

MARINE MAMMAL POPULATION RECOVERIES AND CRITICAL FACTORS

by

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ABSTRACT

Of all the marine taxa, marine mammals seem to have benefited the most from a paradigm shift from exploitation to conservation. Often lauded as symbols of conservation success, some marine mammals have shown remarkable population recoveries after recorded depletions. Others have remained at low levels, continued to decline, or become extinct/extirpated. This thesis provides the first quantitative assessment for marine mammals of (1) global, publicly available population-level abundance data, (2) abundance trends, (3) the relationship between decline and recovery and (4) critical factors to recovery. I compiled a database of 143 population abundance time series for 47 species (37% of marine mammal species) and identified data gaps. Using robust linear regression, I classified population trends for 88 populations over three generations. Approximately one third (35%) were significantly increasing and recovering, one tenth were non-recovering (significantly stable or decreasing), while over half had non-significant or unknown trends. Other marine mammals (sirenians, polar bears and otters) and pinnipeds (most notably the eared seals) showed the highest proportion of recovering populations, likely benefiting from fast life histories and nearshore habitats that conferred visibility and protection. For populations with historical estimates (n=47), I also found a negative relationship between decline and recovery. Larger declines were generally associated with smaller recoveries. With the significant population trends (n=43), I used a variety of modeling approaches—classification trees, generalized linear models (GLMs) and generalized additive models (GAMs)—to assess the relationship between 21 hypothesized intrinsic and extrinsic critical factors and recovery. The results pointed to two critical factors: dominant habitat type and mean habitat disturbance. Primarily coastal species in (on average) more disturbed habitats exhibited higher probability of recovering. Based on the literature, I suggested this was linked to historical exploitation and conservation patterns. Both focused on coastal populations before offshore ones, and coastal populations generally occurred in more anthropogenically disturbed habitats. Economic influences, such as falling return for harvest effort, increasing wealth of harvesting nations and decreasing demand for marine mammal products, may also have played a role. In addition, I identified other possible critical factors to marine mammal recovery status that had some support in the models, but require more investigation: maximum habitat disturbance, species type, and age at maturity. Cetaceans and pinnipeds also appeared to differ in terms of possible critical factors to their recovery. Dominant habitat and weight were likely more important to cetaceans, while trophic level, mean and maximum habitat disturbance may have had more influence on pinniped recovery. As the explanatory power of these models was only moderate, I suggest further investigation into other critical factors. The results suggest the ongoing importance of wildlife proximity and accessibility to humans in determining population recovery. Increased focus on the study and conservation of small, offshore cetaceans, marine mammal populations in low latitudes, and populations in developing nations is needed. Similarly, identification, assessment and protection of important habitat areas with high disturbance is recommended. Overall, this thesis broadens our understanding of available data, critical factors and recovery in marine mammals, as well as mammals and marine species in general.

LIST OF ABBREVIATIONS USED

ACID	Abundance Confidence ID; a system used to incorporate quantitative and qualitative error information into abundance trend estimation
Area_Des	a verbal description of a population's defining area
Area ID	a numeric identification code used to define a population area (unique within a species)
CBD	Convention on Biological Diversity
CITES	Convention on the International Trade in Endangered Species of Wild Fauna and Flora
CMS	Convention on the Conservation of Migratory Species of Wild Animals (a.k.a. Convention on Migratory Species or Bonn Convention)
COSEWIC	Committee on the Status of Endangered Wildlife in Canada
CPUE	catch per unit effort
CV	coefficient of variation
CI	confidence interval
DFO	Department of Fisheries and Oceans Canada
edf	effective degrees of freedom
EEZ	exclusive economic zone
EU	European Union
GAM	generalized additive model
GenTime	generation time
GIS	geographic information system
GLM	generalized linear model
IUCN	International Union for the Conservation of Nature
IUCN Red List	IUCN Red List of Threatened Species
IWC	International Whaling Commission
K	carrying capacity
MMPA	United States Marine Mammal Protection Act
MSYL	maximum sustainable yield level
NMFS	U.S. National Marine Fisheries Services
NOAA	U.S. National Oceanic and Atmospheric Administration
OSP	optimal sustainable population
Other marine mammals	- sirenians, marine and sea otters, and polar bears
pp.	pages
R	R Statistical Analysis Software
r_{max}	maximum intrinsic rate of population increase
SD	standard deviation
SE	standard error
spp.	species
SST	sea surface temperature
UK	United Kingdom
U.S.	United States
USFWS	United States Fish and Wildlife Service

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CHAPTER 1 INTRODUCTION

Humans have a vested interest in assessing and managing changes in animal populations of economic, social, cultural, and ecological importance. With substantial documented historical and current changes in marine ecosystems (e.g. Lotze et al. 2006; Pauly 1995), biologists and managers have taken an interest in the resilience of marine populations in the face of disturbances that affect births, deaths, immigration and emigration (Gotelli 1995). Disturbances can be humans-caused, like hunting or habitat modification, or naturally occurring, such as extreme weather events or prey die-offs.

For many marine species, management has been implemented to mitigate substantial population declines, often from exploitation. However, management philosophies and goals have transitioned over time from managing resources for extraction to increasingly emphasizing conservation. Early in the 20th century, the Lacey Act (1900), the Fur Seal Treaty (1911), the Migratory Bird Treaty Act (1918), and the Convention for the Regulation of Whaling (1931) all aimed at preventing the further depletion and possible extinction of species after substantial depletions. In the 1970s, an growing number of multilateral regulatory mechanisms and agreements aided in monitoring and managing wildlife populations and address their threats, including the Convention on the International Trade of Endangered Fauna and Flora (CITES, 1973), the Convention on Migratory Species (CMS, 1979), and various pollution-related treaties (Mitchell 2002-2010). Many countries also adopted national species and environmental protection legislation (e.g. United States Endangered Species Act, 1973 (Mitchell 2002-2010)). By the 1990s, the Convention on Biological Diversity (1992) highlighted a new emphasis on biodiversity, recovery plans, and not only conserving species, but also populations (Caddy & Agnew 2004; Mace 2005; Mace & Purvis 2008; Mitchell 2002-2010; Schindler et al. 2010).

Among the marine taxa exploited by humans—mammals, birds, reptiles, fish, invertebrates and algae—marine mammals were subject to some of the earliest intense

commercial exploitation that resulted in population depletions and subsequent protection (Lotze 2005; Lotze et al. 2006; Lotze & Milewski 2004). Attitudes towards marine mammals have gradually changed in many areas (e.g. Flowerdew 2004; Lavigne et al. 1999); they've gone from harvested natural resources to wildlife lauded as flagship symbols for the environmental movement (Bosetti & Pearce 2003; Holt 2006; Walpole & Leader-Williams 2002; Zacharias & Roff 2001). Marine mammals have been the subjects of relatively intense scientific study, management and conservation efforts (Aron 1988; Zacharias & Roff 2001). They have also shown some of the most remarkable population increases among the marine taxa (Aron 1988; Freeman 2008; Gerber 1998; Gerber & Hilborn 2001; Lotze et al. 2006; Lotze & Milewski 2004; Lotze & Worm 2009), providing a valuable opportunity to study recovery in marine species. Despite growing interest in marine biodiversity and conservation, we still lack a clear idea of how many marine mammal populations show recovery and what factors are critical to these population recoveries. This thesis aims to fill this knowledge gap.

This study expands previous population dynamics and conservation work on marine species and terrestrial mammals that has concentrated mainly on population declines and extinction risk. Critical factors to various aspects of marine population dynamics have been explored most notably in commercial fishes (Garcia et al. 2007; Hutchings 2000, 2001a, b; Hutchings et al. 2010; Hutchings & Reynolds 2004; Musik 1999; Olden et al. 2007; Reynolds et al. 2005). Similar studies do exist of individual marine mammal populations or subgroupings (de Little et al. 2007; Leaper et al. 2006; McMahon et al. 2005) and terrestrial mammals (Cardillo et al. 2008, 2005). Numerous works have also summarized threats to marine species (Kappel 2005), marine mammals (Schipper et al. 2008) or subgroupings thereof (Reeves et al. 2003; Reijnders et al. 1993), and individual species or populations (IUCN 2008). Given notable increases in numerous marine mammal populations and extensive qualitative discussion of threats, it is time to quantitatively examine marine mammal population recoveries and their correlates.

Although interest in population recoveries is expanding, there is no standard definition of population recovery. Recovery can be described as an increase relative to different

abundance reference points (typically measured as the number of individuals or biomass), including:

- (1) the current population level or trend,
- (2) a population minimum,
- (3) the carrying capacity (K) or a historical population abundance estimate, or
- (4) a percentage thereof (e.g. 50% of K, or maximum sustainable yield level (MSYL)) (Sanderson 2006).

Recovery may also be measured over different time periods, such as an entire time series of data, a set time period (e.g. 50 years, or 1950-2000), or with respect to the species' life history (e.g. three generation times is commonly used by the IUCN (IUCN 2001)). Additional criteria, such as targets for demographic components (e.g. juveniles/adults, males/females), social dynamics, or ecological functions (Sanderson 2006) may be relevant depending on the situation. What definition of recovery is chosen depends on the goals of the study and can alter the conclusions. It can also limit comparison across populations with variable data quality (in terms of time span, number and frequency of data points). Given these issues, I used a basic definition of population recovery as a statistically significant increase in abundance over a specified time period (the one exception being the analysis of magnitude of decline and recovery in sections 2.2.4, 2.3.4 and 2.4.4). This simple and broad definition allowed for comparison across a maximum number of population abundance time series, with the conclusions of this research regarding recovery being broadly interpretable.

The aim of this thesis was a quantitative assessment of the frequency and magnitude of marine mammal recoveries and the critical factors linked to them at a population level, using a robust statistical approach. The analysis focused both on marine mammals overall, while also considering possible differences among notable subgroupings.

In Chapter 2, I sought to assess marine mammal data at a population level in terms of quantity, quality, timespan, collection and estimation methods, taxonomic breadth and depth, and geography. As no publicly available database of global marine mammal population abundance data or trends exists, I developed one from publicly available sources. I provided an assessment of the data available for analysis, as well as its criticisms and knowledge gaps. Using robust linear regression, I estimated general abundance trends for each population, classified population recovery status accordingly, and cross-referenced my findings with the IUCN Red List of Threatened Species. Where historical estimates were available, I also examined the relationship between population

decline and recovery. These analyses provided context on the current state of available marine mammal population abundance data, trends and recovery.

In Chapter 3, I used populations with significant estimated abundance trends from Chapter 2 to conduct the first quantitative examination of critical factors (correlates or drivers) to marine mammal population recovery. I compiled data on intrinsic and extrinsic critical factors hypothesized to be important to marine mammal population recoveries based on the existing literature on marine mammals, terrestrial mammals, and other marine taxa. Employing a variety of modeling approaches (classification trees, generalized linear models (GLMs), generalized additive models (GAMs)) I examined the relationship between various critical factors and recovery across the overall sample of marine mammal populations and relevant subgroupings.

Both Chapters 2 and 3 of this thesis were written with the intention of submitting them for publication in scientific journals with co-authors H. K. Lotze and J. Mills Flemming, hence the use of first person plural (“we”). The appendices have been kept separate (Appendices I and II respectively), but the chapter references have been combined for the purpose of this thesis. I (A. M. Magera) participated in a primary role in the manuscripts and led the data gathering, database construction, methodological decisions, analyses, writing and editing for all chapters. H. K. Lotze first conceptualized the project topic, advised on methodologies, supervised and edited all chapters. J. Mills Flemming advised on statistical methodologies, supervised and edited all chapters. K. Kaschner and L. B. Christensen provided an initial marine mammal abundance database that I substantially expanded in Chapter 2, and used to inform Chapter 3. W. Blanchard and S. C. Anderson also provided statistical advice, and C. Mora provided GIS advice.

CHAPTER 2 RECOVERY TRENDS IN MARINE MAMMAL POPULATIONS

2.1 INTRODUCTION

In the marine realm, mammals appear to have benefited the most of any taxon from a shift from resource exploitation to wildlife conservation. A loose grouping of approximately 127 species, marine mammals include cetaceans (whales, dolphins and porpoises)¹, pinnipeds (true seals, fur seals and sea lions), as well as marine and sea otters, sirenians (manatees and dugongs) and polar bears (Jefferson et al. 2008). Humans throughout history have directly exploited and often depleted marine mammals (Aron 1988; Baker & Clapham 2004; Christensen 2006; Colten 2002; Lotze et al. 2006; Pauly et al. 2005; Reeves 2002; Reeves & Smith 2006; Smith 2005). In the 20th century, substantial population declines afforded marine mammals relatively early and widespread reduction or cessation of commercial exploitation and implementation of conservation measures (Adams 2004; Caddy & Agnew 2004; Lotze & Milewski 2004). Several marine mammals have been held up as key conservation success stories, but despite conservation efforts, not all marine mammal populations have recovered from earlier exploitation-driven declines.

