered or protected species is a common challenge to the usefulness of PVA models, and many practitioners consequently recommend that PVA models be used only to provide assessments of relative risk and relative value of management options, rather than absolute measures of population trajectories. In the case of the Southern Residents population, however, nearly complete demographic data are available from 1976 onwards. This allows highly detailed and situation-specific models to be developed and used for threat assessments. A review of previous PVAs carried out for Southern Resident killer whales is provided in Appendix A of this report.

## **2.2. About the Vortex PVA software**

This report was prepared using the Vortex population model and software. The Vortex population model (Lacy 2000; Lacy et al. 2014a; Lacy et al. 2014b) is used by thousands of population biologists around the world, including independent researchers, government agencies, and teachers in classroom settings. Typical applications include projecting trends, threats, and restoration strategies for wildlife populations. For example, the United States Fish and Wildlife Service and other agencies have used

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<sup>3</sup> **Carrying capacity** is the maximum population size of the species that the environment can sustain indefinitely, given the food, habitat, water, and other life requisites available in the environment.

Vortex to set recovery goals and guide actions for a number of threatened and endangered species.<sup>4</sup> No software program (nor any calculations) can be guaranteed to be completely free of errors, but as a widely distributed and used program, Vortex receives far more testing than similar models that are developed for only specific projects. Vortex simulations have been confirmed to produce population trajectories that are consistent with monitored wildlife populations (Brook et al. 2000a) and with other population models (Brook et al. 2000b). The overall structure of the program was published in Lacy (2000), and the compiled program and documentation are distributed freely at [www.vortex10.org/Vortex10.aspx](http://www.vortex10.org/Vortex10.aspx).

### 2.3. Input variables used in developing the Vortex PVA model for the Southern Resident population

In this section, we outline how the PVA modeling was done, including selection of the input variables. We explain the simulation settings (number of years modeled, number of times the simulation was repeated) and the tests that were run to determine the sensitivity of the model projections to the uncertainty in the input variables.

We conducted the PVA modeling of the Southern Residents population in three parts:

- First, a “baseline” model was developed to represent the best possible trajectories of the population if demographic rates continue as observed in recent decades, and *no additional external threats* such as oil spills, other environmental contamination, noise disturbance, decreasing food supply, increased disease, or increased ship strikes affect the population.
- Second, uncertain model parameter values were systematically altered to determine which would have large effects on the population projections. This “sensitivity analysis” helps determine the confidence we can have in projections given the necessarily incomplete knowledge of the population characteristics. It also reveals to which demographic rates the population performance would be most sensitive if subject to new or worsening threats.

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<sup>4</sup> Black-footed ferret, Mexican wolf (Carroll et al. 2014), Florida panther (Maehr et al. 2002), whooping crane (Mirande et al. 1991), Attwater’s prairie chicken, Puerto Rican crested toad, red wolf (Kelly et al. 1999), Anacapa Island deer mouse (Pergams et al. 2000), Alabama beach mouse (Reed and Traylor-Holzer 2006), Sonoran pronghorn (Hosack et al. 2002), Assateague Island pony (Ballou et al. 2008), Lower Keys marsh rabbit (Forys and Humphrey 1999), Hawaiian forest birds (Ellis et al. 1992), and many other species. Vortex is also a common tool for population analysis by governmental agencies in Canada, Mexico, Costa Rica, Panama, Brazil, Chile, Ecuador, New Zealand, Australia, Indonesia, Malaysia, China, Taiwan, Japan, India, Bangladesh, South Korea, Kenya, South Africa, Spain, Sweden, Norway, Denmark, Italy, UAE, and elsewhere. Vortex has been used before to assess threats to the Southern Resident Killer Whale population (Taylor and Plater 2001), and other species of marine mammals, such as Indo-Pacific bottlenose dolphins (Lacy and Wells 2009), manatee (Marmontel et al. 1997; Castelblanco-Martinez et al. 2012), dugongs (Heinsohn et al. 2004), and Steller’s sea cow (Turvey and Risley 2006).



- Third, estimated impacts of intensifying specified threats (Project related) to the population were added to the model to determine which threats individually could put the population at significant further risk, and what would be the risk of population decline or collapse under the cumulative effects of the several identified new threats.

#### Input variable 1: Primary data source for baseline demographic rates

Demographic rates were calculated from the database on individual animal histories compiled by the Center for Whale Research (CWR 2015). Data from 1976 through 2014 were used. It is recognized that the Southern Resident population experienced moderate population growth from 1976 to 1993, and subsequently experienced a moderate decline. This might indicate that some aspect(s) of the habitat declined in quality recently, or the change in trajectory might be explained by random fluctuations in reproduction and survival, rather than indicating any long-term trend. In addition, the population might have peaked when it reached an ecological carrying capacity – the number of animals that can be supported by the available resource base. By including data back to 1976 for calculation of demographic rates, therefore, we could be over-estimating current conditions. However, to restrict analyses to only the more recent years could under-estimate the ability of the population to grow.

Because the sample sizes are necessarily small, the data are not sufficient to determine accurate estimates of demographic rates for each annual age class. We therefore used the same age class groupings as were used in the recent models of Vélez-Espino et al. (2014a), except that we set an upper limit for female breeding at 45 years rather than 50 years. Thus, we calculated survival and (for adult females) fecundity rates for calves (first year), juveniles (defined as from 1 year through 9 years of age), young mature females (10-30 years), older reproductive females (31-45 years), post-reproductive females (46 years and older), young mature males (10-21 year), and older males (22 years and older). Not all Southern Residents calves and juveniles have been sexed, and the data do not show a significant difference in survival between males and females in these younger age classes. Accordingly, survival was calculated with both sexes combined for calves and for juveniles. Survival rates of young adult females and young adult males have been better than older females and males, so it is appropriate to consider these age classes separately in the analyses. We set an upper limit of 45 years for females breeding because no females in the population have been documented to produce calves at older ages. Killer whales can survive many years after reproductive senescence (Ward et al. 2009a, Ward et al. 2009b; Foster 2012). Although it is not known what age killer whales can reach, and estimates of birth dates for the older whales in the Southern Resident population are uncertain, one female has been estimated to be 104 years old. The next oldest females are estimated to be 87 years and 50 years. We set an upper limit of age to 90 years in our models. However, because females stop breeding long before this, the population growth rate will not be affected by the assumed upper age limit.

We specified the pod (J, K, or L) of each animal, and assigned each newborn in the simulation to the pod of its mother. Southern Residents have not been observed to change pod affiliation, although males will mate with females from the other pods (and also, less often, with females from their natal pod) (Ford et al. 2011). The data on this small population are not sufficient to estimate demographic rates separately for each pod, and it is not known if the pods have differential survival or fecundity. Therefore, we

applied the same demographic rates for all three pods. By tracking the membership of each pod, however, we can project the probability that one or more pods will die out.

As previously noted, the Vortex PVA model that we used is an individual-based model, with the fate of each animal tracked through its lifetime, allowing for determination of matriline, individual variation in reproductive success, loss of genetic diversity, inbreeding, inbreeding avoidance, and any demographic consequences of these processes. We started the projections of population dynamics with the actual ages and sexes of the killer whales alive as of 31 December 2014. We also specified the mother of each animal, where it had been reported (for 76 of 80 living animals) in published sources (CWR 2015; Ford et al. 2011). These designations of maternity are important because we specified in the simulation model that females would not mate with their father, a son, or a maternal half-sibling (i.e. from the same mother). For the oldest animals in the population, mothers or other close relatives are unknown (other than their own offspring). Thus, the analyses will underestimate the accumulation of inbreeding, because living animals may be related in ways not documented.

#### Input variable 2: Impacts of inbreeding

Long-term pedigree information are not available from which the effect of inbreeding (mating between close relatives) could be determined for killer whales or for any cetacean species. The avoidance of matings between related pod members (Ford et al. 2011), however, indicates that the species has reduced fitness when inbred, as has been observed in almost all mammalian species for which data on inbreeding depression are available (Lacy 1997; O’Grady et al. 2009). Lacking data on the severity of inbreeding depression in cetaceans, we assumed in the model that the effect of inbreeding on reproductive success (birth rate and calf survival) is the same as the mean value reported (6.29 “lethal equivalents”) in a survey of impacts on wild species (O’Grady et al. 2009). Inbreeding might also affect other components of fitness – such as longevity – but data on such effects are too few to allow estimation of typical impacts, and we therefore did not include those effects in our population model. We used the option in Vortex to model inbreeding depression as being caused by the presence of recessive lethal alleles,<sup>5</sup> and each initial animal in the model was assigned an average of 6.24 unique lethal alleles across its genome. If inbreeding is instead due in part to other mechanisms – such as deleterious (but not lethal) alleles, or to genetic loci that show heterozygote advantage – then the impacts of inbreeding in early generations projected in the simulation would be the same, but the population would be less able to adapt to inbreeding after many generations than is the case with fully recessive lethal alleles.

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<sup>5</sup> An **allele** is one of a number of alternative forms of the same gene. **Alleles** that cause an organism to die only when present in **homozygous** (2 identical genes) condition are called **lethal alleles**. The gene involved is considered an essential gene.

### Input variable 3: Mortality rates

Mortality rates were calculated from the tallies of deaths each year from 1976 through 2014<sup>6</sup>. The mortality rate for each age-sex class was averaged across the 39 years of data to obtain the mean annual rates. The variation in mortality rates across years has two components – variation in the probability of mortality due to variable environmental conditions (“environmental variation”), and variation in the number of deaths that occur given the independent fates of animals even when exposed to the same probabilities of mortality (“demographic stochasticity”). To determine how much of the observed variation is due to environmental variation, the variance due to demographic stochasticity can be calculated from the expectation for a binomial process<sup>7</sup>, and then subtracted from the total variation across years (Lacy et al. 2014b). Calculated annual mortality rates and environmental variation (represented as a standard deviation) were as follows:

Calves:	17.48% (SD = 17.96)
Juveniles:	2.15% (SD = 2.42)
Young adult females:	0.97% (SD = 0; i.e., the variation in mortality across years was no greater than expected based on the demographic stochasticity if population rates were constant over time)
Older adult females:	2.25% (SD = 0)
Post-reproductive females:	6.29% (SD = 7.77)
Young adult males:	3.03% (SD = 2.53)
Older adult males:	9.80% (SD = 8.68)

The above mortality rates are marginally better (i.e., lower) than the rates presented in Vélez-Espino et al. (2014a), which is due to their use of data from 1987-2011, which omits a prior decade that had better demographic rates. The estimates of annual variation above are all considerably lower than the estimates by Vélez-Espino et al. (2014a) as a result of our removal of the expected demographic stochasticity from the annual variation in observed death rates.

### Input variable 4: Reproductive system

The breeding system is polygamous, with some males able to obtain multiple mates, and females mating with different males over their lifetimes. We assumed in the model that males become sexually mature (actively breeding, which may occur several years after they are physiologically capable of breeding) from 12 to 18 years of age. Thus, in the model, each male was assigned an age of sexual maturity by randomly selecting a value from 12 to 18 (assigned when the male was born). There is evidence that there is variation among males and among females in reproductive success. Genetic evidence indicates

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<sup>6</sup> Mortality was recorded if an individual’s matriline was observed in the population within a year but the individual did not appear.

<sup>7</sup> A binomial process is a random counting system where there are  $n$  independent identical trials, each one of which has the same probability of success  $p$ , which produces  $s$  successes from those  $n$  trials. The simplest example of a binomial process is the toss of a coin.

that the effective population size is about 1/3 of the total size (Ford et al. 2011), as would occur if some animals are more successful breeders than others.<sup>8</sup>

To represent this phenomenon in the PVA model, we specified that each male be assigned a score from 0 to 1 to be used as his likelihood of being a capable breeder (i.e. with full access to breeding females) each year. The mean was set at 0.50, with a standard deviation (SD) of 0.20 in a beta-distributed distribution.<sup>9</sup> This distribution will lead to most males having relative breeding success of 0.3 to 0.7, with a few extreme males having scores below 0.10 or above 0.90.

Similarly, we assigned an individual reproductive success score to each female, used to represent the factor by which the female's probability of breeding each year was below (score < 1) or above (score > 1) the overall mean for females of her age. These scores for variation in female reproductive success had mean 1.0 and SD = 0.2, created by sampling from a beta distribution (mean = 0.50, SD = 0.1) and doubling those values. (It might be expected that individual variation in reproductive success would follow instead a normal distribution (a "bell curve"), but the normal distribution has no limit, which would allow some animals to have probabilities of breeding that are below 0 or above 100%. The beta distribution has a similar shape to a normal distribution when the mean is 0.5, but it does not extend below 0 or above 1, so it is preferred for representing uncertainty in demographic rates.)

The variance among individual females and males in the number of offspring across their lifetimes will cause genetic diversity to be depleted faster and inbreeding to accumulate faster than would occur if mating was assumed random. With the above specification of variance in reproductive success, our models project an effective population size of 37% of the total size, close to the estimate obtained from genetic data (Ford et al. 2011).