Threats to marine mammals are numerous and have changed over time. Historically, marine mammals have been prized sources of meat, oil, fur, baleen and ivory (Baker & Clapham 2004; Christensen 2006; Lotze et al. 2006; Reeves 2002). They have also been captured for display in aquariums, culled when declared nuisances, used for bait, and indirectly exploited as bycatch (Bigg 1988; Kasuya 2007; Read 2008; Reeves et al. 2003; Reijnders et al. 1993; Reijnders 1994; Ward et al. 2009). Numerous marine mammal species were reduced to very low abundances by or during the 1900s, even to the point where they were thought extinct, as in the case of Northern elephant seals (*Mirounga angustirostris*) and Guadalupe fur seals (*Arctocephalus townsendi*) (Gerber 1998; Gerber

¹ River dolphins are also typically classified with marine mammals, and thus we included them here (Jefferson, Webber et al. 2008).

& Hilborn 2001). In some cases populations were regionally extirpated, including the Atlantic gray whale (*Eschrichtius robustus*), the sea otter (*Enhydra lutris*) throughout most of its range, and the walrus (*Odobenus rosmarus*) in parts of the Northwest Atlantic (Lotze & Milewski 2004; Sea Otter Recovery Team 2007). Some species became globally extinct, such as the Japanese sea lion (*Zalophus japonicus*), Caribbean monk seal (*Monachus tropicalis*), sea mink (*Neovison macrodon*) and Steller sea cow (*Hydrodamalis gigas*) (Gerber 1998; Jefferson et al. 2008). Substantial population recoveries have occurred in some cases, as with North Pacific gray whales, Atlantic humpback whales (*Megaptera novaeangliae*), multiple sea otter populations, northern elephant seals, grey seals (*Halichoerus grypus*) in the UK and Northwest Atlantic, and numerous fur seal species (Clapham et al. 1999; Gerber 1998; Gerber & Hilborn 2001; Lotze et al. 2006; Nichol et al. 2005; Thomas et al. 2007; Thomas & Harwood 2008). Direct and indirect exploitation continue for many populations, and coastal development, dams, ship traffic, offshore oil and gas exploration, pollution (chemical, physical and auditory), climate change, disease, and competition for prey (e.g. fish) pose additional threats (Dulvy et al. 2003; Kappel 2005; Lotze et al. 2006; Reeves et al. 2003; Reijnders et al. 1993).

Although it is a commonly used term, “recovery” can have many definitions in different management and conservation contexts. Recovery is defined as “a return to a normal state of health... or strength” (Oxford Dictionaries 2010). In wildlife and resource population analyses, however, we often do not know the “normal state” of a population. It is frequently viewed as a pre-commercial exploitation abundance estimate or carrying capacity (K), and increase of a population to such a reference point indicates recovery (Baker & Clapham 2004; Gerrodette & Demaster 1990). However, neither pre-exploitation nor K estimates exist for many species that lack records of past catch, traded product (e.g. oil, fur), scientific survey, genetic, life history, or population structure data. Furthermore, there is often debate as to whether K estimates should refer to pre-exploitation or current ecosystem conditions (Baker & Clapham 2004; Freeman 2008).

Management bodies often judge recovery with respect to a proportion of K or pre-exploitation size. The U.S. Marine Mammal Protection Act specifies that marine mammals should be managed for an “optimal sustainable population” (OSP) level, defined by the U.S. National Marine Fisheries Services (NMFS) as “a population level between carrying capacity and the population size at maximum net productivity” (Gerrodette & Demaster 1990). OSP is thought to be between 50–85% of K for marine mammals (Gerrodette & Demaster 1990), but generally 60% is used (Gerber et al. 2000). In the absence of either K or pre-exploitation abundance estimates, management bodies may use maximum observed population levels, for example from survey data. This is the case in Canada, where harp seal (*Pagophilus groenlandicus*) populations are managed with a goal of attaining 70% of the maximum observed population level, and all removals are stopped if the population falls to 30% of the maximum (Fisheries and Oceans Canada 2003). However, in cases where qualitative reports of substantial declines predate quantitative records, maximum observed population levels would not represent a pre-exploitation level, and could cause underestimation of declines and overestimation of recoveries.

Other criteria have also been suggested for assessing recovery. Consideration of an ideal population structure (e.g. ratio of juveniles to adults, males to females) may be relevant to recovery, especially when different components of the population may be more or less adversely affected by stresses (Chirakkal & Gerber 2010; Gerber & Heppell 2004; McClenachan & Cooper 2008). Recovery could also be evaluated with respect to a population’s ability to perform its ecological role, or “ecological effectiveness” (Estes et al. 2010). A more basic and practical approach in many data-limited cases has been to view any abundance increase as evidence of a “recovering population” and at least partial recovery (Hutchings 2000). For the analysis of population trends in this study, we used this simple definition, with “recovering” populations being those that show a statistically significant linear increase in abundance.

Descriptions of marine mammal data in the literature often criticize population abundance data for being scant and subject to high uncertainty. This is due to the fact that

catch records are absent for many populations and marine mammals are notoriously difficult to survey accurately for abundance. Abundance estimates are often derived from catch data for valuable commercial species. Thus longer time series with historical population estimates are lacking for many populations (Lotze & Worm 2009). Because marine mammals often have elusive behaviors (e.g. extensive migrations or deep diving) and their aquatic habitats are often remote and large, there are many logistical difficulties and costs associated with surveys and tagging (Amstrup et al. 1999; Gerber et al. 2000; Taylor et al. 2007). With the exception of land-breeding pinnipeds, abundance trend detection is difficult for many marine mammal populations over relatively short time periods (Taylor et al. 2007). Abundance time series data do exist for many species, but typically encompass irregular survey intervals over the past 50 years or less. Current designations of marine mammal populations may not spatially match historical population records, leading to speculation that some populations have changed distributions over time (Kaschner et al. 2006; Whitehead 2002). Distribution changes complicate comparisons of present and historical data in assessments of long-term declines and recoveries.

Collection and modeling methods for marine mammal data have changed over time. These changes, as well as the more recent policy focus on populations as opposed to species, have generally improved the quantity and quality of data (Amstrup et al. 1999; Taylor et al. 2007). Up until the mid-1900s when most commercial marine mammal hunting ended, information on population abundances was typically estimated from log book catch data or trade records (e.g. oil, furs) (Aron 1988; Freeman 2008). Deterministic and stochastic models that borrowed heavily from fisheries science and population ecology (e.g. linear regression, logistic production models, and age/stage structured matrix models (Baker & Clapham 2004; Wade 1999)) started to gain importance in the estimation of abundances in the latter half of the 20th century. In the 1970s, interest in species conservation and species at risk management increased internationally (e.g. Convention on the International Trade of Endangered Species of Wild Fauna and Flora (CITES) and Convention on Migratory Species (CMS)) and nationally (e.g. endangered species legislation, marine mammal protection acts), with regulators and scientists

pursuing more aerial, land, boat and bycatch monitoring (Berta et al. 2006; Gerber et al. 2000). The 1990s onward marked a strengthening of a conservation and sustainability ethos in resource management (Reid & Mace 2003), valuation of biodiversity (Reid & Mace 2003), and species at risk evaluation. Data collection techniques improved, with an increased reliance on standardized line transects, photo-identification and mark-recapture studies, and acoustic monitoring (Berta et al. 2006). Substantial data errors were reported in important data sets, such as Soviet and Japanese whaling records, resulting in adjustments and improvements to models and data quality (Baker & Clapham 2004). Recently, genetic techniques were developed to identify catch misreporting and historical population sizes (Berta et al. 2006). With an upsurge in the amount, regularity, and types of survey and other data, Bayesian and state-space analyses gained popularity (Baker & Clapham 2004; Buckland et al. 2004; Wade 1999). Data are still limited in terms of quantity and historical coverage for smaller, less commercially valuable cetaceans and pinnipeds. Likewise, data from certain regions is still scarce, with more data available from species in North America, Europe, Australia and New Zealand.

Emphasis extended from examining species trends (e.g. International Union for Conservation of Nature (IUCN) Red List of Threatened Species (IUCN 2008)) to increasingly valuing populations as important components of diversity and conservation planning (e.g. Convention on Biological Diversity (CBD) (United Nations 1992) and others (Mace 2005; Mace & Purvis 2008; Schindler et al. 2010)). Populations within the same species may show different abundance trends, so population-level abundance monitoring became increasingly valued. Population-level trend analyses are available (e.g. marine mammal stock assessments in U.S. (Angliss & Allen 2009; Carretta et al. 2009; Waring et al. 2009)), but a quantitative global synthesis of marine mammal population recoveries has not been attempted. Our goal in this study was to summarize publicly available population-level data for marine mammals around the world, estimate abundance trends and assess recovery status across populations, and contribute to understanding recovery in exploited marine populations overall.

2.2 METHODS

2.2.1 Data Compilation

We collected marine mammal population data from around the world, including publicly available published journal articles, online government documents, stock assessment reports, and recovery plans. We required abundance time series with at least three abundance estimates over a span of at least ten years, the minimum time period used by IUCN Red List for assessing population declines (IUCN Standards and Petitions Subcommittee 2010). We built upon a database of marine mammal abundance estimates collected from similar sources by Kaschner (2004) and Christensen (2006). Major sources included: Fisheries and Oceans Canada (DFO), Committee on the Status of Endangered Wildlife in Canada (COSEWIC), U.S. National Oceanic and Atmospheric Administration (NOAA) and NMFS technical and administrative reports, U.S. Marine Mammal Stock Assessment Reports, St. Andrew's Sea Mammal Research Unit reports, Australian and New Zealand government documents, and numerous published primary sources (see Appendix I.A). We collected error information for abundance estimates including coefficient of variation (CV), confidence intervals (CI), standard error (SE) or deviation (SD). Where available, we gathered pre-exploitation abundance estimates and K estimates. In cases where multiple historical estimates were found (e.g. catch vs. genetic data) we recorded them all. We collected data up to 2008 or the next most recent data point. A population is generally described as a group of interbreeding organisms of the same species in a defined area (Gotelli 1995). We chose population abundance data according to consistently defined areas described in the source literature instead of using only populations or stocks defined by monitoring or regulatory agencies, but our definitions often overlapped anyway.

We also collected information on generation times, method of abundance collection and estimation, and data reliability from the IUCN Red List (2008), Taylor et al. (2007), and other source documents. Data came from dedicated and opportunistic aerial, land-based and ship-based surveys, bycatch, catch or catch-per-unit-effort data, extrapolated total population or pup-count data, photo-identification and mark-recapture models, genetic

diversity analysis, combined totals from literature, various model types (including age- or stage-based, simple regression, Bayesian or state-space models), and in some cases unknown or unstated methods. Where abundance estimates had been updated with new model or correction factors, we used the updated abundance estimates and noted their sources. Where year ranges were provided for abundance estimates, we used the mid-point of the range.

Error is present in virtually all marine mammal abundance data, but it may originate from different sources. Abundance estimation from catch, bycatch or product data could be subject to intentional or unintentional misreporting. It may also provide faulty estimates of K or the maximum intrinsic rate of population increase (r_{\max}), both of which may change over time (Baker & Clapham 2004). Historical abundance estimates from DNA have been questioned because of uncertainty over changes in mutation rates, appropriate designation of particular populations, and migration between them, all of which can affect population estimates (Baker & Clapham 2004; Berta et al., 2006; Freeman 2008; Neigel 2002). Surveys also typically do not include all animals and thus must correct for unobserved animals that may be at sea, hidden (under water, ice, rocks, or other habitat features), camouflaged, obscured by poor weather conditions, or otherwise not visible (Amstrup et al. 1999; Berta et al. 2006; Forney & Wade 2006). Methods for correcting these estimates have improved over time. Some species are attracted to survey boats or airplanes while others are repelled, and one must adjust for positive or negative biases in counting (Buckland & York 2002). In line transect studies from the air, boats or land, adequate spatial coverage of species' ranges, transect design and accurate correction factors are important considerations (Forney & Wade 2006). Mark recapture techniques must take into account behavior of different population segments, how consistently marks or tags can be re-identified or recovered, and whether the populations of study are closed or open (Forney & Wade 2006). Similarly, photo-identification studies can give highly accurate population estimates, but are typically only useful for small populations with well-known distributions and distinct individual markings, such as resident killer whales in the North Pacific (Buckland & York 2002; Forney & Wade 2006). Acoustic sensing allows researchers to detect marine mammals underwater and estimate abundance, but

estimates may be difficult when animals are close together (Whitehead et al. 2000). Thus, although they are not the only potential error source, data collection methods can influence abundance estimate reliability.

Error was not always reported in our data sources, so we accounted for error through additional means. We used a modified version of Kaschner's Abundance Confidence Identification (ACID) system (Kaschner 2004) to incorporate error information into subsequent abundance trend estimation. The system combines quantitative error information (where available) with qualitative information about the data source and its reliability (see Appendix I.B for further explanation). We ran comparable robust linear regressions with different weighting mechanisms. The results indicated that the ACID rating gave similar trend information (i.e. trend direction and significance) 77% of the time when compared to weightings using the SE. Thus, we deemed ACID weighting acceptable for incorporating available error information and comparing trends amongst estimates with and without quantitative error information.

2.2.2 Trend Analysis

We were able to compile abundance data for 143 marine mammal populations. Robust linear regressions were fitted to population abundance data over the three most recent generations. Although other time periods were examined², data were not available over uniform time frames or intervals and were generally too sparse to compare amongst most marine mammal populations. Thus, we decided to use the three-generation time period in order to include recovery trends over the largest number of populations. It also corresponded with the criteria used by the IUCN for assessing population decline (IUCN 2001). Fifty-three populations (37%) did not have data for the entire three-generation time period, and in these cases we used the time period for which the data were available (minimum = ten years, cases documented in Appendix I.C). Since some populations were nested by area (Figure 2.1), we considered results with and without nesting.

² The other time periods examined were: the entire population time series, from the minimum population abundance to the most recent data point, 1900–1950, 1950–1970, 1970–1990, and 1990 to most recent data point. The time periods over set intervals were chosen according to important periods in marine mammal management as outlined in the Introduction (Section 2.1).

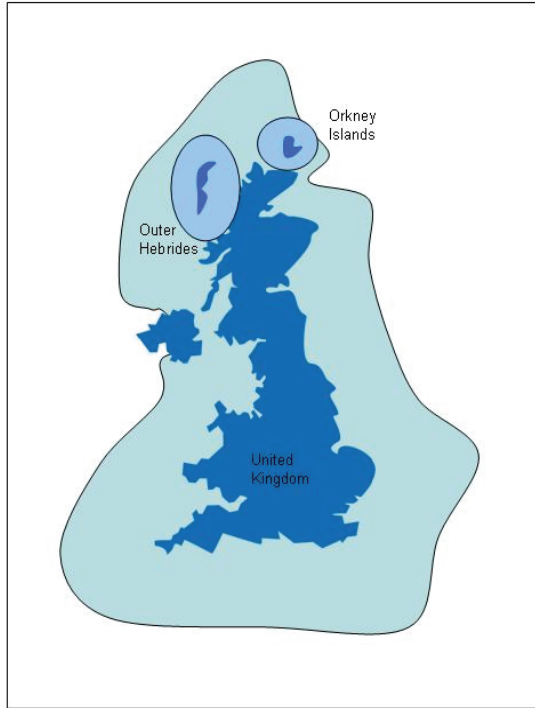


Figure 2.1 Example of population nesting by area. The coastal areas of the Outer Hebrides and Orkney Islands are nested within the overall coastal area of the United Kingdom.

Robust regression was an appropriate analysis procedure due to the high amounts of uncertainty in the data and the need to detect the strongest overall abundance trend signal (Wilkinson & Task Force on Statistical Inference 1999). Robust regression is a powerful tool for down-weighting high influence outliers to capture the most general overall data trend and increase the likelihood of finding a significant result (Wilkinson & Task Force on Statistical Inference 1999; Wright & London 2009). Our data contained variation in data quality, time series length, data intervals, outliers, available error information, and abundance magnitude. Our goal was to determine if there was statistical evidence that a population was increasing, decreasing or stable, as opposed to estimating complex and potentially non-linear population trajectories. To include the abundance data error information, we weighted the data in the robust regression by ACID. We also considered other types of regression (e.g. simple linear regression (both unweighted and weighted by ACID) and robust linear regression (unweighted)), but these were less ideal to address the error in our data. The `lmRob` command in the robust library in R uses an S-estimator

(Wang et al. 2009) to estimate the best robust fit to the data (Franke et al. 1984). An S-estimator has a high breakdown point, or tolerance for highly influential data points before the estimator (in this case, a 50% breakdown estimator) is substantially affected (Franke et al. 1984). We scaled the data by subtracting the mean and dividing by SE in order to allow for easier comparison of regression results among populations. The R code is available in Appendix I.D.

The trend estimates (i.e. slopes) were used to classify each population as Increasing, Decreasing, Stable, or Unknown, and either statistically significant or non-significant at a 95% confidence level. First we determined whether trend estimation was possible. Any populations with insufficient data for trend estimation with robust regression were deemed Unknown. We then classified populations with sufficient data according to the significance and direction of their abundance trend. Significantly Increasing and Decreasing populations had positive or negative slope estimates (respectively) and corresponding critical p-values < 0.05 . Populations with positive or negative slope estimates but with p-values ≥ 0.05 were non-significant. We used additional considerations to designate Stable populations (i.e. slopes very close to zero) from within these non-significant populations. Populations with almost horizontal slopes between -0.1 and +0.1 were deemed Stable. Stable populations were considered significant if their SE was within the SE range of significantly Increasing and Decreasing populations. Finally, we classified population Recovery Status, with significantly Increasing populations designated as “Recovering”, and significantly Stable and Decreasing populations as “Non-recovering”. Populations with Unknown and non-significant trends were not classified as either Recovering or Non-recovering because of the high uncertainty in their trend estimates.

We examined the population trend and recovery classification results for marine mammals overall, as well as for notable taxonomic divisions, including cetaceans, pinnipeds, other marine mammals, and relevant sub-groupings. For cetaceans, we also examined results by main habitat type – coastal or offshore. In many cases, coastal cetaceans were heavily exploited earlier than offshore populations (Reeves & Smith

2006). Anthropogenic habitat disturbance is also higher on average near the coast than in more offshore areas (Halpern et al. 2008).

2.2.3 Comparison with IUCN Data

We compared our population trends (Increasing, Decreasing, Stable, Unknown) to those available through the IUCN Red List. Since our data were mostly collected at a population level, and the IUCN mostly works with data at a species level, we summarized our data at a species level for comparison. Appendix I.E lists the marine mammal trends for the 127 marine mammal species according to the IUCN Red List. Within each species, we selected from our database as many of the largest, non-nested populations as possible. Of these populations, we chose the ones with the largest abundances, and where possible, the majority of the overall species abundance. When we had multiple non-nested and approximately equally sized populations, we took the average trend for the populations as the species trend. If no average was possible (for example, if there were three populations, all with different trends), we listed the population trend as Unknown. We compared the abundance trends from the populations that met these conditions to the corresponding species abundance trends from the IUCN Red List.

2.2.4 Historical Declines and Recent Increases

To assess recovery in various populations with respect to the magnitude of historical decline, we identified all populations with historical population estimates (Appendix I.F). The historical estimates were compared to the minimum and the most recent abundance to estimate the magnitude of decline and recovery with respect to the historical population size. Thus we only assessed populations with evidence of both abundance decline and recovery, as depicted in Figure 2.2. The New Zealand southern right whale population (Figure 2.2a) had an Unknown trend in the above recovery analysis because it lacked data for a robust linear regression over three generations (i.e. 86.4 years). Using all available data over a longer time period, however, allowed us to include this population in the decline-recovery analysis, although its recovery was minimal. The southern Australian Afro-Australian fur seal (*A. pusillus*) population (Figure 2.2b) shows a situation where multiple historical population estimates extended further into the past

than three generations (i.e. 28.2 years). In this case, we used the mean of the declines and recoveries relative to the historical population estimates. Although we used pup count data for some trend determination over three generations, we used the regular data for examining the decline-recovery relationship.

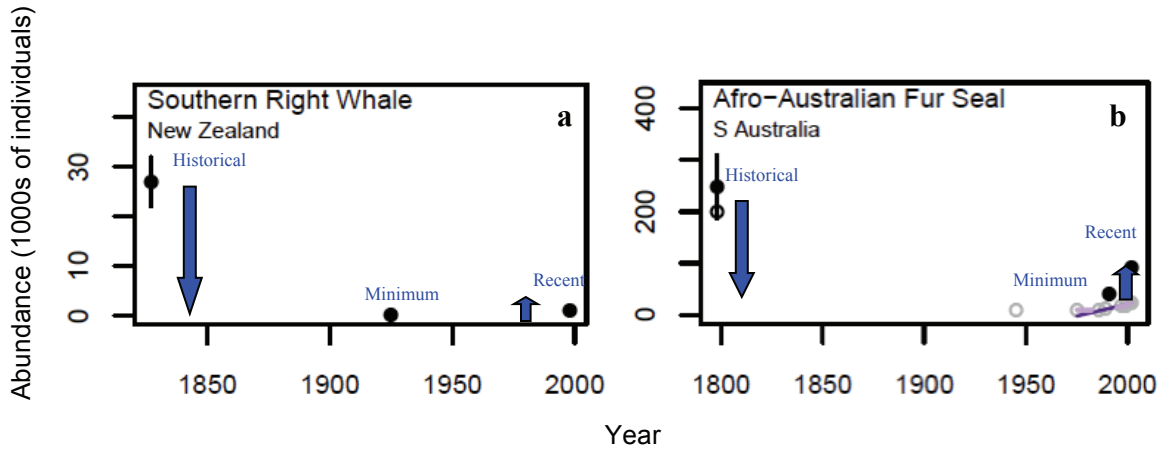


Figure 2.2 Examples of populations with historical, minimum and recent abundance estimates, from which we can estimate the magnitude of decline and recovery (blue arrows). Solid points = abundance data with quantitative error information (95% confidence interval bars). Empty points = abundance data with no stated quantitative error information. Black points = regular data that was collected from the entire population. Grey points = pup count data. Purple line = robust regression line.

To assess the relationship between decline and recovery, we used visual inspection and generalized linear models (GLMs). We tried GLMs with two different families: binomial (logit link) and quasi (identity link). The response variable was a percentage, which is typically represented as a number between 0-100% and a binomial distribution (as a corresponding proportion between 0 and 1). However, some estimates of recovery magnitude compared to historical estimates exceeded 100% (1). Thus in this case the response variable appeared to be better represented by a quasi-normal distribution. Model fitting was achieved through an iterative least squares approach (McCullagh & Nelder 1989).

2.3 RESULTS

2.3.1 State of Available Marine Mammal Population Data

Overall, we were able to compile 157 population abundance time series for 47 species of marine mammals (i.e. 37% of the 127 currently recognized marine mammal species) with at least three abundance estimates over three generations or at least ten years. Some of these populations represented duplicate pup-count and regular (i.e. entire population) count data. In these cases, we favored regular data over pup count data unless the regular data were much sparser than the pup count data. With these duplicate populations removed, we had 143 population abundance time series in total. A breakdown of species over different types of marine mammals in this study compared to all marine mammal species is depicted in Figure 2.3. Groups with low representation in our data (<50% of known species represented) included the sirenians and cetaceans, especially toothed whales, dolphins and porpoises. No species of beaked whales (n=21 species globally) or river dolphins (n=4 species globally) were included. Groups with high representation (>50% of known species represented) were the baleen whales, pinnipeds and other carnivores (sea otters, polar bears). We found it difficult to obtain time series that met our criteria for many smaller cetacean species (notably porpoises, beaked whales and river dolphins), Antarctic true seals, and sirenians. We were able to obtain three generations of abundance data for 90 of the 143 overall populations.