Genetic data indicate that females usually mate with males from the other pods, but occasionally do mate within their own pod (Ford et al. 2011). However, no cases of father-daughter, mother-son, or maternal half-sibling matings were observed, even though the within-pod matings could make such inbreeding likely if mating were at random. Thus, it appears that killer whales generally avoid mating with those relatives in their own pod that can be reliably determined as close relatives. To include this inbreeding avoidance in the model, we specified that females would not mate with their fathers, sons, or brothers or half-brothers from the same mother. This will reduce the likelihood and extent of any damage caused by inbreeding in the closed Southern Residents population, but could also lead to a situation in which some females might be unable to find a suitable mate if the population becomes small enough so that no unrelated breeding males are available.

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<sup>8</sup> Effective population size is the number of breeding individuals in an idealized population that would show the same amount of dispersion of allele frequencies under random genetic drift or the same amount of inbreeding as the population under consideration.

<sup>9</sup> In probability theory and statistics, the beta distribution is a family of continuous probability distributions.

#### Input variable 5: Reproductive rates

Breeding rates – expressed as the proportion of the females of an age class that produce a calf each year – were calculated to be:

12.04% for young adult females (age 10-30), with SD = 3.54

7.88% for older females (age 31-45), with SD = 4.15

0% for post-reproductive females (age > 45)

The above standard deviations expressing environmentally caused variation in rates across years were adjusted by removing the part of the observed variation that would be expected to be due to the demographic stochasticity (chance fluctuations in numbers breeding) even when population mean rates are constant.

Our estimated fecundities are all a little higher than those estimated by Vélez-Espino et al. (2014a) from the 1987-2011 data. Our estimates of annual variation are lower because we removed the demographic stochasticity.

#### Input variable 6: Carrying capacity

For our purposes, carrying capacity is the maximum population size of Southern Resident killer whales that the environment can sustain. For the initial tests of the importance of estimates of demographic rates to the population trajectories, we set the upper limit on population size to 300, so that the “carrying capacity” would not restrict population growth under the best conditions tested. (In the projections, the Southern Resident population never reached this limiting size.) In later analyses of the effects of various threats, we set the carrying capacity to  $K = 150$ , on the assumption that even under conditions that can allow growth, the population would not exceed 1.5x the largest size observed in recent decades.<sup>10</sup> Only rarely in our models (when individual simulated populations experienced unusually lucky good years) did any iteration reach this limit of 150. Setting  $K = 150$  rather than  $K = 300$  had minimal effect on the baseline model, and in none of our models did the  $K$  of 150 restrict growth in more than a few percent of the independent simulations.

#### Simulation settings

We projected the Southern Residents population for 100 years with the above input values. The simulation was repeated 10,000 times (independent iterations) to obtain precise estimates of means and variances in measures of population performance. For analyses of variants on the input rates (see “sensitivity tests”, below) and for comparisons among alternative scenarios, fewer iterations are needed to obtain good estimates of the relative impact of altered input values, and tests of alternative models were run with 1000 iterations of the simulation.

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<sup>10</sup> NOAA (2014) estimates the historic population size of Southern Residents was about 140 whales.

## Sensitivity tests

Sensitivity tests were done to determine the sensitivity of the model projections to the uncertainty in 11 demographic input variables described above. We ran 100 iterations each of 1,000 combinations of input parameters sampled from ranges. The sampled parameters were evenly spaced across the range set for each, with the sampling done according to a “Latin hyperspace” design so that the combinations of the 11 rates were evenly distributed. This method of sampling provides high statistical power for determination of the effect of each parameter. The ranges sampled for each variable were:

Inbreeding effects:                      Lethal equivalents = 3.145 to 9.435 ( $\pm 50\%$  around the baseline value)

Male variance in Reproductive Success: SD = 0 to 0.4

Female variance in Reproductive Success: SD = 0 to 0.4

Birth rate:                                       $\pm 10\%$  around the baseline values

Annual variation in birth rate:               $\pm 10\%$  around the baseline values

Calf mortality rate:                            $\pm 10\%$  around the baseline values

Annual variation in calf mortality:           $\pm 10\%$  around the baseline values

Juvenile mortality rate:                       $\pm 10\%$  around the baseline values

Annual variation in juvenile mortality:       $\pm 10\%$  around the baseline values

Adult mortality rate:                            $\pm 10\%$  around the baseline values

Annual variation in adult mortality:           $\pm 10\%$  around the baseline values

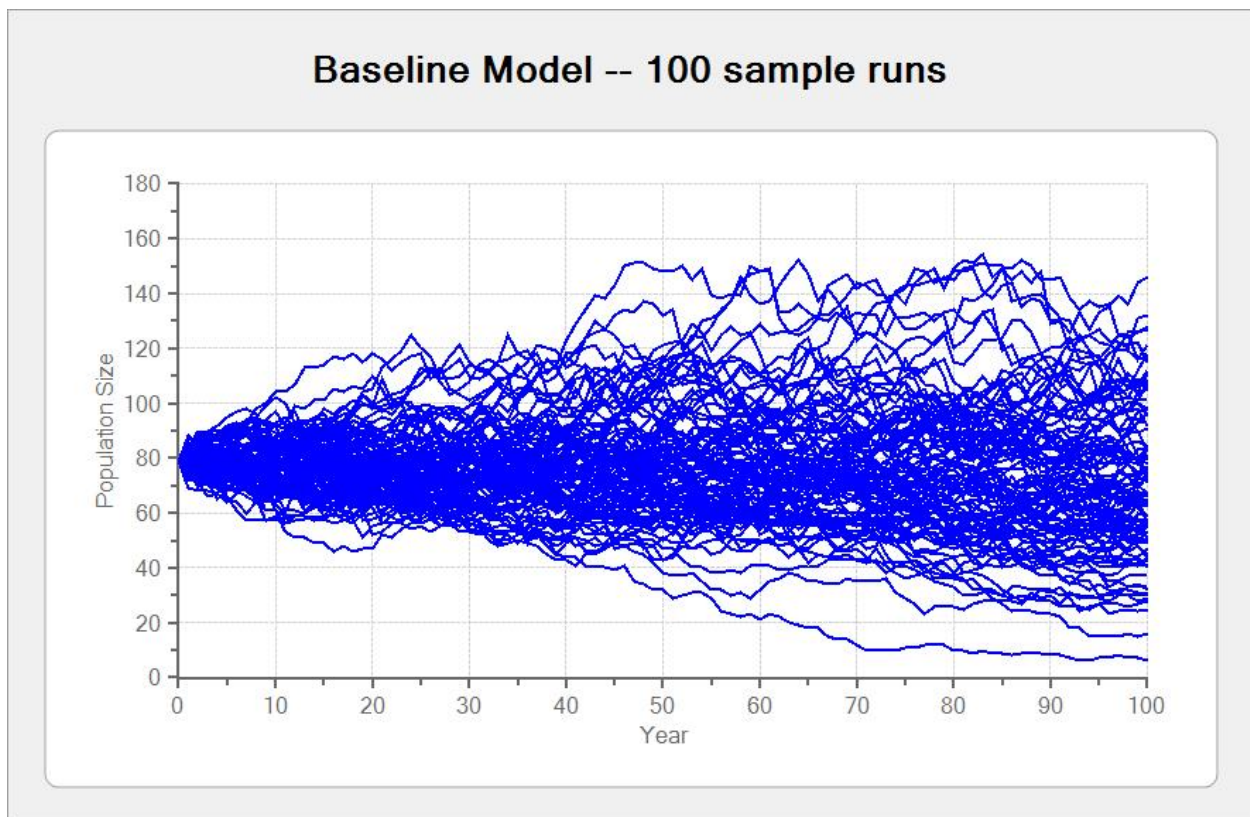
Thus, for each basic demographic rate (life table values for fecundity and mortality), we tested a range of  $\pm 10\%$  around the baseline value. For several model variables that describe other aspects of the population dynamics and are very uncertain, we tested wider ranges of values (see Table 1 below).

The above ranges for sensitivity tests are different from a common practice of examining the amount of change in the population growth for a constant proportional change in each survival and fecundity rate (“elasticities”). The apparent standardization of sensitivities of growth to changes in variables via such elasticities is arbitrary and an artifact of the age classes used for the demographic projections. It is arbitrary because the same proportional change in different demographic rates may not be likely or achievable for the population of interest. (E.g., it might be possible to shift an 80% calf survival rate up by 10%, but it is not possible to similarly shift an adult survival rate of 99% up by a “comparable” 10%.) For other model variables, such as the inbreeding depression, it is not clear that a 10% change in the value has the same meaning as a 10% shift in other demographic rates measured on very different and not always linear scales. The standardization achieved through elasticities is artifactual because very different results can be obtained if ages are binned into more or fewer age class categories for the calculations. Although strict comparison of the effect of proportional changes in model parameter values is usually not meaningful, the sensitivity tests can be useful guides as to which model parameters are the most important determinants of population trajectories, *over the range of values that are chosen for testing*. Thus, it is often useful to vary parameter values by amounts that reflect our uncertainty in each input value.

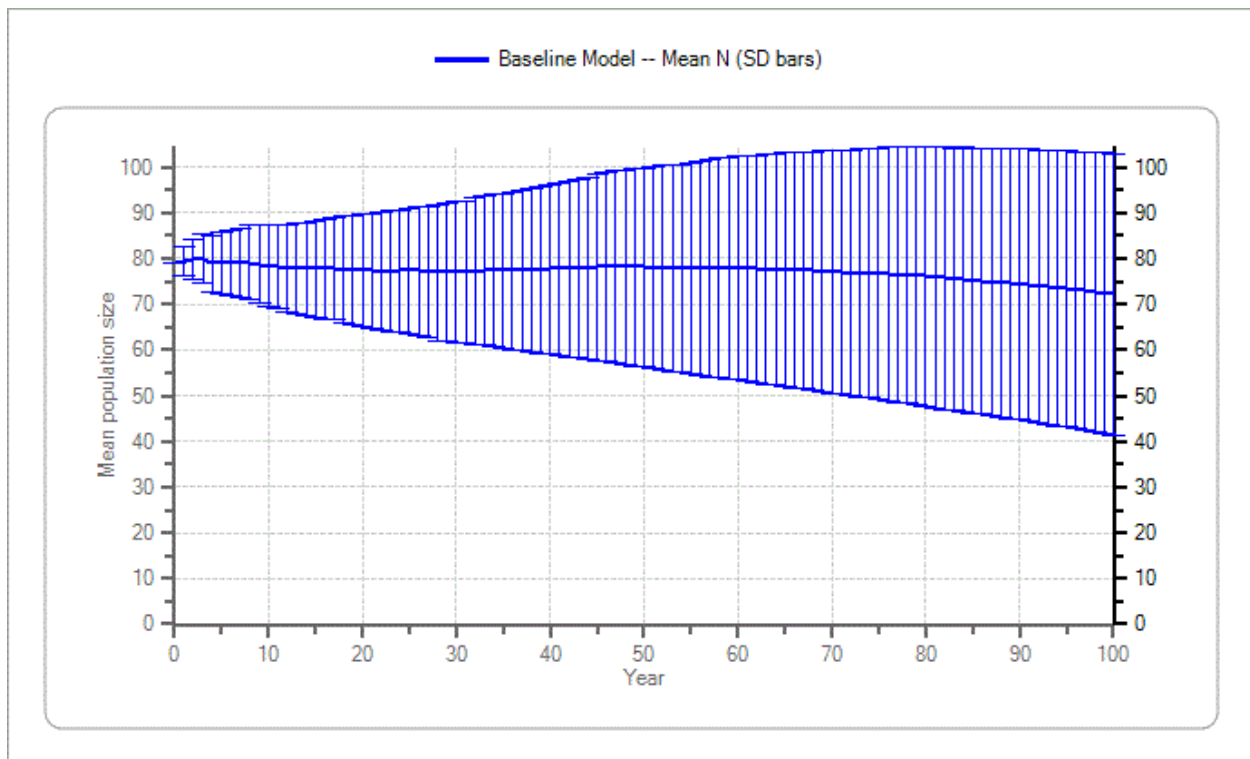
### 3.0. Results of modelling

#### 3.1. Projections for the Southern Resident population under the status quo (baseline model)

With the above model input values, we can project the trajectory of the Southern Resident population under our best understanding of the conditions that have occurred over the past few decades. Across 10,000 iterations, the baseline model projects a mean population growth rate of  $r = -0.002$  (i.e. 0.2% decline per year), with fluctuation across years of  $SD(r) = 0.045$  (i.e. approximately  $\pm 4.5\%$  growth). The following graphs illustrate the model with a sample of 100 iterations of the simulation – showing projections with an average slight decline but with much variation among the possible trajectories (Figures 1 and 2). Of course, the real population will experience only a single trajectory out of the range of possible futures. The model also projects a reduction in genetic diversity (measured as heterozygosity) after 100 years to 93% of the starting value. This is equivalent to the individuals in the population becoming inter-related on average to an extent a little more closely than first cousins are.