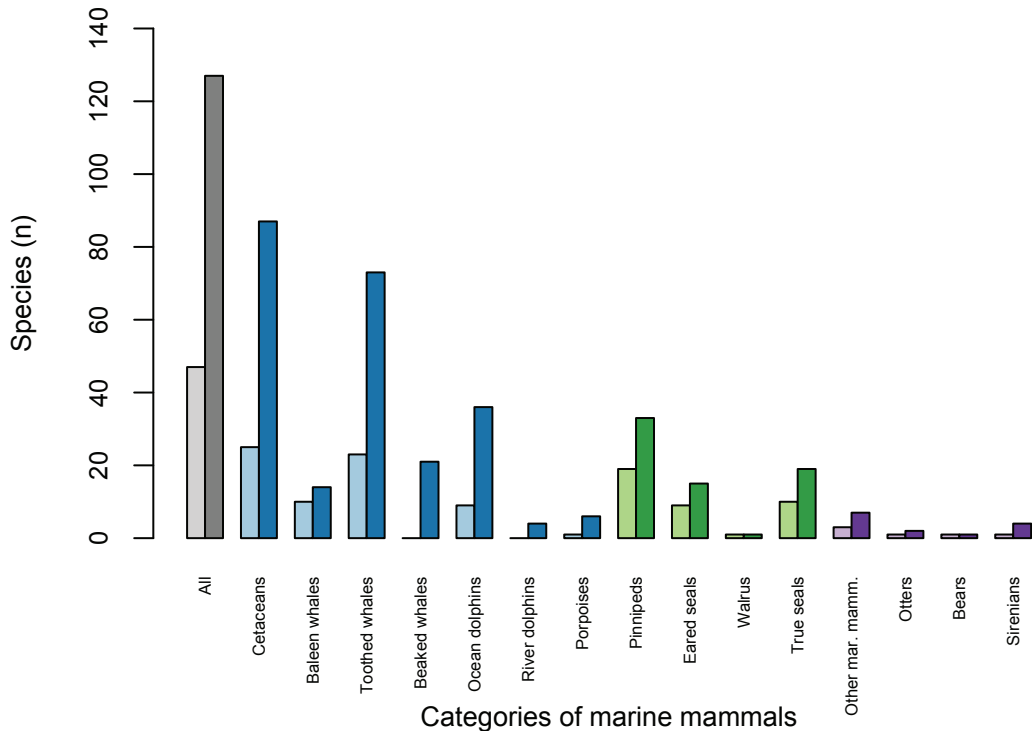


Figure 2.3 Summary of marine mammal species represented in population level data in this study (light bars) compared to marine mammal species overall (dark bars) by major taxonomic groupings. Colors represent main taxonomic divisions: all marine mammals (grey), cetaceans (blue), pinnipeds (green), and other marine mammals (marine and sea otters, polar bears and sirenians) (purple).

2.3.2 Marine Mammal Population Trends

We classified population trends determined by weighted robust linear regression over three generations for 143 non-duplicated populations from 47 species. Examples of population trends are depicted in Figure 2.4 and classification results are summarized in Figure 2.5. Abundance time series plots for each population with trend lines of robust linear weighted regressions and a Loess curve (additive model) are depicted in Appendix I.G, and regression results by population are available in Appendix I.H.

Since some individual population trends were nested within each other and not independent, we analyzed trends for populations chosen by the smallest ($n = 111$) and the largest ($n = 88$) non-overlapping areas. The overall results were similar, so we only

reported the results for the largest non-overlapping areas. A number of populations had significant trends: 35% were Increasing and thus Recovering, while 3% were Stable and 7% were Decreasing. Several populations had non-significant Increasing (22%), Stable (5%) or Decreasing (7%) trends, and 22% of population trends were Unknown.

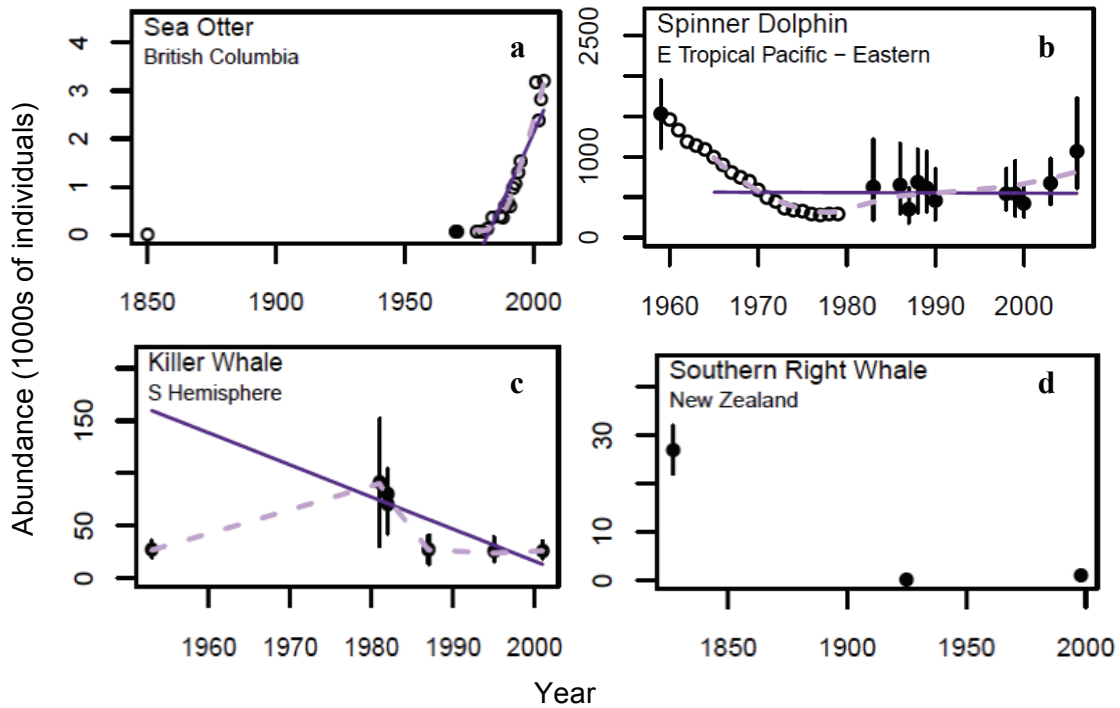


Figure 2.4 Examples of Increasing (a), Stable (b), Decreasing (c), and Unknown (d) population abundance trends over three generations or at least ten years, with robust weighted linear regression line (solid dark purple) and a Loess curve (additive model; dashed light purple). Solid points = abundance estimates with reported error (95% confidence intervals). Open points = abundance estimates without reported error.

If we look at specific groupings of marine mammals (Figure 2.5a), the results indicate that proportionally more sirenian, polar bear and sea otter populations (i.e. “Other”, 71%) and pinnipeds (50%) were significantly Increasing than marine mammals overall (35%) or cetaceans (16%). From the pinnipeds, the eared seals (67%) showed a higher percentage of significantly Increasing populations than the true seals (44%). Among the cetaceans, all taxonomic groups showed relatively few significantly Increasing

populations (19% baleen whales, 14% toothed whales, 17% dolphins and porpoises). Primarily coastal cetaceans, however, had proportionally more significantly Increasing populations (32%) than primarily offshore cetaceans (6%).

If we consider just the populations with statistically significant abundance trends, the majority of all groups of marine mammals, except for toothed whales, dolphins and porpoises, and offshore cetaceans, were Recovering (Figure 2.5b). Marine mammals overall, the pinnipeds, other marine mammals, and coastal cetaceans showed the highest numbers of Recovering populations as compared to Non-recovering populations.

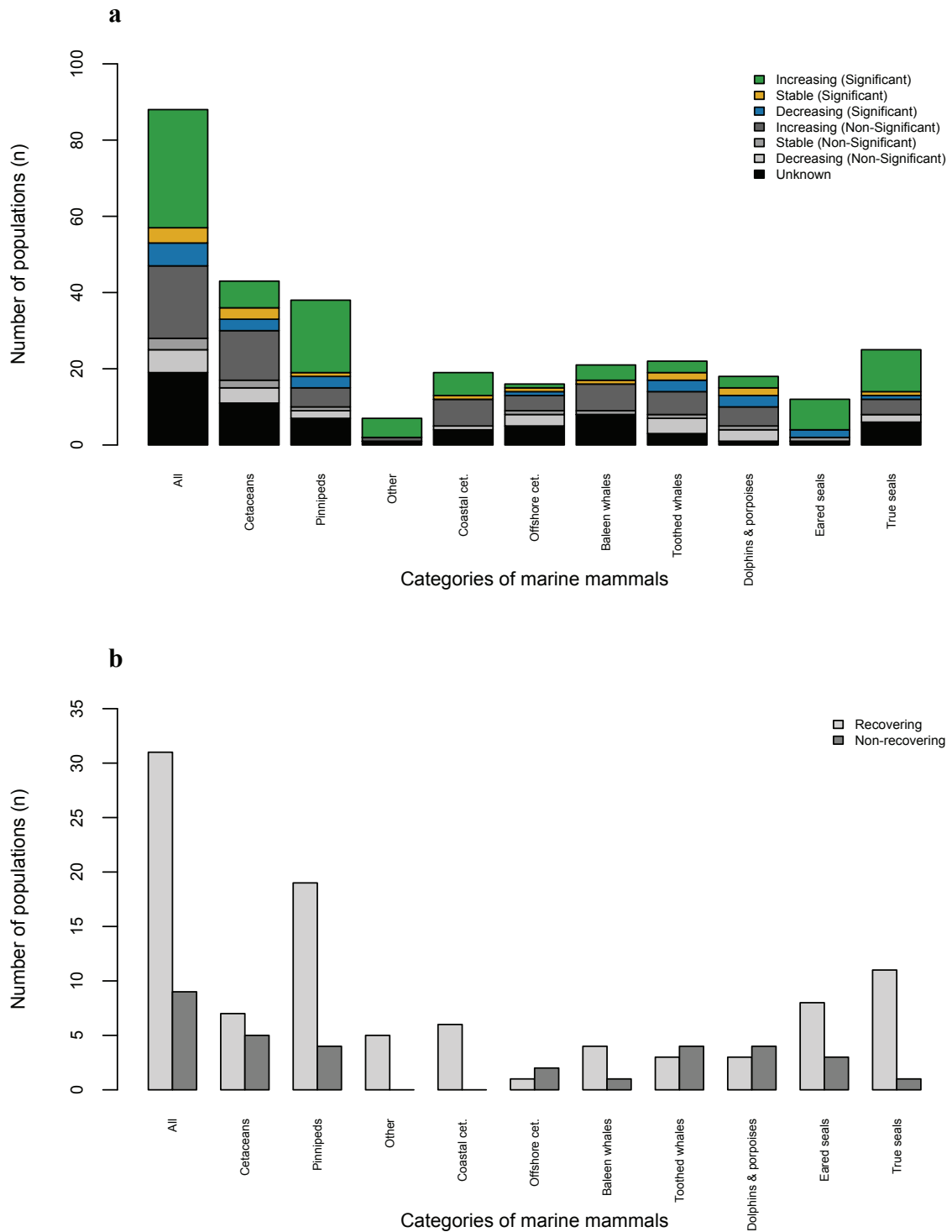


Figure 2.5 Trend classification (a) and recovery status (b) from robust weighted linear regressions for 88 (non-nested, including the largest possible areas) marine mammal populations, sorted by noteworthy categories. In (b) “Recovering” includes significantly Increasing, and “Non-recovering” includes significantly Decreasing or Stable trends. “Other” includes sirenians, polar bears and sea otters.

2.3.3 Comparison with IUCN Data

We were able to compare 26 of the 47 species for which we had population level data to the IUCN classifications (Figure 2.6, Appendix I.E). Most trend classifications were similar, with approximately 35–42% of species showing Increasing trends, less than 10% Stable, 12–19% Decreasing and 39–46% Unknown trends (Figure 2.6a). However compared to all 127 mammals in the IUCN database, our data over-represented Recovering and under-represented Non-recovering populations (Figure 2.6b), partly due to the large percentage (58%) of species classified as Unknown by the IUCN (Figure 2.6a).

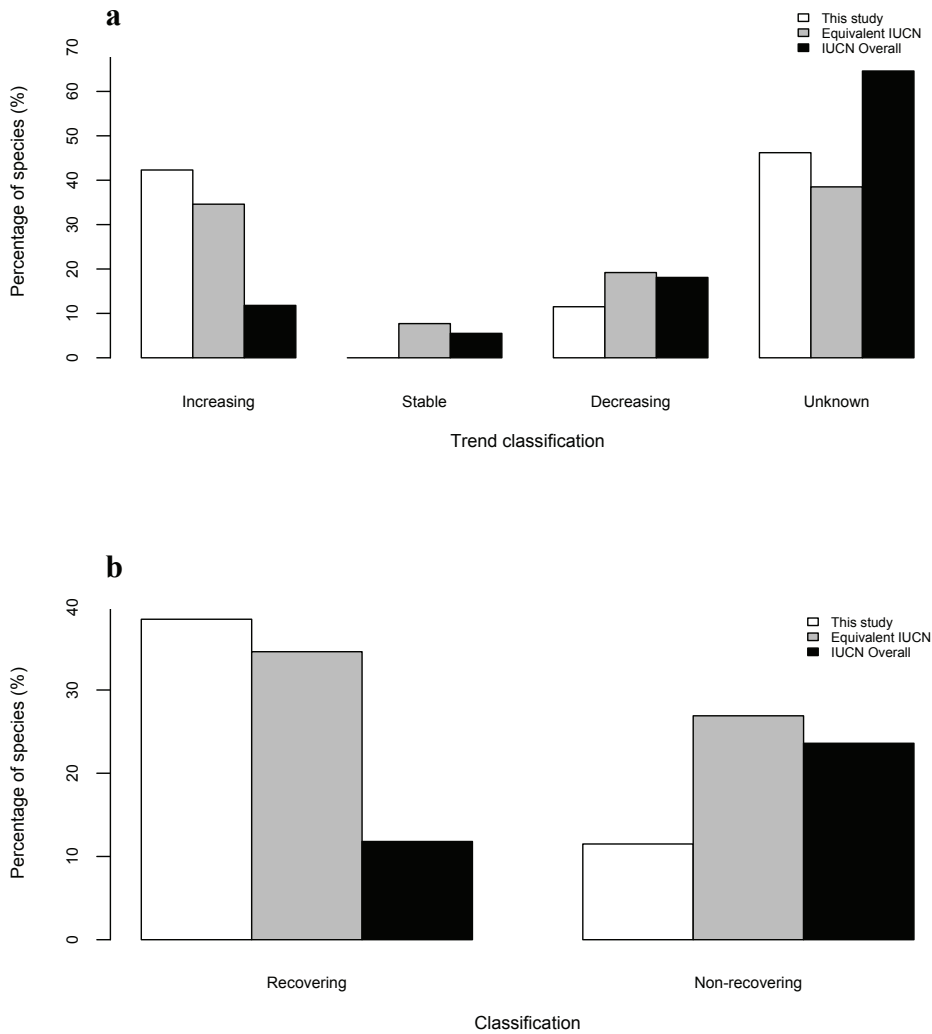


Figure 2.6 Percentage of species (n=26) in abundance trend categories (a) and recovery classifications (b) from this study, the equivalent IUCN species, and all marine mammal species (n=127 IUCN Overall).

2.3.4 Historical Declines and Recent Increases

Among all non-duplicated populations ($n = 143$) in our database, we had 47 non-nested populations that included a historical, minimum and recent population estimate (listed in Appendix I.F). Relative declines and recoveries ranged from virtually zero to close to 100%, with some population recoveries even exceeding the best available historical population estimates that we could find. In general, the relationship between decline and recovery appeared negative and linear (Figure 2.7a). However, there was a higher variation in recoveries with high declines: five populations with very high declines (>90% of historical level) also showed very high recoveries (>90% of historical level). The negative relationship was confirmed with a GLM (quasi family, identity link). The results indicated a proportional decline was highly significantly related to recovery (p -value = 0.000003, slope = -0.7984). With an approximate R^2 value of 0.387, the model explained a moderate amount of the data variation. The residual plots for the model showed higher variance at lower values and some deviation from normality at the tails (Appendix I.I). The outlier populations with very large declines and recoveries included: Afro-Australian fur seals (South Africa and Namibia), harbour seals (Washington coast, Oregon), and humpback whales (North Atlantic, North Pacific).

On average, all marine mammal populations declined by 71% and recovered to 61% of their historical abundance (Figure 2.7b). Recovery responses were generally more variable within each group compared to declines, and pinnipeds (phocids & otariids) showed the most variation. Coastal cetaceans and other marine mammals (in this case, $n=1$ sea otter population) showed the greatest mean declines (93% and 96% respectively). The two groupings that had the lowest mean declines, dolphins and porpoises (41%) and toothed whales (49%), showed the highest mean recoveries (89% and 78% respectively). Coastal cetaceans showed the lowest recoveries (43%).

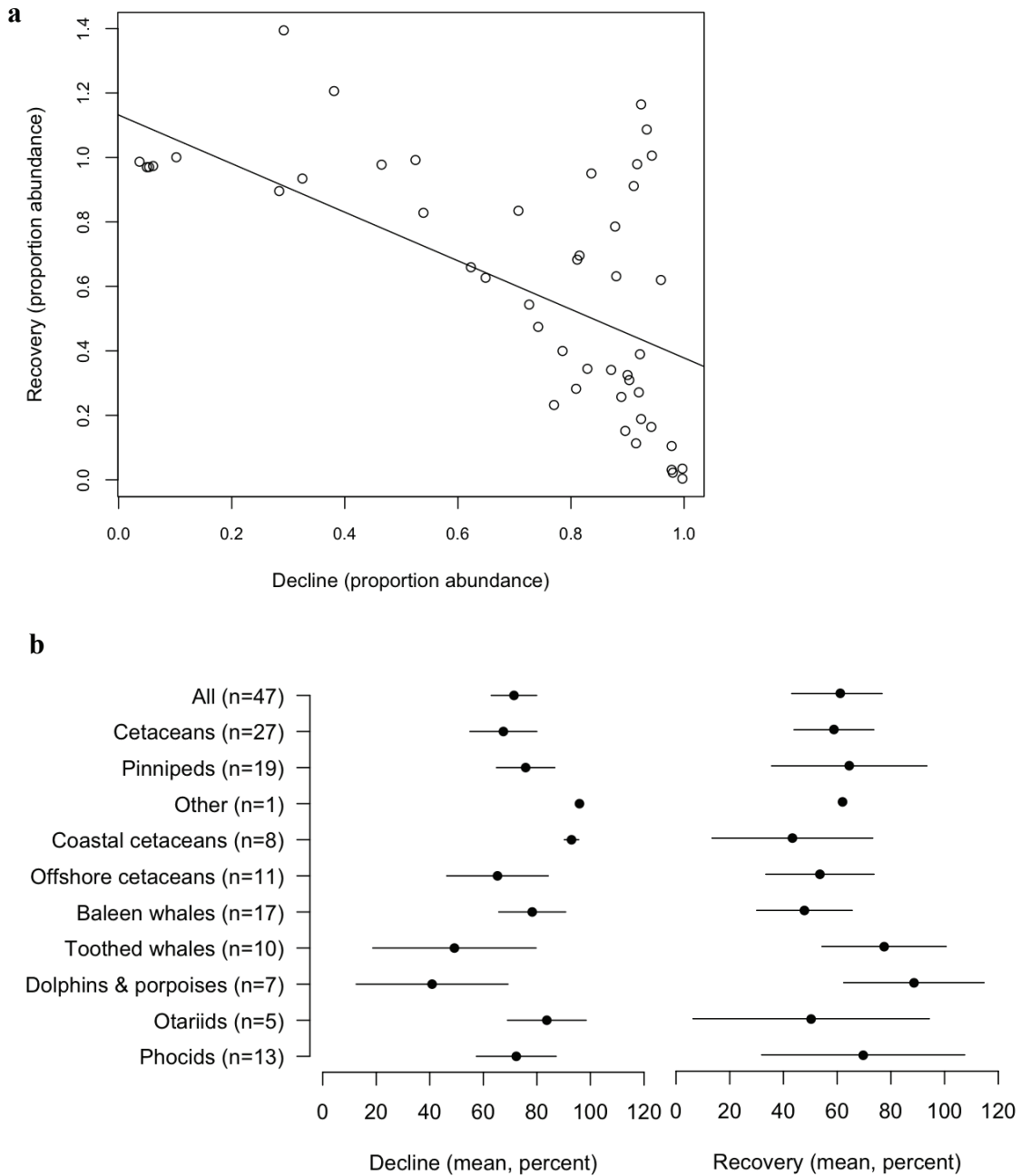


Figure 2.7 Decline and recovery relative to historical population level for 47 non-nested marine mammal populations with historical, minimum and recent abundance estimates (with regression line) (a) and averaged over relevant categories (b).

2.4 DISCUSSION

Aiming to better understand recovery in marine mammal populations, we assessed the available marine mammal population data, compiled abundance time series for 143 marine mammal populations, and classified their population trends and recovery status. We cross-referenced our findings with IUCN Red List species-level trends. For 47 populations with historical estimates, we also investigated the relationship between magnitude of decline and recovery relative to historical population size. Our investigation quantified recovery for marine mammals at a population level.

2.4.1 State of Available Marine Mammal Population Data

Population level abundance data are limited in many ways for marine mammals, but we compiled a substantial number of time series that spanned three generations or at least ten years (n=143). These abundance time series provided representation for 37% of marine mammal species worldwide. Other available species and population data that we did not locate in this study could easily be included in our database for further investigations. Populations with better time series information shared some common characteristics. First, they typically had either present or past commercial or cultural value such as many large whale populations and pinnipeds, or were iconic or charismatic species such as killer whales (*Orcinus orca*) or common bottlenose dolphins (*Tursiops truncatus*). Second, species with good data were generally easier to monitor because of some combination of factors that made them accessible and visible. These factors included aspects of their behavior, such as the regular use of haul-out and breeding areas by numerous pinniped species (Taylor et al. 2007), consistent coastal migration routes as for the gray whale on the west coast of North America (Swartz et al. 2006), or long times spent at the water surface, as with North Atlantic right whales (*Eubalaena glacialis*) (NMFS 2005). Habitat or body size characteristics could have also contributed to better time series information. Abundance data collection may be easier for animals in accessible coastal areas, with smaller, well-known ranges, with large body size (e.g. great whales), or with individually identifying markings (e.g. killer whales) (Aron 1988; Gerber 1998; Taylor et al. 2007).

Definite gaps in our knowledge of marine mammal abundance trends exist, namely for beaked whales, river dolphins, sirenians and Antarctic phocid populations. Beaked whales are typically pelagic deep-divers with large ranges and low densities (Taylor et al. 2007). Relative lack of commercial value and recognition in the public sphere may have contributed to the lack of monitoring and data. Short (typically <10 years), sparse, recent time series do exist for some beaked whales, but their offshore distribution and deep-diving behavior has hampered data collection (Taylor et al. 2007). Time series data will likely improve due to interest in the susceptibility of these species to acoustic disturbance, especially from seismic and naval sonar testing (Jepson et al. 2003; Taylor et al. 2007). Many river dolphins are similarly cryptic, live at low densities or do not gather in social groups. A lack of conservation and monitoring plans with standardized population and habitat assessment techniques has limited data availability for them (Reeves et al. 2003). Although intensely studied, West Indian or Florida manatees (*Trichechus manatus*) are difficult to observe and reliable abundance estimates are challenging to obtain (Lefebvre et al. 2009). Lack of management has also contributed to a lack of time series data for Amazonian (*T. inunguis*) and West African manatees (*T. senegalensis*) (Reeves et al. 1996; Silva & Araujo 2001). Despite intensive shoreline and aerial survey efforts in many areas of the dugong's (*Dugong dugon*) range, low densities and large ranges have inhibited reliable abundance estimates (Marsh et al. 2002). Many Antarctic true seal populations do have recent population estimates and are thought to have healthy populations, but they lack longer time series or historical estimates (Reijnders et al. 1993). Abundance monitoring of Antarctic species may become more important for assessing and managing the effects of climate change and expanding Antarctic fisheries (e.g. krill) (Lake et al. 2008; Southwell et al. 2008).

The time spans for which data were available varied between different groupings of marine mammals. Three generations of data were available for 63% of populations, while shorter time series were typically available for dolphins, porpoises, small whales, polar bears (*Ursus maritimus*), and sirenians. These data gaps are not surprising considering that many of these populations were not heavily commercially exploited, and thus abundance records likely only began recently with management or recovery monitoring.

Populations of great whales, Pacific dolphin species, northern true seals, belugas (*Delphinapterus leucas*) and narwhals (*Monodon monoceros*) made up the majority of the populations with historical abundance estimates. Historical populations estimates for commercially valuable great whales typically came from either (1) catch data or product trade records, or (2) back-casting or genetic techniques (Alter et al. 2007; Baker & Clapham 2004; Roman & Palumbi 2003). Numerous dolphin species are found in Pacific U.S. waters. They are a management concern under the U.S. Marine Mammal Protection Act (MMPA), and were impacted by the Pacific tuna fishery that was established in the 1960s (Gerrodette et al. 2008; Wade et al. 2007). Many northern phocids, belugas, narwhals, and bowhead whales are still exploited commercially or for subsistence use by aboriginal groups, and have been subject to intense study and management (e.g. COSEWIC 2004, 2005; Fisheries and Oceans Canada 2003; Reeves 2002). Commercial pinniped hunts exist in Canada, Greenland, Namibia, Norway and Russia for several true and fur seal populations (Fisheries and Oceans Canada 2003; Kirkman & Lavigne 2010). With the lack of historical catch or abundance data for many populations, the development of genetic techniques for estimating historic population size (Alter et al. 2007; Roman & Palumbi 2003) may provide insight into pre-exploitation estimates in coming years.