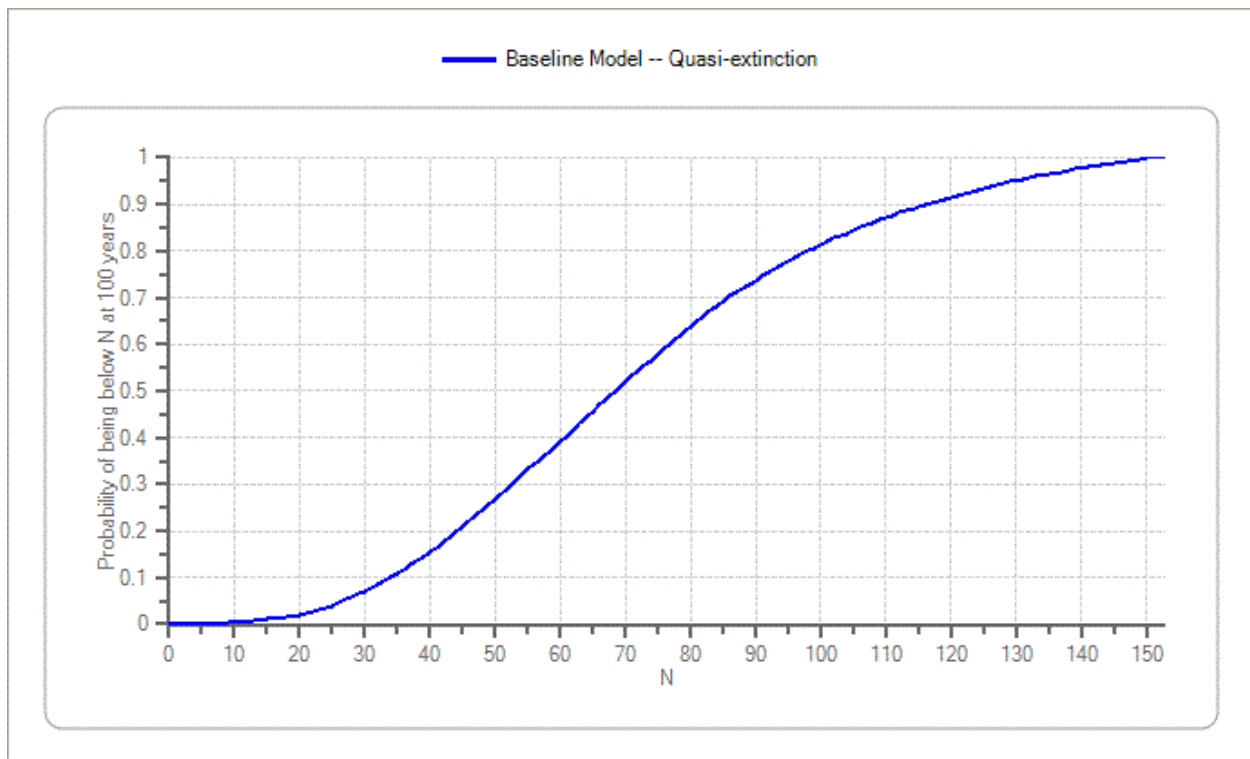
**Figure 1.** The baseline model projects a mean or average Southern Resident population growth rate of  $r = -0.002$  (i.e. 0.2% decline per year).



**Figure 2. The distribution of simulated Southern Resident population trajectories with means and SD of the projected population sizes.**

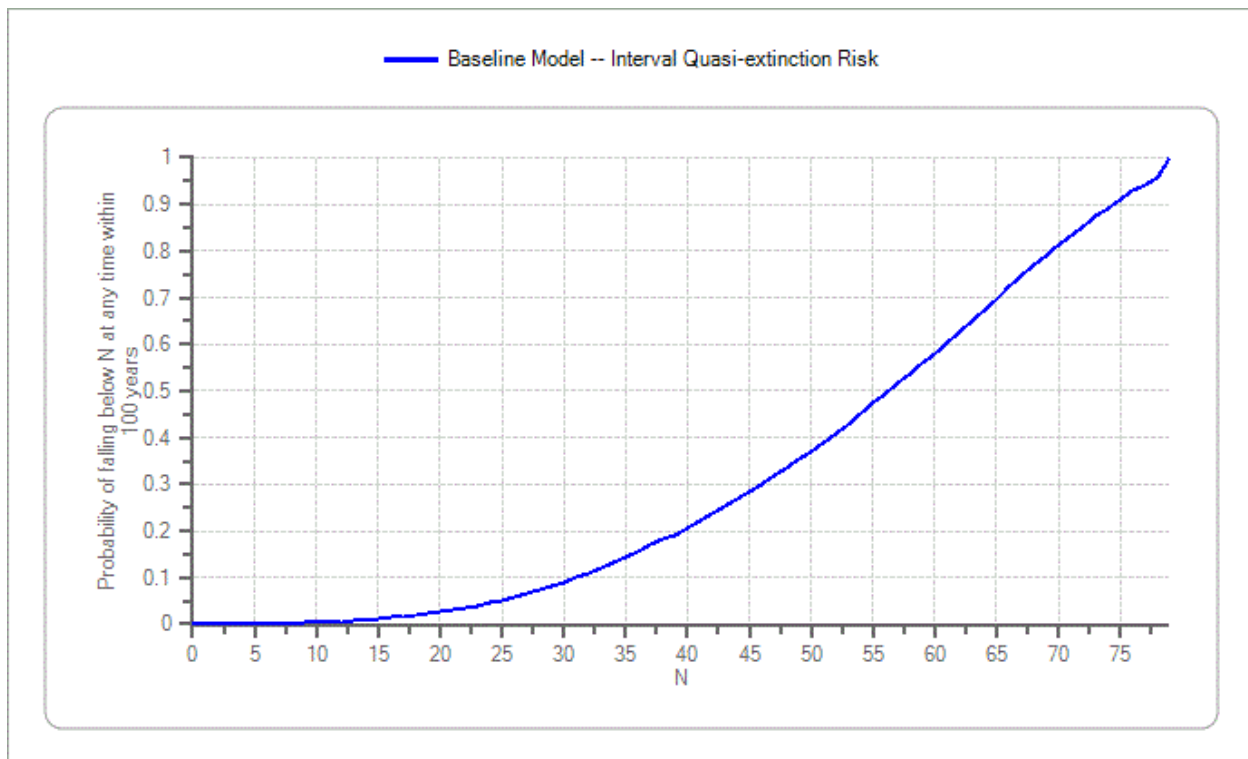
The model predicts no complete extinctions (no animals remaining), but sometimes the population is reduced to a much smaller size. The risk of population reduction can be represented by a graph of “quasi-extinction” – the probability that the population will have declined below any given  $N$  at the end of 100 years. The following quasi-extinction graph shows, for example, about a 7% probability of the population being at  $N < 30$  after 100 years (Figure 3). Quasi-extinction threshold is the minimum number below which extinction is very likely due to genetic or demographic risks. For this review, the quasi-extinction threshold is 30 killer whales, a level at which the Southern Resident are unlikely to persist. Graphs of this style will be used in this report to show the effects of various scenarios on the likelihood of population collapse.





**Figure 3. The probability of the population becoming quasi-extinct ( $N < 30$ ) after 100 year is about a 7%.**

It is also sometimes useful to look at an “interval quasi-extinction” graph – which shows the probability of the population falling below any given  $N$  at any time during the 100 year simulation. For example, the graph below shows that there is about a 9% chance of the “baseline” population falling below  $N = 30$  at any time over the next 100 years (Figure 4).



**Figure 4. The chance of the “baseline” population falling below  $N = 30$  at any time over the next 100 years is about a 9%.**

#### Model validation

As stated above, the Vortex population viability analysis program and manual are available free from [www.vortex10.org/Vortex10.aspx](http://www.vortex10.org/Vortex10.aspx). The input files that we created for modeling the population are available at [www.vortex10.org/SRKW-Vortex.zip](http://www.vortex10.org/SRKW-Vortex.zip), so all input values are available for review and the analyses can be repeated and extended by others.

The baseline model projects a very slight average decline, with a mean population growth rate of  $r = -0.002$ , and a variation across years of  $SD(r) = 0.045$ . The observed mean growth rate from 1976 to 2014 was  $r = 0.002$ , with a variation of  $SD(r) = 0.042$ . The observed growth rate was higher (mean  $r = 0.017$ ) before the peak of  $N = 94$  individuals in 1993 and has subsequently been negative (mean  $r = -0.009$ ). Thus, the baseline PVA model accurately reflects the population dynamics since 1976; although projections forward in time should be made with the caution that it is not known which recent time span best represents the current and future conditions if threats remain at the status quo. The mean age of living animals projected in the model is 24.2 years, while the observed current mean age is 21.2 years. This difference may reflect the consequence of animals having been removed from the population in previous decades, thus reducing the number of older animals currently in the population.

Other PVA models, based on fewer and less recent years of data have projected either lower (e.g. Taylor and Plater 2001; Vélez-Espino et al. 2014a) or higher (e.g., Olesiuk et al. 1990) population growth rates. These differences are consistent with the models that used demographic data from years of decline

projecting continuing decline, and the models relying on data from earlier years of growth projecting continued growth. We used demographic data over the full span of years starting in 1976, and our population model predicts almost no mean change in population size – as has been observed over that 39-year time span.

### 3.2. Sensitivity testing of important model parameters

For the model parameters that might have significant effect on population growth, and yet the values currently and in the future are uncertain, we ran simulations with higher and lower values to determine the importance of each to the population performance. For each model parameter that was tested, the Table 1 below gives the value used in the baseline model, the minimum and maximum values of the range that was tested, the population growth rates that resulted from the min value (r-min) and max value (r-max) for that parameter while all other parameters were held at their baseline, and the % of variance in population growth (as a percent of the total variation accounted for by the varied parameters) due to variation in that parameter when all other parameters were simultaneously and independently varied across their ranges of uncertainty. Cells with two or three values for the rate are for the several age categories.

**Table 1. The importance of model parameters that potentially affect the population growth rate of the Southern Residents. The higher the %variance the greater the importance of the parameter.**

Parameter	Baseline	Min tested	Max tested	r-min	r-max	%variance
Inbreeding depression	6.29	3.145	9.435	-0.0005	-0.0029	6.1
Variance in male RS	0.20	0.00	0.40	-0.0017	-0.0023	0.4
Variance in female RS	0.20	0.00	0.40	-0.0017	-0.0019	0.0
Mean birth rate	0.1204 0.0788	0.1084 0.0709	0.1324 0.0867	-0.0062	0.0019	83.0
SD in birth rate	0.0354 0.0415	0.0319 0.0374	0.0389 0.0457	-0.0020	-0.0018	0.0
Calf mortality	0.1748	0.1573	0.1923	-0.0012	-0.0029	3.6
SD in calf mortality	0.1796	0.1616	0.1976	-0.0017	-0.0019	0.0
Juvenile mortality	0.0215	0.0194	0.0237	-0.0011	-0.0028	3.6
SD in juv. Mortality	0.0242	0.0218	0.0266	-0.0015	-0.0019	0.0
Adult mortality	various (see text)	base * 0.9	base * 1.1	-0.0010	-0.0028	6.4
SD in adult mortality	various (see text)	base * 0.9	base * 1.1	-0.0018	-0.0018	0.0

As shown in the table above, the estimates of environmental variation (EV, expressed as SDs) for each demographic rate had no effect on the population growth rate (within the range tested). Therefore, although these estimates of annual variation in rates are uncertain, refining the estimates would not change any conclusions about threats and the viability of the population.

Variance in reproductive success of males had a very small effect. Inbreeding depression and each of the mortality rates had moderate effects, while the birth rate (calves per adult female) dominated the variation in population growth. This is counter to a commonly reported trend for sensitivity of survival rates being more important than fecundity in long-lived species. However, this difference can be ascribed simply to the difference in whether sensitivity is tested for survival vs. mortality. (e.g. a 1% change in a survival rate of 90% is the same as a 10% change in the equivalent 10% mortality rate. Thus, growth rate will often be most sensitive to a change in survival, less sensitive to the same proportional change in fecundity, and even less sensitive to the same proportional change in mortality.)

Note that the significant impact of a shift in inbreeding depression indicates that the population is small enough so that the effects of inbreeding are likely to be damaging to the prospects for the population. This effect would be exacerbated further if we did not include in the model an avoidance of very close inbreeding (within matriline). If the effect of inbreeding depression on calf survival is removed entirely from the model, then the projected growth rate becomes slightly positive, at  $r = 0.0006$ .

### **3.3. Examination of potential threats**

The sections below describe the modeling to examine the likely impacts of several kinds of existing or potential threats to the Southern Residents. Text descriptions of these scenarios and brief summaries of the results are presented, followed by a summary table comparing results across these various scenarios.

#### Modeling of impacts of Chinook salmon abundance

Several factors have modified the Southern Residents' habitat, including changes in prey availability, contaminants, and vessel traffic. Reductions in salmon and other prey along much of the west coast of North America during the past 150 years, especially from Washington to California (Nehlsen 1997, Kope and Wainwright 1998), have likely lessened the region's carrying capacity for resident killer whales (Krahn et al. 2002). Resident whales likely forage selectively for Chinook salmon over other available salmonids because of the large size, high fat content, and year-round availability of this species in coastal waters (Ford et al. 1998, Ford and Ellis 2005). Ford et al. (2005) found that trends in the mortality rates of southern were strongly related to fluctuations in the abundance of Chinook salmon. Birth rates were also correlated with Chinook salmon abundance, but more weakly than mortalities.