We also found geographical biases in the data, which was typically from North America, Europe (especially northern Europe), and to a lesser extent Australia, New Zealand, Japan, South America and southern Africa. This bias is generally mimicked in global marine fish abundance datasets (e.g. Hutchings et al. 2010; Reynolds et al. 2005; Worm et al. 2009) and reflects the availability of financial and logistic resources for monitoring and assessment in richer nations. With the increasing interest in the value of global biodiversity, perhaps monitoring will expand to other more data-poor areas. Population abundance monitoring is important for both conservation (e.g. recovery plans) and sustainable extractive management to assess trends and reference points for conservation goals and management targets (Worm et al. 2009).

2.4.2 Marine Mammal Population Trends

Our synthesis of population trends for marine mammals was useful to obtain an overview of recovery trends. Amalgamating data from numerous different sources posed challenges, but we chose analytical techniques accordingly. Using a robust regression over three generations allowed us to estimate in a statistically sound manner the dominant recent abundance trends for the largest number of marine mammal populations, as scaled to life history and comparable to IUCN methods (IUCN Standards and Petitions Subcommittee 2010). The analysis of decline and recovery relationships, however, allowed us to incorporate populations with longer time spans (but insufficient data over three generations) into the study. Our basic definition of “Recovering” populations—those showing a statistically significant increase in abundance—also worked well for the challenges we faced, including non-uniform data time-spans and different life histories. In other analyses, depending on the goal, more specific definitions of recovery may be appropriate. Only in a few cases did this method not capture what by sight appeared to be the true trend of the data: the harbour seal (*Phoca vitulina*) population for all of Great Britain (Recovering) and sperm whales (*Physeter macrocephalus*) south of 60 degrees latitude in the southern hemisphere (Non-recovering). Both populations had relatively short time series (< 20 years), and the harbour seal population was highly variable. Sperm whales are typically difficult to monitor for abundance (Whitehead 2002), and the population time series had high leverage points over a short time period. We removed these two populations from our results summary, although including them would not change the results substantially.

Overall, 35% of populations were significantly Increasing compared to 3% Stable and 7% Decreasing, while 22% of the populations had Unknown and 33% non-significant trends. The large proportion of non-significant trends points to the difficulty of studying these animals and estimating their population size with any accuracy, and the need for better monitoring efforts for certain groups. Improvements in (1) increasingly commonly used techniques such as acoustic monitoring, tagging, photo-identification and mark-recapture, as well as (2) computerized database and analysis technologies, (3) modeling, and (4) data sharing among organizations may improve data quality and quantity.

Despite the data gaps, the populations with good data showed some interesting patterns. A large percentage (50%) of the pinniped populations were Increasing and Recovering. Their fast life history characteristics may have helped promote recovery. Management and conservation efforts, in terms of limiting direct exploitation, bycatch and trade, and either the isolation or protection of important haul-out or breeding habitats likely also contributed to recoveries in some populations (Reijnders et al. 1993). Coastal cetaceans were also recovering relatively well, possibly because of their early exploitation and subsequent relatively early management, conservation, and attention in the public sphere. Large, coastal cetaceans were often the first species hunted in an area because of their commercial value and relatively easy access (e.g. North Atlantic right (Clapham et al. 1999), gray (Swartz et al. 2006), and humpback whales (Clapham et al. 1999)). International concern over steep declines in numbers by the 1900s for most populations lead to some of the first multilateral conservation agreements, protection from international trade, domestic exploitation bans or regulations, habitat protection, and recovery planning (Aron 1988; Bhargava 2005; Gerber 1998). Numerous marine mammals also became endearing symbols of the environmental movement (Lavigne et al. 1999). Less visible or charismatic species, such as more predominantly offshore or smaller cetaceans, may have suffered in terms of population recovery both because they were often exploited after the depletion of more easily accessible coastal species, but also because later onset of or lack of directed management. Some toothed cetaceans, such as the sperm, pilot (*Globicephala* species) and killer whales, also have highly developed social structures that may be important to survival. As a result they may suffer the effects of selected removal and small population size more severely than less social marine mammals (Wade & Reeves unpublished; Whitehead et al. 2004). With the trend estimates derived from this study, we aim to further investigate the critical factors to population recovery in more detail (refer to Chapter 3).

2.4.3 Comparison with IUCN Data

In order to verify our population-level trends, we compared our results with IUCN assessment for those species where we did have the majority of abundance data at a

population level. This included 26 species, approximately 20% of all marine mammal species worldwide. For these, we did have good agreement with the equivalent IUCN trend determination for the same species, which strengthens confidence in our results. However, we clearly had more Increasing (i.e. Recovering), and fewer Decreasing, Stable and Unknown species (populations) compared to the global IUCN assessment of all 127 marine mammals (Figure 2.6). This is primarily attributable to the lack of data that met our criteria for many rare or difficult to monitor species (see Section 2.3.1), as well as the large proportion of these data-deficient species in the IUCN database.

2.4.4 Historical Declines and Recent Increases

Many populations with available time series did not have pre-exploitation or K estimates of historical population size. However, we were able to obtain estimates of historical population size and thus examine relationships between decline and recovery for 33% (n=47) of the non-nested populations. As shown for marine fish populations (Hutchings 2000, 2001), smaller historical population declines were significantly associated with more successful recent recoveries. The large proportion of populations with >60% to >90% declines highlights the substantial declines in many marine mammal populations.

We also found differences in declines and recovery between different types of marine mammals, with the smaller, typically less commercially valuable toothed whales, and especially porpoises and dolphins showing the smallest declines and greatest recoveries. Easily accessible coastal cetaceans and other marine mammals showed the largest declines. Recovery among marine mammal populations showed quite high variability, but on average otariids (eared seals), and baleen, offshore and coastal cetaceans seemed to show the smallest recoveries, likely because of heavy historical exploitation (otariids, baleen and coastal cetaceans) or lack of management (offshore cetaceans).

Other studies have quantified declines and recoveries in marine mammals. Christensen (2006) estimated historical baselines for exploited cetaceans and pinnipeds and found a cumulative decline of 22% (range = 0–62%) in numbers. The largest declines were in the great whales (64%, range = 40–79%), corresponding with periods of increased catches

(Christensen 2006) and comparable to declines we estimated for the baleen whales. The overall marine mammal declines, however, presented a lower decrease in terms of overall numbers than calculated in our study, likely for two reasons. Christensen (2006) limited her assessment of marine mammal declines to 1800–2000, and by this time numerous populations (e.g. North Atlantic right whales) had already been substantially depleted. In addition, declines were assessed in terms of cumulative numbers across all populations (Christensen 2006), as opposed to within each individual population as in our study, thus offering different representation of decline. A second recent study of historical baselines for large marine animals (not limited to a specific period) estimated a decline of approximately 96% for pinnipeds, otters and sirenians, and a recovery to approximately 25% of historical abundance (Lotze and Worm 2009). Whales declined by approximately 82% and recovered to approximately 32% of historical levels (Lotze & Worm 2009). The pinniped, sea otter and sirenian category was not directly comparable to any of our categories, but for pinnipeds, our study presented smaller declines and larger recoveries. This may have been because the Lotze and Worm (2009) study included populations that did not exhibit any recovery, including extirpated populations, while our study did not. The whale category only included great whale populations (mainly baleen) and was comparable to our baleen whale decline and recovery results.

Although there was relatively high variability in population recoveries after large declines, most populations showed minimal population recovery following very high declines, possibly indicating Allee effects (Hutchings & Reynolds 2004). Only five populations that underwent very large declines (>90% of the historical population abundance) also showed very high (>90%) recoveries. This reflected a similar finding in certain fast-growing clupeid populations, which recovered to levels that were not observed in any other types of fish after declines of similar magnitude (Hutchings 2000; Hutchings & Reynolds 2004). Two possibilities for explaining these outliers are that historical population estimates underestimated true pre-commercial exploitation population size, or ecosystem conditions changed in these areas to favor substantial population growth and larger abundances. However, these populations have relatively early age at maturity (4-5.5 years) and have been afforded some type of protection (Boyd

2002; Brown et al. 2005; David & van Sittert 2008; Gerber 1998; Hoesel 2002; Jeffries et al. 2003; Perry et al. 1999; Whitehead & Mann 2000). More investigation is necessary to determine if these are true outliers and what factors may have contributed to these substantial recoveries.

2.5 CONCLUSION

Despite scarce data for many species and regions, lack of historical abundance estimates and often high error associated with available data, we were able to summarize and estimate general population trends for 143 marine mammal populations. Overall, 35% of marine mammal populations are recovering from former exploitation, especially pinnipeds, coastal cetaceans and other marine mammals (i.e. polar bears, otters and sirenians). Dolphins and porpoises and offshore cetaceans showed relatively few recovering populations. On a species level, our results were comparable to assessments performed by IUCN, suggesting that our robust, weighted regression over three generations is a useful and appropriate method for estimating general population trends. However, compared to all marine mammal species assessed by IUCN, our data appeared to over-represent recovering populations due to a lack of data for data poor populations, most notably the sirenians, river dolphins and beaked whales. We also found that populations with smaller historical population declines were more likely to show strong population recoveries in more recent times, while those that have been extensively depleted showed more variability in their recovery success, but tended to have smaller recoveries. It is our hope that the synthesis and compiled database are useful tools for other researchers interested in marine mammal population trends, and that enhanced monitoring of marine mammal populations will produce more complete and accurate abundance estimates in the future. Reliable abundance estimates are critical for better management, conservation and evaluation of recovery of marine species.

CHAPTER 3 CRITICAL FACTORS TO MARINE MAMMAL POPULATION RECOVERIES

3.1 INTRODUCTION

One important focus in conservation biology is assessing the extinction risk of vulnerable species and populations. Investigating critical factors (correlates and possible drivers) affecting extinction can help us to understand which organisms are more at risk and why. This information is essential to informing effective management actions. In the marine realm, examining extinction risk and its correlates is relevant for species still undergoing substantial population declines, such as many bony fish (Hutchings et al. 2010; Worm et al. 2009), sharks (Dulvy et al. 2008; Ferretti et al. 2010) and invertebrates (Anderson 2010; Fisher & Owens 2004). In contrast, marine mammals—the cetaceans, pinnipeds, sirenians, marine and sea otters, and polar bears—have shown numerous population increases in recent decades following substantial, mainly exploitation-driven declines (Aron 1988; Freeman 2008; Gerber 1998; Gerber & Hilborn 2001; Lotze & Worm 2009). Thus, for marine mammals, a more pertinent question has become, “What are the critical factors for recovery?”

Understanding marine mammal population dynamics is valuable because many species are culturally, economically and ecologically important (Bowen 1997; Hovelsrud et al. 2008; Kareiva et al. 2006; Schipper et al. 2008). They are noteworthy symbols in traditional and contemporary cultures, are hunted commercially and for subsistence purposes, and are increasingly valuable for tourism (Hovelsrud et al. 2008; Kareiva et al. 2006). They shape marine ecosystems from both the bottom up (e.g. grazing sirenians and dead whales contribute to nutrient cycling) and top down (e.g. transient killer whales prey on other marine mammals) (Bowen 1997). A better understanding of the critical factors to marine mammal recovery will enhance our knowledge of population dynamics and recovery in long-lived marine animals and inform management and conservation strategies.

Critical factors to population decline or recovery are typically separated into two groups. Intrinsic factors are population or species-specific and are typically life history and ecological traits such as age at maturity, maximum intrinsic population growth rates (r_{\max}), range size, trophic level, and social structure. Extrinsic factors include predation, interspecific competition, anthropogenic habitat disturbance, or environmental change. Intrinsic and extrinsic factors can interact, with intrinsic factors influencing a population's response to external factors (Cardillo et al. 2008; de Little et al. 2007; Fowler 1981; Long et al. 2007; McMahon et al. 2005; Reynolds et al. 2005).

Several studies have investigated potential intrinsic and extrinsic factors for broad taxonomic and geographic groupings. These factors have been broadly summarized and used to assess the conservation status of populations and species, most notably by the International Union for the Conservation of Nature (IUCN) Red List of Threatened Species (IUCN 2001). Life history factors related to extinction and recovery are well summarized for vertebrates (Collen et al. 2006), mammals (Cardillo et al. 2008), large mammals (Cardillo et al. 2005), and declining species of primates and carnivores (Purvis et al. 2000). However, studies on mammals have typically either excluded the marine component (Cardillo et al. 2008, 2005), or focused on single or small groups of marine populations and species (e.g. de Little et al. 2007; Leaper et al. 2006; McMahon et al. 2005). Roberts and Hawkins (1999) summarized intrinsic and extrinsic factors affecting declines in marine species in general, with only a few examples for marine mammals. In the aquatic environment, critical factors have been more explicitly studied in fish population dynamics (Garcia et al. 2007; Hutchings 2000, 2001a, b; Hutchings et al. 2010; Hutchings & Reynolds 2004; Musik 1999; Olden et al. 2007; Reynolds et al. 2005), and Hutchings and Reynolds (2004) provide a good summary of hypothesized critical factors to fish stock recovery. Building on previous literature on terrestrial mammals and marine fish, this study aimed to investigate critical factors to marine mammal population recoveries.