Ward et al. (2009b), Ford et al. (2015), and Vélez-Espino et al. (2014b) all provide estimates of the relationship between abundance of Chinook salmon and demographic rates for Southern Residents. The details of the data used to quantify Chinook abundance, the co-factors considered, and the statistical

methodologies differ in many details between these studies. Vélez-Espino et al. examined fecundity for young and old females separately, and examined impacts on survival rates of different age classes, while the other papers assessed relationships with pooled demographic data. Ward et al. used Pacific Salmon Commission indices of Chinook abundance off the west coast of Vancouver Island; Ford et al. used Pacific Salmon Commission indices for the coastal region for coastal regions from SE Alaska to Oregon; and Vélez-Espino et al. used indices for terminal run abundance and ocean abundance for various salmon stocks and combinations of stocks in the region. All three studies examined the relationships with various time lags (0 to 2 years), although for projecting long-term population viability in simulation models, it is not important if changes in fecundity due to changing Chinook abundance occur in the year of the Chinook index or with a lag of a year or two.

All three previous studies identified large effects of Chinook salmon abundance on Southern Resident demographic rates. Ward et al. and Vélez-Espino et al. found large effects of Chinook abundance on fecundity, whereas Ford et al. and Vélez-Espino et al. reported significant relationships with mortality. However, Vélez-Espino et al. found the relationships of Chinook abundance with fecundity had greater influence on projected population growth than did the effect on survival, while Ford et al. reported a weaker (but still significant) effect on fecundity compared with mortality.

Both Ward et al. and Vélez-Espino et al. used regression models to determine the relationship between salmon abundance and  $\text{logit}(\text{birth rate})$ . The regressions provided by both studies can be rescaled so that Chinook abundance index is set to 1.0 for the average over the span of data (1976-2014 for our demographic analyses), and so that the regression predicts the observed birth rate when Chinook index = 1. After that rescaling, the relationship for overall fecundity reported in Ward et al. and for fecundity of the younger (more productive) females reported in Vélez-Espino et al. (for terminal run of Fraser late stock) are very similar and are both approximately:  $\text{logit}(\text{birth rate}) = -3.0 + \text{Chinook}$ , in which Chinook is the abundance relative to the long-term average.

This relationship leads to a predicted shift from a birth rate of 12% to 18.5% if the Chinook abundance increases by 50%, and a shift down to 7.6% if abundance decreases by 50%. The linear relationship reported by Ford et al. would lead to smaller but still significant shifts (up to 13.3% and down to 9.2%, respectively) in the birth rate.

Vélez-Espino et al. reported a stronger effect on fecundity of older females in relation to the Puget Sound terminal run, but a similar slope for Fraser + Puget abundance. If the intercept in the above regression is adjusted so that the fecundity of the older breeding females is correctly predicted at the baseline of Chinook = 1, then the relationship for that age class becomes:  $\text{logit}(\text{birth rate}) = -3.46 + \text{Chinook}$

Ford et al. (2015) provide the relationship of mortality to Chinook abundance in a form that is easily transferred to the Vortex model, namely:

Mortality index (relative to the expected value) =  $-2.6504 \times \text{Chinook (relative abundance index)} + 4.0066$   
Rescaling this relationship so that the mortality index is 1 when Chinook = 1 gives:

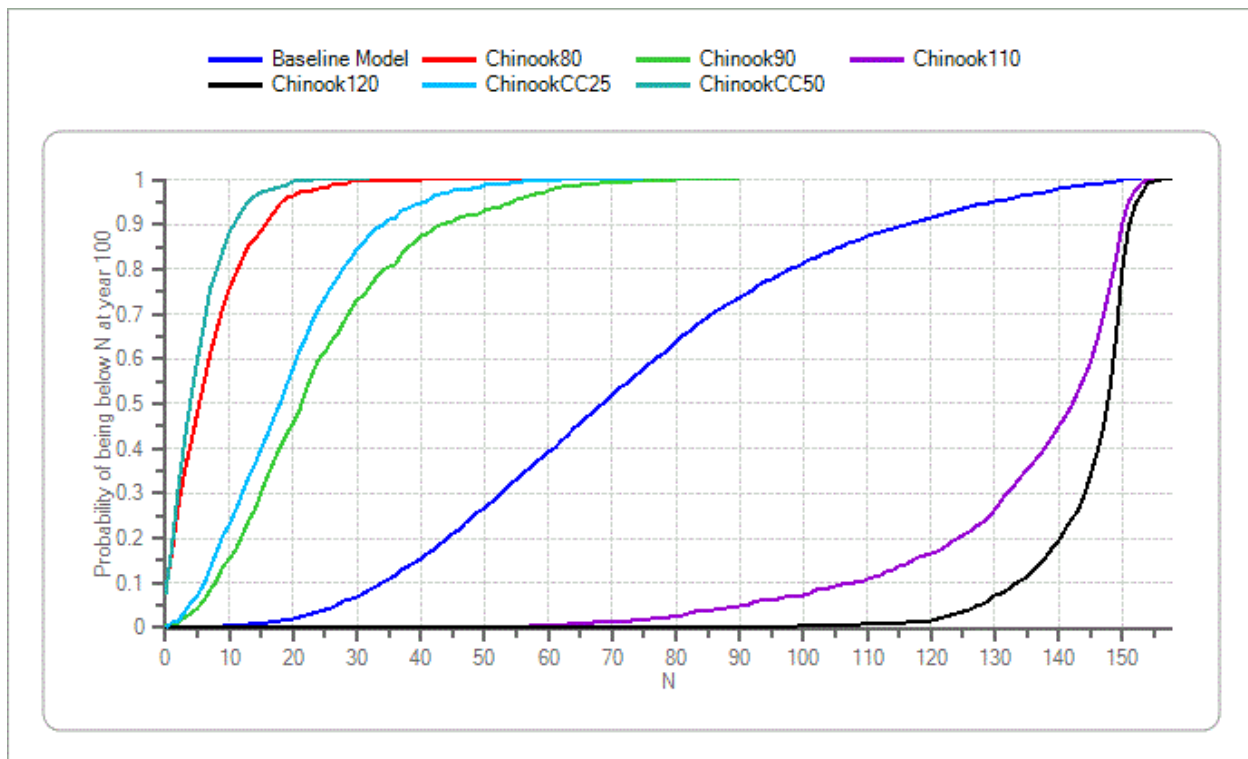
Mortality index (relative to the baseline) =  $-2.6504 \times \text{Chinook (relative abundance index)} + 3.6504$   
This relationship translates to a 26% increase in mortality for each 10% decrease in Chinook abundance.

The rescaling of the relationships above was confirmed to produce the same population growth in the Vortex model ( $r = -0.002$ , with  $SD = 0.045$ ) as was projected from the baseline model, as it should. These general relationships can then be used for projecting the primary impacts of changing Chinook abundance on population viability. For purposes such as managing threats via individual stocks, or assessing also the lesser impacts on other demographic rates, the more specific regression analyses presented in Vélez-Espino et al. (2014b) would provide models more tailored to specific questions.

With the above relationships of Southern Residents demography to Chinook abundance, we modeled the fate of the Southern Residents if Chinook numbers were set to 80%, 90%, 100%, 110%, or 120% of current (baseline) levels. Muñoz et al. (2014) also projected that Chinook could suffer a catastrophic decline within the next 60 to 90 years due to climate change raising the water temperatures occasionally above the thermal tolerance of the Chinook. Although the time course of any decline in Chinook is unknown as global temperatures steadily rise, we examined scenarios in which Chinook decline gradually but steadily by 0.25% per year or 0.50% per year (resulting in a 25% or 50% loss over 100 years).

As found in other studies, reducing the abundance of Chinook is projected to have a substantial negative impact on the Southern Residents population. The combined effect on fecundity and survival result in the mean population growth falling to  $r = -1.4\%$  or  $-2.6\%$  for a 10% or 20% reduction in prey. Moreover, the probability of extinction rises to 4% or 39%, respectively, whereas the probability of the population declining to below 30 animals rises to 73% or over 99%. Conversely, increasing Chinook abundance can lead to relatively robust population growth (up to 1.9% with 20% more prey) and protection from extinction or serious decline. If a decline of 25% or 50% occurs gradually over the next 100 years because of climate change (or other factors), the consequences for Southern Residents population viability are about comparable to an immediate loss of about half the magnitude.

The quasi-extinction graph below demonstrates the dramatic effect that can occur with shifts in the abundance of Chinook prey (Figure 5).



**Figure 5. The graph illustrates the effects that can occur with varying abundances of Chinook prey, which is the primary food for Southern Residents. Reducing the abundance of Chinook is projected to have a substantial negative impact on the Southern Residents population, whereas increasing abundance leads to robust population growth and protection from serious decline or extinction.**

### Modeling oil spill impacts

While the probability of either Northern or Southern Resident killer whales being exposed to an oil spill is low, the impact of such an event is potentially catastrophic. Southern Residents are at risk of an oil spill because of the existing tanker traffic that travels in and out of Puget Sound and the Strait of Georgia (Baird 2001, Grant and Ross 2002) and the proposed expansion of tanker traffic associated with Project.

Impacts of oil spills are tested in the model by adding two types of catastrophes – large oil spill and smaller oil spill. Catastrophes are assumed to occur at random infrequently (i.e., with low probability of occurrence in any given year) but to affect survival or reproduction when they occur. In the model, the impacts are deaths that occur in the year of the spill. The deaths occurring because of an actual spill may occur over several years, but presumably the females weakened by the spill would not be successful breeders before they die from the spill, so they can be removed from the population in the model at the time of the spill.

The initial frequency of a big or “worst case” spill ( $>16,500 \text{ m}^3$ ) is based on an analysis by Foschi (2014). He used Kinder Morgan’s projections, which were calculated as return periods (in years) for oil spills of different volumes (Table 34 of their TERMPOL Report 3.15.), to derive a 10% probability of an oil spill in 50 years, corresponding to a 0.21% chance per year. The initial frequency of smaller spill ( $>8,250 \text{ m}^3$ )

was estimated to be 42% in 50 years, corresponding to a 1.08% chance per year. The basis for the Kinder Morgan estimates is not clear, and it is difficult to consider the threats of smaller volume spills (<8,250 m<sup>3</sup>) because the reports do not clarify the average volume or the distribution of volumes of those small spills. To encompass some of the uncertainty, we therefore also tested the projected effects of frequencies of large and smaller spills that are double those stated above.

The mortality caused by the spills is the product of the percent of the Southern Resident population that would become exposed to damaging doses of oil products and the percent that die from that exposure. Based on the percent overlap of oil coverage and critical habitat, as determined from Trans Mountain Pipelines oil spill models (Modeling the Fate and Behavior of Marine Oil Spills for the Trans Mountain Expansion Project. 2013. [NEB Exhibit No. B21-9 to B23-28, V8C TR 8C 12 TR S9 and V8C TR 8C 12 S9a APPE, A3S5G9 to A3S5H5]. EBA File: V13203022. Prepared for Trans Mountain Pipelines ULC.), we estimate that about 50% of the Southern Residents would encounter a large spill. We estimate that half this percent (25%) would encounter a smaller spill (of half the oil volume) (Figures 6 and 7)).<sup>11</sup> We also assumed that a Southern Resident that has direct exposure to a large spill would have 100% mortality. Small spills are assumed to cause 50% mortality to those Killer Whales that are exposed to the oil. Thus, the overall mortality due to a large spill in the critical habitat would be 50%, and overall mortality due to a smaller spill would be 12.5%.

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<sup>11</sup> Whether an oil spill would directly affect the Southern Residents depends largely on traffic levels, the size of the whale population (i.e., the larger the population the greater the probability of exposure), and the distribution of whales relative to the spill. All of the Southern Residents are periodically in the same location at the same time (known as a “super pod”), making the whales very vulnerable to a catastrophic event like an oil spill during such times (NOAA 2014).



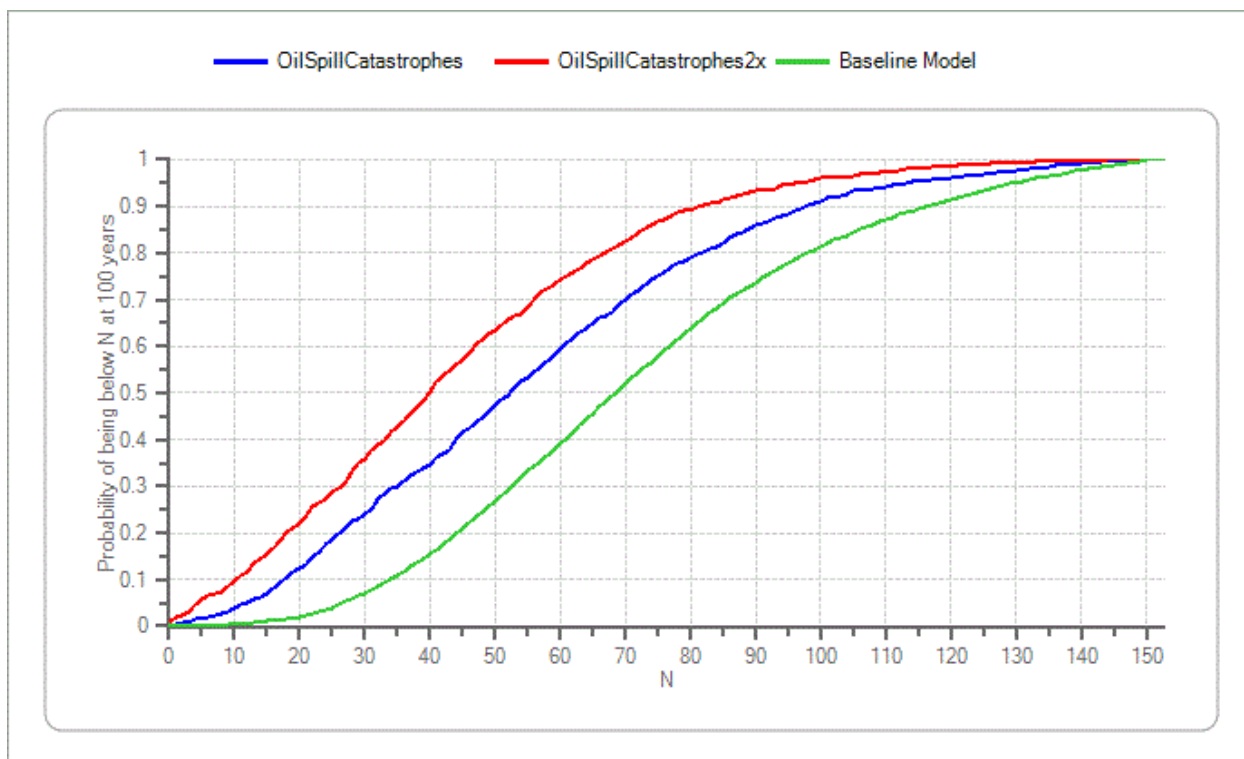


Figure 6. The figure shows the probability of oil presence and dispersion within the Salish Sea following an oil spill during summer. The overlap with critical habitat of Southern Resident killer whales is significant.



**Figure 7.** The figure shows the probability of oil presence and dispersion within the Salish Sea following an oil spill during the fall. The overlap with critical habitat of Southern Resident killer whales is significant.

Oil spills of the frequency estimated and with the estimated extent of overlap of oil with critical habitat would cause some depression of mean population growth (to  $r = -0.005$  as opposed to  $r = -0.002$  without oil spills) and the mean final population after 100 years ( $N = 56$  vs.  $N = 72$  with no oil spills). The probability of complete extinction would rise to 1%, but the probability of quasi-extinction (below  $N=30$  threshold) rises to 24.3% (vs. 7.1%). If oil spills occur at a frequency twice that projected by Kinder Morgan, then the mean prospects for the population are worse ( $r = -0.008$ , final  $N = 46$ ) and there becomes a 35.8% chance of quasi-extinction below the  $N = 30$  threshold (see graph below) and a 3.5% chance of complete extinction of the Southern Residents. Thus, the impact on mean long-term population growth of rare oil spills could be moderate, because in most years no spill occurs, but the effect on probability of the population dropping to low numbers (e.g., quasi-extinction below  $N = 30$ ) is more substantial, with a possibility of complete extinction within 100 years due to the potential of catastrophic decimation of the population to a small number from which it could not recover.



**Figure 8.** This figure shows the effects of oil spills on the mean population growth rate of Southern Resident killer whales. The rate of occurrence of various sized oil spills was determined using an analysis of spill probably frequencies provided by Kinder Morgan in the Trans Mountain Pipeline application. These are given in Table 34 of their TERMPOL Report 3.15.

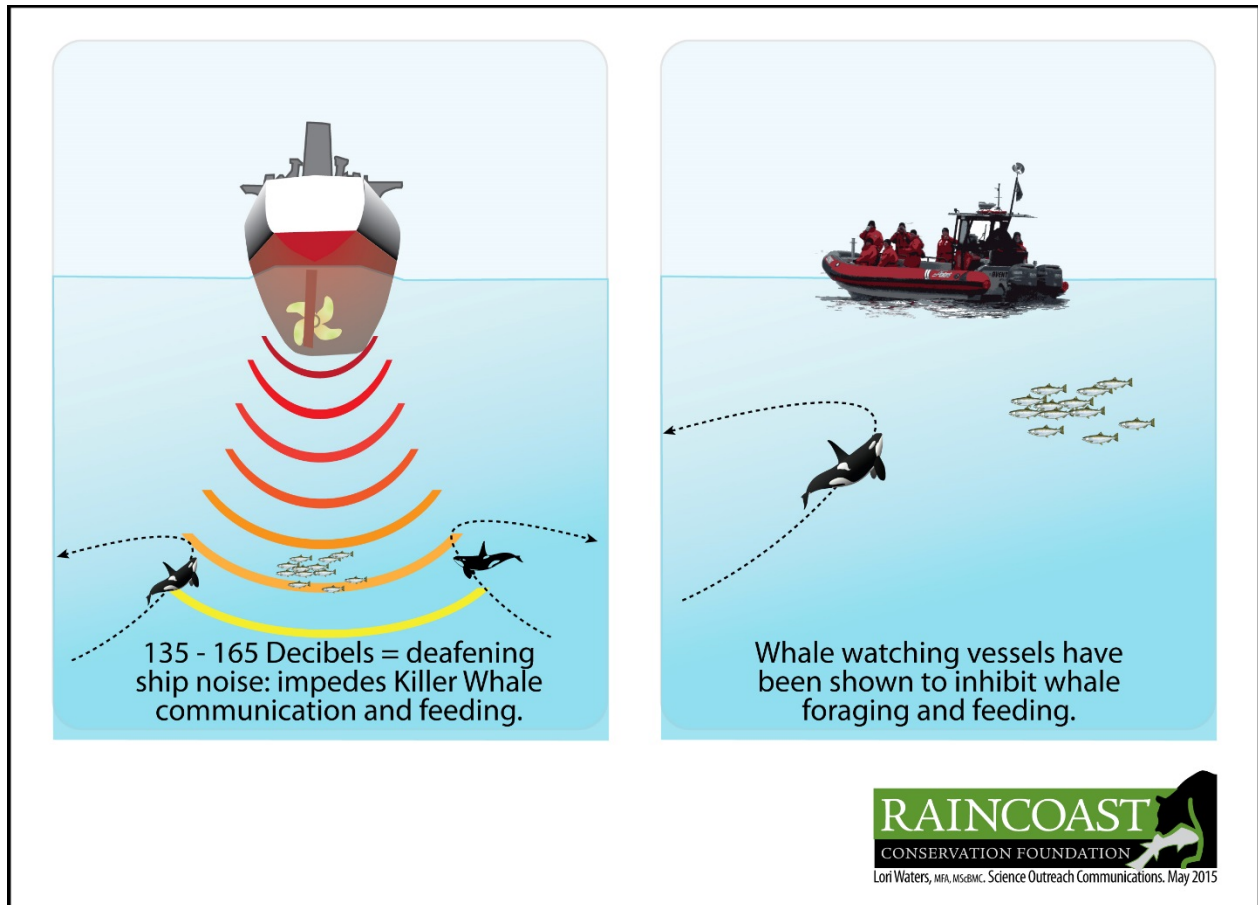
#### Modeling impact of increased boat noise

Noise from boats near Southern Residents can disrupt feeding activity and reduce foraging efficiency by masking echolocation (Figures 9 and 10). However, the reduced feeding activity will likely have a much larger impact than the reduced foraging efficiency, and we will focus our analyses on the former.

Southern Residents reduce feeding activity by 25% around boats. Presently, boats are present an estimated 85% of the time that Southern Residents forage (there is no evidence that they have shifted foraging activity to the nighttime to avoid recreational and whale-watching boats), and they are foraging in the presence of boats an estimated 78% of that time. Thus, feeding is expected to be reduced by 16.6% ( $= 25\% \times 85\% \times 78\%$ ) due to disturbance by boats (Bain 2002, Williams et al. 2006, Lusseau et al 2009, Lusseau and Bejder 2007)

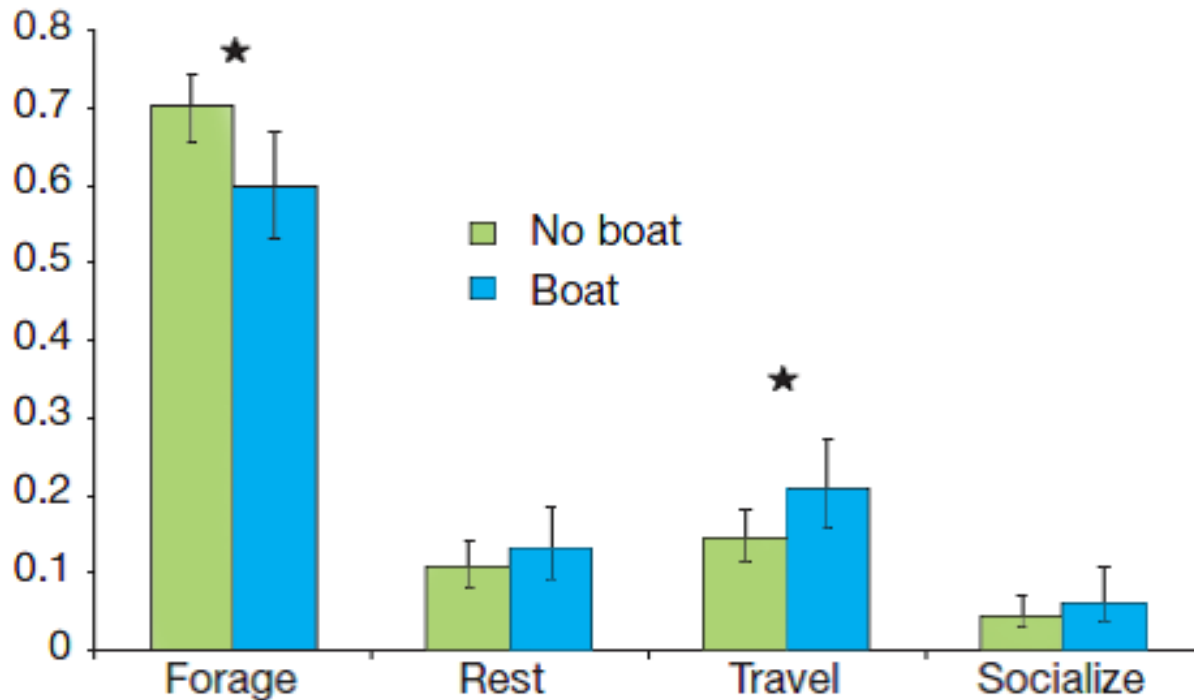
With increased shipping traffic associated with the Project, Southern Residents could be around boats up to 100% of the time – according to the proponent tankers would be a “near continuous” presence. Thus, feeding could potentially be reduced by up to 19.5%.





**Figure 9. Noise from boats near Southern Residents can physically disrupt feeding activity and reduce foraging efficiency by masking echolocation.**

## Southern Resident Behavior Changes With Boat Presence

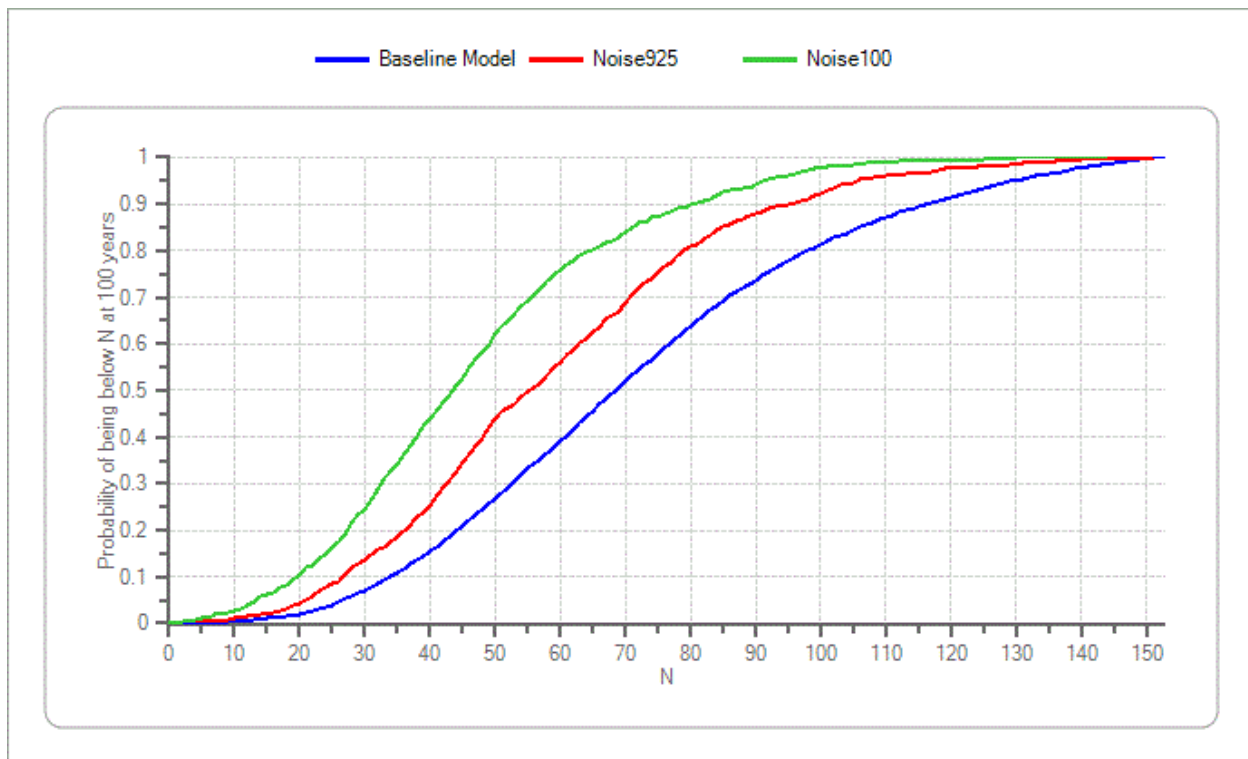


**Figure 10.** This figure shows the amount of time Southern Residents from J, K, and L pod spent foraging, resting, traveling, and socializing with and without the presence of boats in two areas near San Juan Island. When vessels were present, the whales foraged significantly less and travelled more. Figure from NOAA (2014), Data from Lusseau et al. 2009.