Main hypotheses and findings of relevant studies on critical factors affecting decline and recovery are summarized below. In the cases reporting only population declines we proposed the relationship between the stated factor and recovery.

Intrinsic factors:

- Life history traits: In terrestrial mammals, body size may show a positive or negative relationship with decline (and presumably recovery), depending on taxonomic group (Cardillo et al. 2008). Olden et al. (2007) indicated that body size in freshwater and marine fishes is positively correlated with decline; we suggest smaller species should have a higher probability of recovery. Hutchings and Reynolds (2004) indicate that the suggestion of fecundity as a possible recovery correlate is not theoretically or empirically supported in marine fishes. Moreover, as almost all marine mammals give birth to one young at a time (Jefferson et al. 2008), fecundity is not a useful measure. Collen et al. (2006) found a positive relationship between decline and age at first reproduction in Asian vertebrates, and we suggest that earlier maturing populations should have a higher probability of recovery. The influence of gestation length on population decline (and likely recovery) in mammals can vary (Cardillo et al. 2005, 2004; Purvis et al. 2000).
- Trophic level: Purvis et al. (2000) and Cardillo et al. (2004) revealed that trophic level is positively associated with extinction risk in declining species and carnivores. A similar relationship has been suggested for marine species (Roberts & Hawkins 1999). We propose lower trophic level species should have a higher probability of recovery.
- Social interactions: For highly social organisms such as the cetaceans, some literature suggests an inverse relationship between the importance of social interaction and recovery. Social disruption may inhibit strong population increases in toothed whales with highly developed social structures (Jackson et al. 2008; Wade & Reeves unpublished). Disruption of mother-calf bonds may be partially responsible for lack of recovery in spotted and spinner dolphin populations (*Stenella attenuata* and *S. longirostris*) in the Eastern Tropical Pacific that have been subject to high incidental mortality in the tuna fishery (Wade et al. 2007). The importance of social interaction has been tied in with Allee effects and lack of recovery in some great

whales, namely western North Pacific gray whales (*Eschrichtius robustus*) and North Atlantic right whales (*Eubalaena glacialis*) (Jackson et al. 2008), as well as polar bears (*Ursus maritimus*) (Thiemann et al. 2008), sea otters (*Enhydra lutris*) (USFWS 2005), and the eared seals (otariids) at very low population levels (Gerber & Hilborn 2001).

- **Habitat area:** Habitat area or range size has been negatively associated with population decline in several species (Cardillo et al. 2008, 2005, 2004; Purvis et al. 2000; Roberts & Hawkins 1999). We suggest populations with larger habitat areas should have a greater probability of recovery. Because of difficulties in discerning habitat boundaries, lack of marine habitat fragmentation, and the migratory nature of certain species (e.g. most large whales), habitat area has been less of a concern for marine species than terrestrial ones (Dulvy et al. 2003).
- **Habitat type:** Habitat type (e.g. coastal, offshore, pelagic, demersal) is thought to be important for fish population dynamics because of differences in exploitation and disturbance patterns across habitat types (Hutchings & Reynolds 2004). Coastal species may be affected more than offshore species as nearshore areas are typically more anthropogenically disturbed (Schipper et al. 2008).
- **Genetic diversity:** Loss of genetic variation is thought to have negative effects on recovery in marine fishes (Hutchings & Reynolds 2004). Remarkably, it has not appeared to be a limiting factor in the recovery of several marine mammal populations reduced to incredibly low levels, including many otariids (Gerber & Hilborn 2001) and Hawaiian monk seals (*Monachus schauinslandi*) (Schultz et al. 2009). It has, however, been suggested to hamper substantial recovery in North Atlantic right whales (NOAA & NMFS 2006).
- **Phylogenetic proximity:** Phylogenetic relatedness is also a consideration in assessing population dynamics correlates (Cardillo et al. 2008, 2004; Collen et al. 2006; Fisher & Owens 2004; Fritz & Purvis 2010; Purvis et al. 2005, 2000; Reynolds et al. 2005). Phylogenetic proximity can influence extinction (and conversely recovery) probability, especially in terms of interactions with life history characteristics and trophic level. For example, pinnipeds have high mass-specific production rates for mammals (Sibly & Brown 2007), and thus we suggest they may be more adept at

recovering after population declines than cetaceans or other marine mammals. The influence of phylogenetic proximity on other factors is less clear (Purvis et al. 2005). Some extrinsic factors, like exploitation pressure, are thought to be more linked to phylogenetic patterns than others, such as habitat loss (Fritz & Purvis 2010).

Extrinsic factors:

- **Climate:** Temperature (typically measured through sea surface temperature, or SST) can have strong effects on marine ecosystem and population dynamics. Temperature affects primary productivity and thus prey abundance and distribution. Changes in temperature can also impact physical habitat suitability, for example through ice melting or loss of coastal habitat features to sea level rise (Croxall et al. 1992; Kaschner et al. 2006; Lehodey et al. 2006). Effects of temperature changes on a population can vary, but global warming is predicted to negatively impact marine mammals dependent on polar regions and with small, restricted ranges (Laidre et al. 2008; MacLeod 2009; Simmonds & Isaac 2007). Temperature changes have been linked to population dynamics in numerous marine mammals, including southern right whales (*E. australis*) (Leaper et al. 2006) and many pinnipeds (Sydeman & Allen 1999).
- **Species interactions:** Changes in facilitation, competition and predation may be important in determining decline and recovery in marine fishes (Hutchings & Reynolds 2004) and elasmobranchs (Ferretti et al. 2010). The same has been suggested for certain marine mammal populations, such as Antarctic minke whales (*Balaenoptera bonaerensis*) (Ruegg et al. 2010), and Northwest Pacific marine mammal communities (Springer et al. 2003). Interspecific interactions are difficult to quantify and more evidence is needed to support these ideas (Kareiva et al. 2006).
- **Disease:** Disease outbreaks have influenced population dynamics in some marine mammals, such as harbour seals (*Phoca vitulina*) in northern Europe (Hall et al. 2006) and sea otters in California (USFWS 2003).
- **Exploitation:** Mortality from direct and incidental exploitation can negatively affect population recovery (Hutchings 2000; Hutchings & Reynolds 2004) and has been suggested as the most important threat to marine populations (Hutchings & Reynolds 2004; Roberts & Hawkins 1999). Large-scale commercial exploitation has resulted

in depletion of many marine mammal populations (Lotze and Worm 2009). Today, some commercial exploitation (e.g. common minke whales (*Balaenoptera acutorostrata*) and certain pinnipeds) and subsistence hunts (e.g. numerous Arctic species, long-finned pilot whales (*Globicephala melas*) in the Faroe Islands) continue (Clapham & Van Waerebeek 2007; Fisheries and Oceans Canada 2008; Hovelsrud et al. 2008; Kirkman & Lavigne 2010; Reeves & Smith 2006; Reijnders et al. 1993). Indirect catch by fishing operations and entanglement in fishing gear impact many populations. Bycatch has been cited as an impediment to recovery of New Zealand sea lions (*Phocarctos hookeri*) (Chilvers 2008) and multiple small cetaceans (Young & Iudicello 2007). However, harbour and grey seals (*Halichoerus grypus*) from numerous populations are bycaught with apparently little effect on population abundance (Belden et al. 2006).

- Habitat disturbance: Habitat loss or modification can negatively affect population recovery (Hutchings and Reynolds 2004), and numerous studies found a positive relationship to extinction risk. We propose a negative relationship with recovery (Cardillo et al. 2008, 2005, 2004).
- Management effectiveness and timing: Early and extensive management of exploitation, habitat alterations and trade could be linked to greater recoveries (Hutchings & Reynolds 2004). However, some highly managed marine mammals, such as North Atlantic right whales and Hawaiian monk seals still show a lack of recovery (NOAA & NMFS 2006; Reynolds et al. 2009).

In this study, we investigated which intrinsic and extrinsic factors are most critical to recovery across marine mammal populations. We were not able to test all variables listed above, but chose those for which good data were available and which have been suggested to be more important for marine mammals. Because marine mammal population abundance data quality and quantity vary widely, we used a dataset of statistically significant population trends based on our analysis in Chapter 2. We defined recovery in the most basic sense as a statistically significant population increase. Our main objective was to better understand those factors related to whether or not marine

mammal populations show signs of recovering, rather than factors determining the magnitude or rate of recovery.

3.2 METHODS

3.2.1 Data Compilation

We compiled publicly available marine mammal abundance data, and estimated population trends with robust linear regression. Robust linear regression allowed us to down-weight any high influence outliers and capture the strongest overall trend signal (Wilkinson & Task Force on Statistical Inference 1999; Wright & London 2009). We used datasets with a minimum of ten years or three generations of data, depending on availability. This time period allowed for a broad comparison of population trends over data sets that lacked standard time frames, data intervals, and historical population estimates. It scaled the analysis to the species' life history, as is commonly done by the IUCN in assessing population trends (IUCN 2001). A further explanation of trend determination and classification is contained in Chapter 2.

We selected all populations with statistically significant abundance trends (i.e. Increasing, Decreasing or Stable; 95% confidence level), and classified the Recovery Status of each as Recovering or Non-recovering (see Chapter 2). Recovering populations showed a statistically significant positive slope (> 0.1) and Increasing trend, and Non-recovering populations showed significantly Stable ($-0.1 \leq \text{slope} \leq 0.1$) or Decreasing trends ($\text{slope} < -0.1$). Populations with Stable trends were mostly at low abundance levels and therefore could show abundance increases. In total, we had 43 non-nested marine mammal populations from 25 species (see Appendix II.A for a full list). For nine pinniped populations, we used pup count data since adequate regular population data were not available (Seber 1986). Abundance data and trends are plotted for each population in Appendix II.B. A breakdown of Recovering and Non-recovering populations for different data groupings analyzed in this study is shown in Figure 3.1.

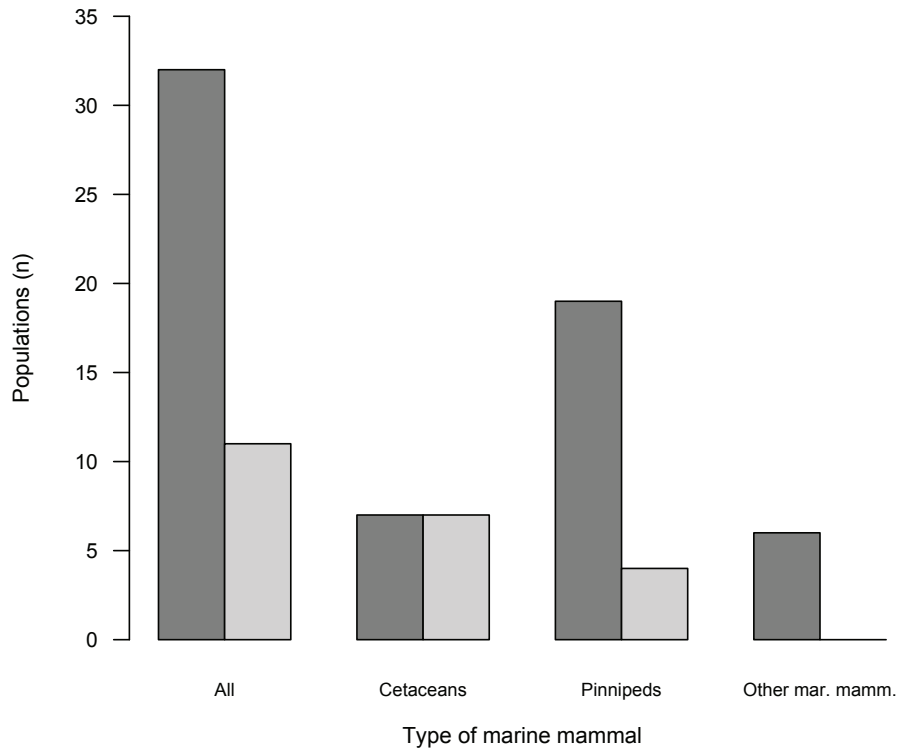


Figure 3.1 Recovering (dark grey) and Non-recovering (light grey) populations of all marine mammals (n=43), cetaceans (n=14), pinnipeds (n=23) and other marine mammals (i.e. polar bear & sea otter, n=6) in this study. Abundance data and trends for each population are shown in Appendix II.B.