If we assume that the effect on demographic rates of reduced feeding activity is the same as a comparable reduction in prey, then we can use the relationships described above for the effects of reduced Chinook abundance to estimate also the effects of reduced feeding activity due to the presence of boats. Thus, the foraging success relative to the baseline conditions with current levels of disturbance by boats would be:

Proportional time spent feeding =  $(1 - (0.25 \times 0.78 \times BT)) / (1 - (0.25 \times 0.78 \times 0.85)) = (1 - (0.195 \times BT)) / 0.83425$ , with BT being the proportion of the time that boats are present.

We tested values of BT = 85% (baseline), BT = 92.5%, and BT = 100% to determine if increase disturbance of feeding behavior could have a significant influence on Southern Resident demography. With boats always present (BT = 100%), the reduction in foraging is about 3.5% and this resulted in accelerated population decline ( $r = -0.007$ ), smaller mean size ( $N = 47$ ), 1% probability of extinction, and 25% chance of falling below 30 animals. The impact of an increase in boat presence of half as much (BT = 92.5%) caused proportionately about half as large shifts in population viability relative to the baseline (Figure 11).



**Figure 11. This figure show that increasing disturbance of feeding behavior above current levels would affect Southern Resident killer whale demography, resulting in accelerated population decline, smaller mean population size, and increased chance quasi extinction.**

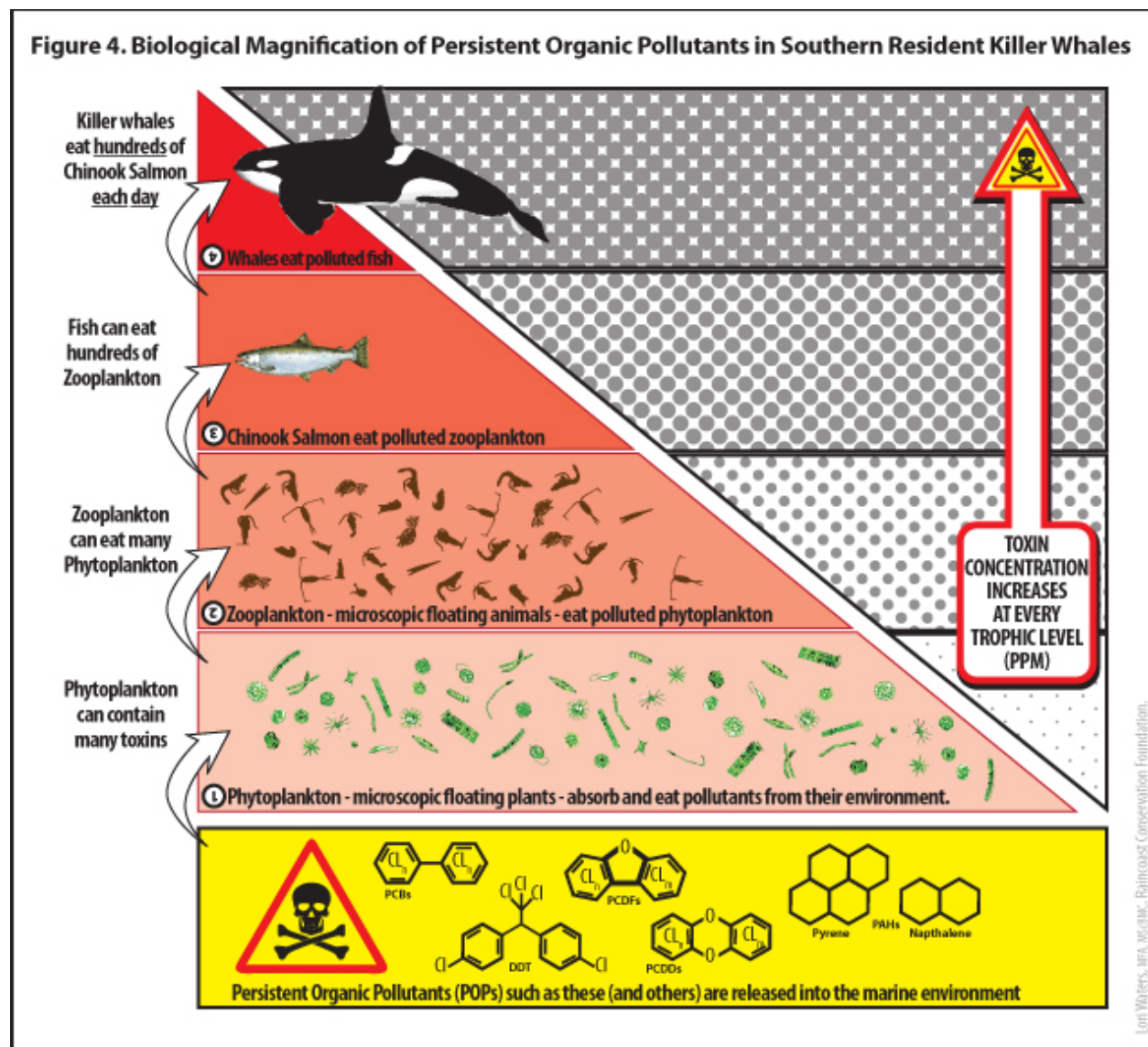
Clearly, increased recreational, fishing, whale-watching, and shipping traffic can affect Southern Residents also in other ways, such as increased frequency of injury from boat strikes, and an increase in the small scale pollution from spilled fuel and emissions. The effect of additional boat strike mortality can be assessed with the models presented below for “Modeling population impacts of human-caused deaths”, although we have not attempted to determine how the frequency of such injuries will change. We also have not tried to assess the health effects on Southern Residents of increased pollution of the water and air.

#### Modeling impact of PCBs on Southern Residents

PCB burdens in Southern Residents are at harmful levels (Garrett and Ross 2010) and considered a primary ongoing threat by the Recovery Strategy in Canada (Fisheries and Oceans Canada 2011) and the U.S. (National Marine Fisheries Service). The detrimental health effects of carrying large contaminant burdens interact with other threats such as prey limitations and disease, and increase susceptibility to other threats emanating from vessel traffic, such as acoustical disturbance or oil spills (Figure 12). Our basic model of accumulation, depuration,<sup>12</sup> and impact on calf survival of PCBs was based on the

<sup>12</sup> The process of freeing from contaminants; in this case PCBs.

methodology of Hall et al. (2006, 2011, 2012), with modifications in rates for Southern Residents as described below.



**Figure 12. Biological magnification of persistent organic pollutants in Southern Resident killer whales.**

We assumed that Southern Residents obtain the initial load of PCBs from their mothers, but that most of that initial load is removed, primarily through a growth dilution, by the time that the animals reach 10 years of age (Hickie et al. 2007). The impact of PCB on population growth is being modeled only as the reduction in survival of calves due to the PCB loads of their mothers, so the initial PCB level before age 10 years is not important in our model. Note that we did not attempt to project the effect of PCBs on disease susceptibility, as was done in Hall et al. (2012).

We initially modeled the accumulation of PCBs as a linear function:  $PCB = 1 + 5 * Age$ , extrapolating back to a conservative estimate of 1 mg / kg remaining from the initial PCB load obtained from the mother,

and accumulating thereafter at a rate of 5 mg/kg/y. Breeding females are projected to have a 0.77 proportional reduction in their PCB levels through depuration when they raise a calf. The rate of accumulation that we used is higher than the mean (2.96 mg/kg/y) that has been reported in a population of bottlenose dolphins that does not have high PCB levels in adults (Wells et al. 2005), and within the range tested for cetaceans by Hall et al. (2011). This rate of accumulation leads to a mean PCB level in our simulations of 57 mg/kg in breeding adult females ( $9 < \text{Age} < 46$ ) and 106 mg/kg in males 10 y and older. These mean projected PCB loads are consistent with few data on Southern Residents reported by Ross et al. (2000), who found  $55 \pm 19$  mg/kg in two adult females and  $146 \pm 33$  mg/kg in four adult males.

For the impact of maternal PCB on calf survival, we assumed a linear regression on  $\text{logit}(\text{survival})$ , of the same form as used by Hall et al. (2006). We determined the slope and intercept that fit the two observed data points for Southern Residents ( $\text{survival} = 0.8252$ , mean PCB = 55.4 [Ross et al. 2000]) and Northern Resident Killer Whales ( $\text{survival} = 0.9218$  [Vélez-Espino et al. 2014a], mean PCB = 9.3 [Ross et al. 2000]). This yielded a relationship of:  $\text{logit}(\text{survival}) = 2.65 - 0.02 * \text{PCB}$ .

This relationship predicts a calf survival rate of 93.4% in the absence of PCBs, consistent with the higher estimates of calf survival reported for growing killer whale populations (such as Northern Residents).

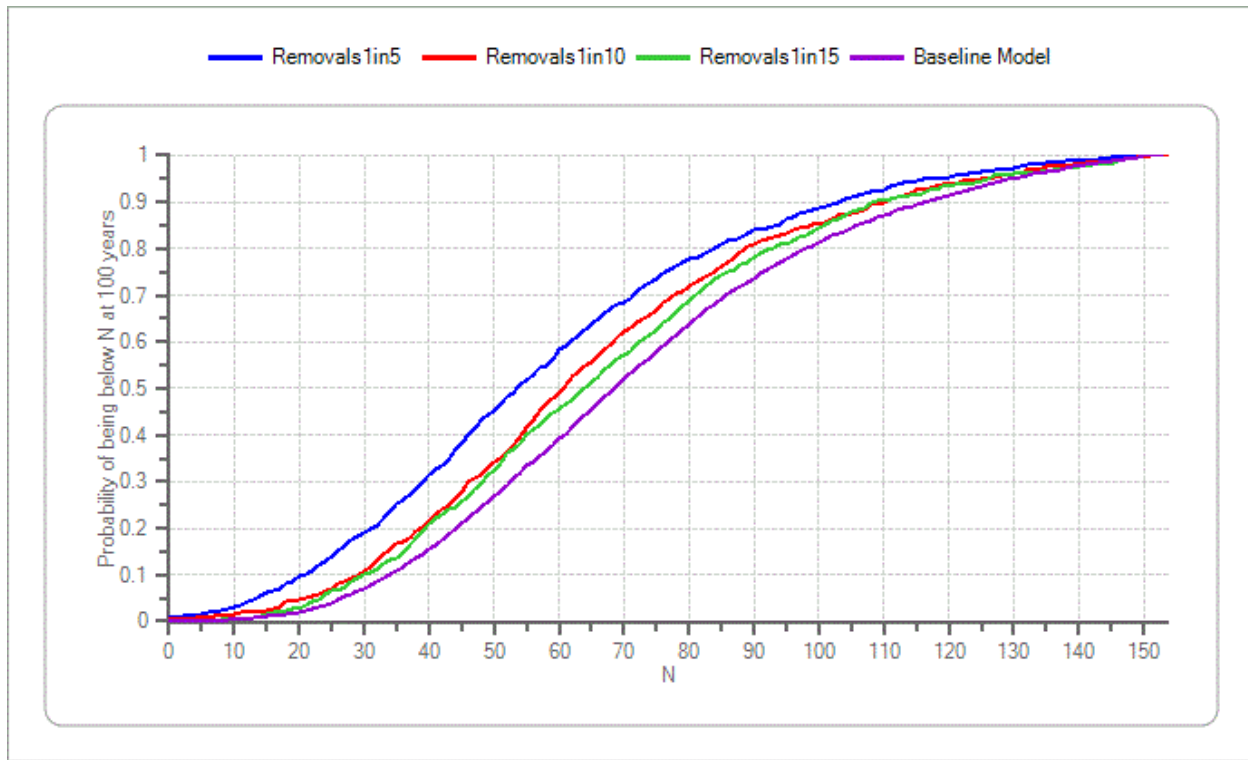
When the accumulation, depuration, and impact on calf survival of PCBs were added to our baseline model, the mean population growth was  $r = -0.002$ . This is the same as the baseline model without consideration of PCBs, as is expected because the effect of PCBs on calf survival was scaled so as to produce the baseline survival rate with the average level of PCBs in the mothers. If the PCB level is set to 0 for all animals in the model with consideration of PCBs, then the mean population growth is projected to be  $r = 0.003$ . This suggests that PCB effects model can be a basis for examining likely effects of increased or decreased PCBs in the population.

#### Modeling population impacts of human-caused deaths

Various human activities have a risk of causing a fatal injury to a Killer Whale. These include accidental collisions with recreational or commercial boats, entanglement in fishing gear, and intentional harm to animals. Documented causes of death include ingested fishhook with trailing line, trauma from ship strikes, and *Salmonella* septicemia (Gaydos and Raverty 2007). Although such events are likely rare, in a small population with low birth rates, even a few extra deaths might cause significant damage to the population growth, size, and even persistence. To explore the possible population consequences of additional deaths (or removals of any sort) caused by human activities, we ran simulations in which one KW was removed on average every 15 years, 10 years, or 5 years, which reflects the rate of documented human induced mortalities for the Southern Residents during the last 30 years (K. Balcomb pers. Comm., Gaydos and Raverty 2007). In the model the removals were stochastic (with constant probabilities of the loss of an animal over time), had equal probability of the removed animal being male or female, and removed adults ( $> 9$  years of age) otherwise, without regard for their age.



The removal of one additional adult Killer Whale from the population every 10 years or every 15 years had little effect on population growth (from  $r = -0.002$  to  $r = -0.003$ ), and caused a small increase (from 7% to 10%) in the probability that the population would be below 30 animals after 100 years. Removal of an animal every 5 years had a more noticeable impact on average population growth (reducing to  $r = -0.005$ ), caused a 2% probability of extinction and 19% probability of being below 30 killer whales (Figure 13).



**Figure 13.** Various human activities have a risk of causing a fatal injury to a killer whale. These include accidental collisions with recreational or commercial boats, entanglement in fishing gear, and intentional harm to animals. To explore the possible population consequences of additional deaths (or removals of any sort) caused by human activities, we ran simulations in which one killer whales was removed on average every 15 years, 10 years, or 5 years as shown in the figure.

## Summary and comparison of the impacts of potential threats

The table below summarizes the impacts of several levels of each of the kinds of threats that we have examined (Table 2). For each threat model, the columns show the mean population growth rate, mean population size after 100 years, standard deviation in population size, probability of complete extinction, and probability of quasi-extinction (defined as being at or below  $N = 30$  after 100 years). Note that for the Baseline scenario, 10,000 independent iterations were run. For each alternative scenario, 1,000 iterations were run, resulting in outcomes that are less precise. Usually the last digit shown is within  $\pm 1$  of the value that would be obtained with many more iterations of the scenario.

**Table 2. Summary of the kinds impacts of potential threats that we examined at several levels.**

Threat model	mean r	final N	SD(N)	Pr[extinct]	Pr[N ≤ 30]
Baseline	-0.002	72	31	0.1%	7.1%
Chinook80	-0.026	7	7	39.4%	99.4%
Chinook90	-0.014	24	15	4.2%	73.1%
Chinook110	0.008	135	19	0%	0%
Chinook120	0.019	145	8	0%	0%
ChinookCC25	-0.016	20	11	6.4%	84.6%
ChinookCC50	-0.027	8	4	50.6%	99.9%
PCB90	-0.002	71	32	0.1%	8.9%
PCB110	-0.003	63	28	0.5%	11.0%
OilSpills	-0.005	56	31	1.0%	24.3%
OilSpills2x	-0.008	46	28	3.5%	35.8%
Noise92.5	-0.004	59	26	0.3%	13.8%
Noise100	-0.007	47	23	1.0%	24.5%
Removal15y	-0.003	68	31	0%	10.3%
Removal10y	-0.003	65	31	0.6%	10.9%
Removal5y	-0.005	58	30	2.0%	19.1%
Cumulative	-0.012	33	23	8.6%	53.5%

Threat models tested (see text for further explanation of each):

- Baseline = no additional threats
- Chinook80 = Chinook reduced to 80% of current
- Chinook90 = Chinook reduced to 90% of current
- Chinook110 = Chinook increased to 110% of current
- Chinook120 = Chinook increased to 120% of current

- ChinookCC25 = Chinook projected to decline by 0.25% per year due to climate change
- ChinookCC50 = Chinook projected to decline by 0.50% per year due to climate change
- PCB90 = PCB accumulation rate set to 90% of baseline
- PCB110 = PCB accumulation rate set to 110% of baseline
- OilSpills = Large and smaller oil spills at annual probabilities of 0.21% and 1.0835%, respectively
- OilSpills2x = frequency of spills doubled over the above
- Noise92.5 = Feeding time reduced because of boat presence 92.5% of the time
- Noise100 = Feeding time reduced because of boat presence 100% of the time
- Removal15y = remove on average an adult every 15 years
- Removal10y = remove on average an adult every 10 years
- Removal5y = remove on average an adult every 5 years
- Cumulative = OilSpill + Noise100 + Removal10y

From the above results, it is clear that even small changes in the abundance of Chinook could have substantial impacts on the Southern Residents population. A 10% increase in prey changes the population to a positive population growth, and eliminates the chance of extinction or dropping to very small size. A 10% decrease in prey results in a 73% (in contrast to 7% for the baseline) probability of declining below 30 animals. A 20% reduction in prey leads to almost a 100% chance that the Southern Residents population will fall below 30 animals. If Chinook decline gradually down to 75% or 50% of current numbers due to climate change over the next century, then the effects on measures of population growth and viability are about half as severe as when a comparable decrease occurs immediately.

A change of 10% in the rate of accumulation of PCBs has a relatively small effect.

Adding the expected possibility of oil spills to the model moderately decreases long-term average population growth, considerably increases the probability of a major decline to below 30 animals, and leads to a low but not insignificant possibility of complete extinction.

Noise disturbance at the 100% level, because of adverse effects on foraging, decreases long-term average population size, accelerates the probability of population decline, and increases the chance of quasi extinction.

Removing an additional animal every 10 to 15 years caused only slight decreases in population performance, as expected considering that 1 animal every 10 years removes, on average, a little more than 0.1% of the population. Removing an animal every 5 years is enough to accelerate decline noticeably and cause some chance of extinction.

Note that the amounts of change tested above do not necessarily represent projections of the changes to expected threats, because often data on which to make such predictions are not available. However,

the ranges tested do allow comparison of the magnitude of impacts with several plausible levels of each threatening process.

### Modelling the cumulative impacts of threats

The above tests examine each threat on its own, but the Southern Resident population may be facing increasing pressures from multiple threats. We tested one scenario that combines some threats likely to intensify if there is an increase in shipping of oil through the critical habitat of the Southern Resident population and no adequately compensatory actions are taken to offset threats. In this cumulative impacts model, we imposed the effects of the forecast frequency of oil spills (as in the “OilSpills” model above), the effects of noise on foraging efficiency if boat traffic increases substantially (“Noise100”), and the impact of the death of one additional animal per 10 years due to boat strikes (“Removal10y”).

The cumulative impact of those three threats together resulted in a population decline of more than 1% per year, resulting in a mean final population size of only 33 animals, a 8.6% probability of complete extinction of the Southern Residents, and more than 50% probability that the final population would be less than 30 animals and, therefore, probably on a course toward nearly inevitable extinction. The following 3 graphs present the results of this cumulative effects model on various measures of population viability, in comparison with the models of the 3 threats individually and the baseline “status quo” model (Figures 14, 15, 16).

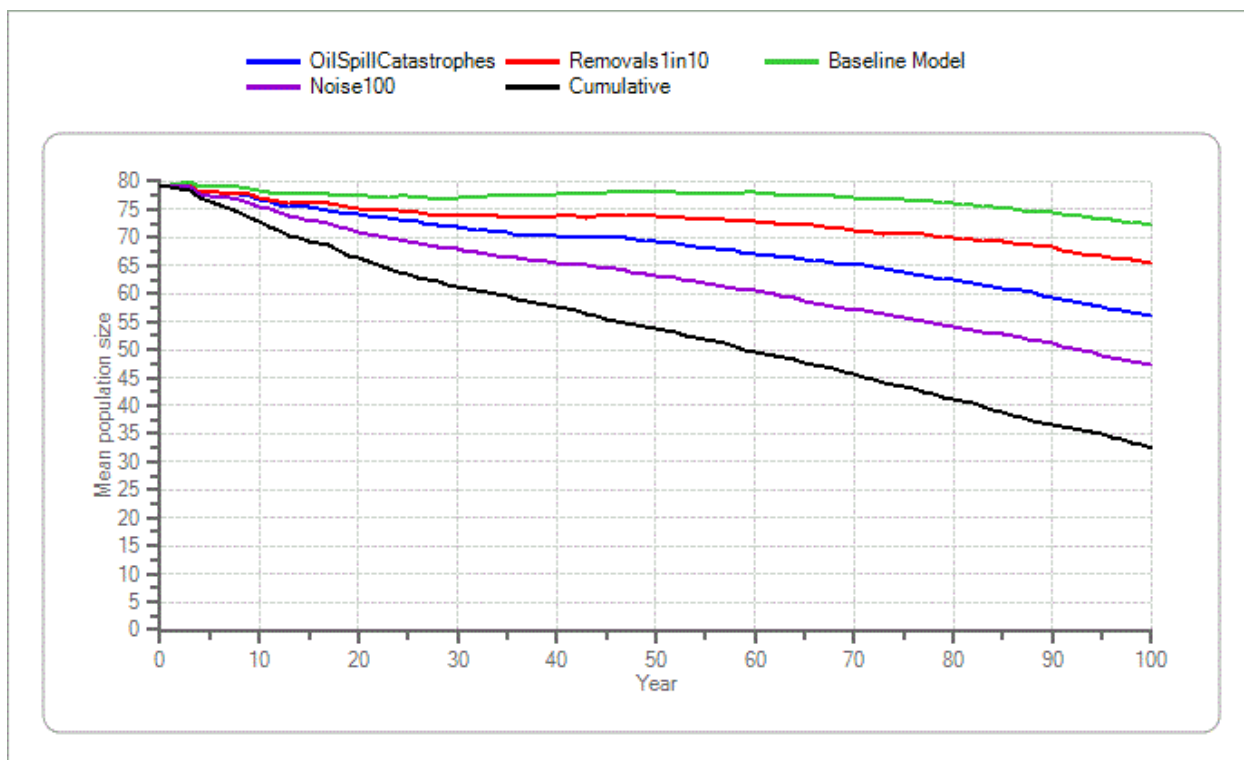


Figure 14. The graph shows the mean population size averaged across 1,000 iterations of each simulation.

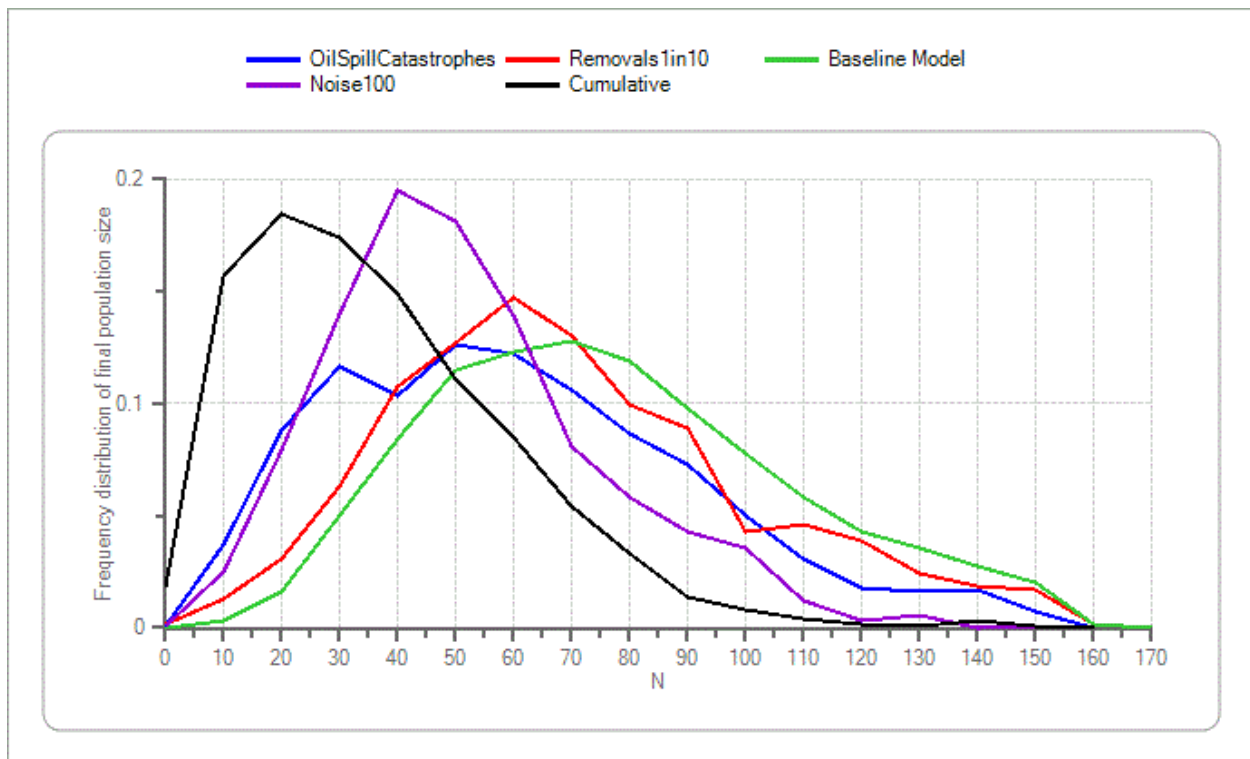
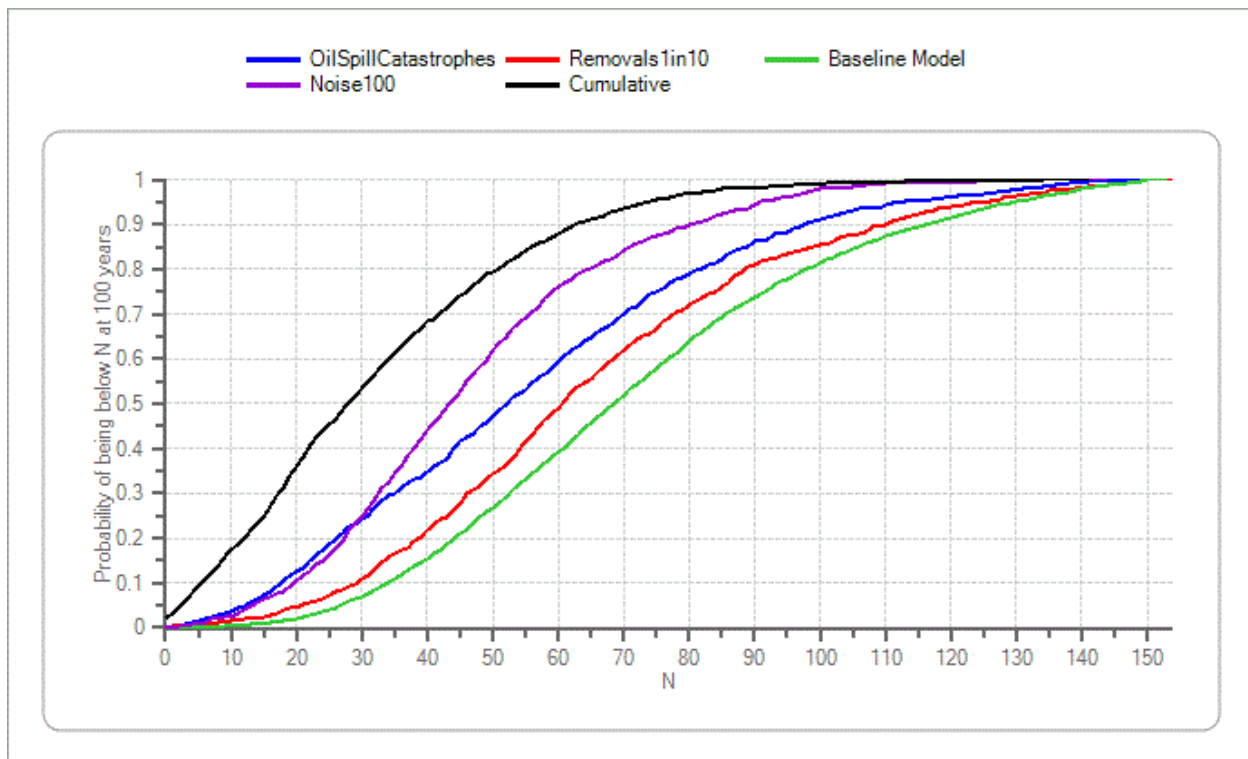


Figure 15. The graph shows the distribution of population size in the 1,000 iterations of each simulation, and the range of final population size that was generated by each of the models.



**Figure 16. The graph of quasi-extinction shows the probabilities for each model of the population size being below 30 killer whales at 100 years.**

#### 4.0. Conclusions

The Southern Resident population has experienced almost no population growth over the past 4 decades, and has declined in the last two decades. Models projecting population changes based on average demographic rates and the fluctuations in those rates across time project that under the status quo conditions the population will most likely remain about at its current size or continue a very slow decline. Potential population growth is inhibited in part by the very small size of the population and the consequent lack of available unrelated mates for breeding females. Thus, even without modeling new or increased external threats associated with the Project, it is clear that the population cannot withstand additional negative pressures.

In our modeling, we projected the impacts of several kinds of threats that may become worse over time through the approval of the Project. The factor projected to have the largest effect on depressing population size and possibly leading to extinction was a reduction of the Chinook prey base. Noise disturbance that affects foraging efficiency for Chinook has a moderate but significant influence on population viability. Large or medium oil spills occurring at the frequency suggested in Kinder Morgan's own oil spill analysis could depress long-term average population growth and lead to a considerable chance of the population declining below 30 animals (quasi-extinction). Progressively smaller impacts were seen with disturbance of feeding by boats, removal (human-cause death) of an animal every 5 years, and small changes in the rate of accumulation of PCBs (used as proxy for environmental contamination) acquired from the environment. However, it should be noted that all of the threats

tested caused some reduction in population viability. Reduction of some of the existing pressures on the population is necessary for population growth to resume and for there to be a reasonable expectation of recovery to a more viable level.

In our models the probability of complete extinction (no remaining animals) within 100 years in our analysis of Project effects is low. However, because individual killer whales can live to be almost 100 years old, and a demographically collapsing killer whale population will often have at least a few individuals still alive 100 years from now, this appearance can be misleading. The probability of the population dropping below 30 animals (about the size of one current pod) is the more relevant measure of threat to population persistence. That probability is unacceptably high in all of the scenarios to which we added new threats associated with the Project.

We combined into one model the three threats that are projected to result from the marine shipping of oil through the critical habitat associated with the Project: the possibility of oil spills at the frequency estimated by Kinder Morgan, projected effects of noise if there becomes high frequency of shipping traffic, and occasional additional mortalities due to boat strikes (one in 10 years). This cumulative effects model indicates that the Southern Residents population becomes vulnerable to extinction (8.6% probability within 100 years), and faces more than 50% probability of decline below 30 animals. We have not yet examined the many other possible combinations of cumulative impacts of threats occurring together, including the effect of the above three threats if compounded or offset by changes in other pressures such as changes to the abundance of Chinook salmon. Avoidance or full mitigation of these threats will be required to give the Southern Residents population a good chance to persist, and improvements to current conditions for the population will be required to permit the growth that is necessary to meet recovery criteria.

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## Appendix A. Review of Previous Southern Resident Population Viability Analyses

In recent years, numerous Population Viability Analyses (PVAs) have been used to estimate growth rates and extinction risk of the Southern Residents (Plater 2001, Taylor and Plater 2001, and Krahn et al. 2002, 2004, Vélez-Espino et al. 2013, 2014). Although methodologically similar, these PVAs differ somewhat in biological details, time frames, and suppositions as appropriate for the specific objectives of the various analyses. As would be expected, in all analyses extinction risk increased when the frequency and magnitude of catastrophes such as oil spills were elevated, or carrying capacity<sup>1</sup> declined (Taylor and Plater 2001, and Krahn et al. 2002, 2004). Similarly, declines in prey availability (Vélez-Espino et al. 2013, 2014) were shown to adversely affect population persistence. Based on these analyses and assuming that no attempt is made to alleviate or lessen current threats to the population's viability, a slow decline and likely extinction of the Southern Resident population can be regarded as inevitable – this is the trajectory that protection under the Species at Risk Act is intended to halt. Unless wholly mitigated, the addition of disturbances such as increasing shipping traffic and catastrophic events such as oil spill will hasten the demise of the species.

### 1.0 2001 PVAs

In the first comprehensive PVA of Southern Residents, Plater (2001) used demographic data from 1974–2000 to estimate mortality and fecundity rates. Depending on model assumptions regarding the maximum population size that the environment could sustain indefinitely (i.e. carrying capacity), sex ratio at birth, and potential effects of risk factors on reproduction and survival, the time to extinction ranged from an estimated 113 to greater than 300 years.

A second series of PVAs incorporated a much wider range of assumptions and risk levels (Taylor and Plater 2001), using data from the 1996–2000 decline to estimate mortality and fecundity rates. These models included the multiple impacts of higher inbreeding, oil spills, epizootics (disease events), and reduced food supply. Addition of these threats resulted in the prediction of a greatly increased risk of extinction - a 33-100% chance of extinction in 100 years. Regardless of the assumptions made in any given PVA in this series of PVAs, each calculated that the population would go extinct within 200 years and the median predicted time to extinction ranged from 54 to 112 years, depending on the model assumptions.

The estimated risk of extinction in this second series of PVAs was very sensitive to assumptions regarding the average probability of survival and reproduction (i.e. survival rates) of Southern Residents in the future. When a PVA assumed that the previous 29 years were a good indicator of future population trends, then the estimated probability of extinction was much lower than if a more pessimistic assumption was made that the previous 10 years, during which the population declined, were a good indicator of the future. Under the pessimistic assumption, uncertainties with respect to the level of carrying capacity, and the rate and magnitude of catastrophes, had relatively little effect on the extinction probability, which was high regardless. In contrast, under the more optimistic prediction using the 29-year series of survival rates, the risk of extinction was strongly influenced by the assumption made about carrying capacity and was to a lesser extent influenced by assumptions about the level and magnitude of catastrophes.

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<sup>1</sup> The **carrying capacity** is the maximum population size of the species that the environment can sustain indefinitely, given the food, habitat, water, and other life requisites available in the environment.

## **2.0 2002 and 2004 PVAs**

Two associated PVAs of Southern Residents were conducted by the National Marine Fisheries Service's Biological Recovery Team to synthesize the potential biological consequences of a small population size, a slowly increasing or a declining population trend, and potential risk factors (Krahn et al. 2002, 2004). In both analyses, the probability of the population going extinct was estimated using demographic information from the yearly census of the population. Notably, the original PVA (Krahn et al. 2002) was adjusted and updated (Krahn et al. 2004) to incorporate data concerning the Southern Resident population collected through 2003. Because the two PVAs are nearly identical, we only describe the results of the modified and most recent PVA.

The recovery team determined both the probability of extinction (defined as <1 male or female) and the probability of "quasi-extinction" (defined as < 10 males or females) were determined, because the recovery team believed that a population at the quasi-extinction level would be destined to extinction, even though literal extinction might still take decades given killer whales' long lifespans.

When the team assumed that growth rates in the future would be most accurately predicted by the full 29-year time series of available data on the population (the most optimistic scenario considered), the model predicted the probability that Southern Resident would become extinct was <0.1–3% in 100 years and 2–42% in 300 years. If the quasi-extinction threshold was used instead of actual extinction, the predicted probability of meeting the threshold ranged 1–15% in 100 years and 4–68% in 300 years. For both scenarios, the higher percentages in each range were associated with assumptions of higher probability and higher magnitude of catastrophic mortality events (e.g. oil spills), and associated with a smaller carrying capacity of 100 whales.

When it was assumed that the population survival for the previous 10 years would best predict the future (the most pessimistic model), the analysis predicted a probability of extinction of 6–19% in 100 years and 68–94% in 300 years. If a quasi-extinction threshold was used instead of actual demographic extinction, the predicted probability of meeting the threshold ranged from 39–67% in 100 years to 76–98% in 300 years.

## **3.0 2014 PVA**

Vélez-Espino et al. (2014) assessed the population status of Southern Residents and the population's potential responses to non specific management actions that putatively would improve specific vital rates (i.e., improve sex- and age-specific survival probability and fecundity rates). The authors applied status-quo conditions, and assumed no environmental or demographic stochasticity or future catastrophic events. Given these conditions and assumptions, and an initial population size of 88, the authors estimated the Southern Residents' expected population size to be 84 in 10 years, 78 in 20 years, 71 in 30 years, and 68 in 35 years,. Only a small fraction of the projected populations exceeded the initial population size of 88 at 10 and 20 years, but at 35 years all projections were below 88 and some were as low as 55-60.

Projections of population size under demographic stochasticity showed that the probability of falling below 30 individuals was greater than zero at about 55 years in the future. However, inclusion of both environmental and demographic stochasticity increased the probability of falling below 30 individuals, which was greater than zero at 10 years, 50% at 47 years and approximately 80% at 100 years. Even without the inclusion of demographic stochasticity, there was a zero probability of Southern Residents reaching 120 individuals in 14 years and thus meeting the U.S. target to "downlist" the Southern

Residents from their endangered status (National Marine Fisheries Service 2008). Moreover, when the time horizon was fixed, rather than fixing the carrying capacity, there was an extinction risk of 49% in 100 years with an expected abundance of 15 individuals during this timeframe.