For each population, we compiled data on twenty-one intrinsic and extrinsic factors that may be critical to recovery (Table 3.1). We anticipated some of these would be highly correlated (see Section 3.2.2). Detailed information on data and sources for each critical factor are provided in Appendix II.A.

Table 3.1 Intrinsic and extrinsic factors hypothesized to influence recovery in marine mammal populations. Units and data type, if present, are indicated in brackets. See Appendix II.A for data and sources for each marine mammal population.

Intrinsic factors	Extrinsic factors
Length , mean or median female (m) (continuous)	Mean Habitat Disturbance (continuous)
Weight , mean or median female (kg) (continuous)	Maximum Habitat Disturbance (continuous)
Gestation Time (months) (continuous)	Direct Exploitation (categorical, 2 levels – yes or no)
Interbirth Interval (years) (continuous)	Bycatch (caught as) (categorical, 2 levels – yes or no)
Age at Maturity (years) (continuous)	Exploitation Management (categorical, 3 levels – none, partial, full)
Trophic Level (continuous)	Exploitation Management Implementation Time (categorical, 4 levels – recent, mid, distant past, NA)
Habitat Type (categorical, 3 levels - terrestrial/nearshore, terrestrial/nearshore & oceanic, oceanic)	Habitat Management (categorical, 3 levels – none, partial, full)
Dominant Habitat (categorical, 2 levels – coastal, coastal and offshore (both) & offshore)	Habitat Management Implementation Time (categorical, 4 levels – recent, mid, distant past, NA)
Habitat Area (km squared) (continuous)	Trade Management (categorical, 3 levels – none, partial, full)
Importance of Social Interaction (categorical, 3 levels – low, medium, high)	Trade Management Implementation Time (categorical, 4 levels – recent, mid, distant past, NA)
Species Type (categorical, 3 levels – cetacean, other, pinniped)	

As r_{max} was not available for many populations included in our study, we used a selection of individual life history characteristics (Table 3.1, Appendix II.A). Life history information was obtained from a variety of published primary articles, reviews, government technical reports, government websites, and in some cases personal communications (see Appendix II.A). Trophic Level information came from a summary of marine mammal trophic levels (Pauly et al. 1998).

Habitat description data (Type, Dominant and Area) was derived both from literature and data extraction in ArcGIS 9.3.1 (ESRI 2009). Habitat Types for each marine mammal species are summarized in the IUCN Red List under the Classification Schemes tab (www.iucnredlist.org). We condensed the results into three categories: terrestrial/nearshore, terrestrial/nearshore & oceanic, and oceanic. Dominant Habitat (coastal or coastal and offshore (both) & offshore), however, described the habitat where the population spent the majority of its time according to IUCN and Jefferson et al. (2008). For example, humpback whales (*Megaptera novaeangliae*) may be found in both coastal and offshore habitats, but they are mainly a coastal species outside of migration times (Reilly et al. 2008). To assess Habitat Area, we used maps of species/population ranges or descriptions from (1) the IUCN Red List (searchable by species, (IUCN 2008)), (2) stock assessment reports and recovery and (3) other source documents. We used ArcGIS 9.3.1 to plot the ranges from IUCN maps constructed by Schipper et al. (2008), including important migration, feeding, breeding, and nursery areas for each population. For some pinnipeds and coastal cetaceans we used the typical foraging area around a land feature as a buffer to approximate the population habitat area. For example, female grey seals typically forage within ~100 km from haul-out sites on Sable Island (Breed et al. 2009).

An intrinsic factor that is not often evaluated in wildlife population dynamics is the importance of social interaction. Based on available literature on marine mammal social organization and culture, and input from an expert on the topic (Dr. Hal Whitehead, personal communication), we developed an index for the Importance of Social Interaction as: (1) low = the species presents few sustained social bonds, which in some species includes minimal mother-offspring interaction aside from initial nursing period (e.g. most pinnipeds), (2) medium = species with important fission/fusion social bonds (e.g. most small, toothed cetaceans) or mostly solitary lives with strong, sustained mother-calf bonds and group formation for feeding and mating (e.g. most baleen whales, sea otters, walrus) (Connor 2000; Connor et al. 2000), and (3) high = species with matrilineal and strong family ties important for socialization, feeding, and mating (e.g. large toothed

whales) (Connor 2000; Connor et al. 2000; Trillmich 2002; Whitehead 2002; Whitehead et al. 2004; Williams & Lusseau 2006).

To incorporate a measure of phylogenetic relatedness we included the categorical variable Species Type (cetacean, pinniped, or other). The “other” category encompassed polar bears and sea otters, which we grouped together due to small sample size and to differentiate them from the cetaceans and pinnipeds.

For extrinsic critical factors, we included three main categories: habitat disturbance, exploitation and management. Habitat disturbance was assessed using Halpern et al.’s (2008) cumulative human impact score, which combines measures for 17 recent anthropogenic factors on a grid of 1 km² cells of the ocean from 1985–2009 (typically 1999–2003). Using ArcGIS 9.3.1, we matched population range polygons described above to Halpern et al.’s (2008) scores and extracted the mean and maximum habitat disturbance for each population’s range. Some highly migratory populations had very large ranges, while other populations had very small and well-defined ranges. We therefore extracted both a mean and a maximum. The Maximum Habitat Disturbance helped us to evaluate whether populations were exposed to very high levels of disturbance in part of their range, even if overall Mean Habitat Disturbance was relatively low. Factors included in the habitat disturbance index were pollution (nutrient enhancement, organic, inorganic), human population density, commercial and artisanal fishing and bycatch, oil rigs, invasive species, shipping, and climate change (SST, UV radiation, and ocean acidification) (Halpern et al. 2008). One notably absent factor was noise, which affects marine mammals, in particular beaked whales (family Ziphiidae) (Horowitz & Jasny 2007; Nowacek et al. 2007; Weilgart 2007). Incidentally, abundance data for these species was not available and hence they were absent from our analysis. Efforts are underway to include ocean noise in a revised cumulative habitat impact score; in the interim we assumed oilrigs, shipping lanes, and human population density served as a proxy.

Regarding exploitation, we examined the presence or absence of direct and indirect (bycatch) exploitation on recovery (Table 3.1) based on data from the IUCN and other sources. We further investigated the degree (no, partial, full ban) and time of implementation of three categories of management: (1) exploitation, (2) habitat, and (3) trade management. For Exploitation Management, partial bans included catch limits, regulated harvest periods, co-managed aboriginal or subsistence hunts, or complete bans on harvest where illegal harvest was still documented (as in the case of some large cetaceans despite the International Whaling Commission's commercial whaling moratorium of 1986). For Trade Management, a complete ban occurred when a population was listed on the Convention on the International Trade of Endangered Species of Fauna and Flora (CITES) Appendix I, which bans international trade. We also considered regional bans, for example under the U.S. Marine Mammal Protection Act (MMPA) if they covered the population's range. Populations listed on CITES Appendix II or III (which permit sustainable, regulated trade) or with only portions of their range or population regulated were classified under partial bans. Populations with any type of Habitat Management within their range (e.g. protection of a pupping area) had partial Habitat Management, while populations with protection over their entire range had full Habitat Management. For all types of management, we examined the time period in which the management actions were implemented with respect to the life history of the population in question. Management Implementation Time was classified as (1) recent past = less than one generation before the most recent abundance estimate, (2) mid past = between one to three generations, (3) distant past = more than three generations before the last abundance record in the data series, and (4) NA= no management was implemented and time period did not apply. Data on exploitation management came from the same sources as the direct and indirect exploitation data and additional sources. Habitat and trade management data were mainly obtained from the IUCN Red List (IUCN 2008), as well as a number of other sources.

3.2.2 Statistical Analysis

We performed all statistical analyses using R Statistical Analysis Software (R Development Core Team 2010) (code available in Appendix II.C). We modeled all

populations (n=43) simultaneously as well as in two subgroups: cetaceans (n=14) and pinnipeds (n=23). We did not separately analyze subsets of other marine mammals because of the lack of available data (n=6, no sirenians).

First, we investigated the correlation among critical factors to reduce collinearity in the analysis. We used the `cor()` command in R with the Spearman's Rho method to deal with the large number of ordinal and categorical variables (R Development Core Team 2010). For variable pairs with >0.7 correlation (a standard cutoff point for high correlation), we removed the variable that was highly correlated with the highest number of other variables. Variables with multiple correlations were removed first. We also considered the correlation of generation time with other life history characteristics, but did not exclude any variables on this basis. Exploratory analysis also suggested two variables with large ranges should be log transformed: Weight and Habitat Area.

We used classification trees, generalized additive models (GAMs), and generalized linear models (GLMs) to explore relationships between our binary response variable, Recovery Status (Recovering or Non-recovering) and the hypothesized critical factors (independent variables). Classification trees use binary recursive partitioning to split the data into groupings of similar data according to the dependent and independent variables (Clark & Pregibon 1992). We employed classification trees, using the `tree` command in the `tree` library in R (R Development Core Team 2010), for initial data inspection, identification of data structure, and as a comparison with more complex modeling approaches (Clark & Pregibon 1992; Crawley 2003). Generalized additive models (GAMs) were used to assess whether any of the independent variables interacted with the response variable in a non-linear fashion (Wood 2006). Penalized likelihood maximization was used to fit GAMs (Flemming et al. 2010), where the flexibility or “wiggleness” of each smoothed function and any reduction in fit was penalized to adjust the model likelihood (Flemming et al. 2010). A balance between model flexibility and fit penalties was achieved by multiplying each penalty by a smoothing parameter which was estimated using generalized cross-validation in the `mgcv` package in R (Flemming et al. 2010). We constructed the GAMs with a binomial family and a logit link. We used thin plate regression splines to estimate the smooth functions. This approach also shrunk completely to zero those terms that were

not important in the model fit, thus aiding in model selection (Wood 2006). We also investigated whether the use of generalized linear models (GLMs) was more appropriate, and used a logit link to correspond to the binomial response and error structure. Model fitting was achieved through an iterative least squares approach (McCullagh & Nelder 1989).

For model selection with GAMs and GLMs, we considered (1) minimizing Akaike information criterion (AIC), (2) significance of the model variables at a 95% confidence level (p-value = 0.05), (3) adjusted, approximated or regular R^2 (as available), and (4) equal variance of residuals and normality in the data (residual plots) (Crawley 2003). These four model selection criteria addressed model fit, complexity and adherence to assumptions (Johnson & Omland 2004). We aimed for significant p-values < 0.05 for all variables in final models, but also considered models that included variables with $0.05 \leq \text{p-value} < 0.15$ if they improved model fit according to the above criteria. Considering the complexity of marine ecosystems and the associated uncertainty, instead of selecting only one best model we considered multiple competing good models and discussed the statistical and biological support for each (Buckland et al. 1997; Burnham & Anderson 2002; Johnson & Omland 2004). We determined relative importance of covariates based on significance and consensus across the collection of good models as an approximation of multi-model inference (Burnham & Anderson 2002; Cantoni et al. 2007). We classified “critical factors” as those that were significant covariates or were included in the best classification tree model³, and were included in at least two model types. “Possible critical factors” were either (a) significant in one type of good model and/or (b) possibly important ($0.05 \leq \text{p-value} < 0.15$) in at least one type of good model or included in the best classification tree model. We used backward model selection, starting from a full model and removing variables. We then re-visited the models using forward selection, starting from a null model and adding variables (Venables & Ripley 2002).

³ Critical p-values are not calculated for covariates in classification tree models.

3.3 RESULTS

In the overall marine mammal population dataset, high correlation (>0.7) was estimated among Length, Direct Exploitation, Interbirth Interval, Habitat Management, Importance of Social Interaction and other variables; thus we removed them from further analyses. For the same reason we removed Trade Management from the cetacean dataset, and Gestation Time, Habitat Type, and Habitat Area (log transformed) from the pinniped dataset. With small sample sizes high correlation among numerous variables was understandable. Figure 3.2 depicts the distribution of significant and possibly important correlates in relation to Recovery Status, with similar plots for all independent variables in Appendix II.D. Table 3.2 shows the different types of final models that offered good alignment in terms of highly and moderately significant covariates. Detailed model outputs and plots in are available in Appendix II.E.

3.3.1 Marine Mammals Overall

For marine mammal populations overall we identified two critical factors: Dominant Habitat and Habitat Disturbance, and several possible critical factors: Trophic Level, Species Type, Maximum Habitat Disturbance, and Age at Maturity (Figure 3.2a, Table 3.2). Detailed models outputs and plots are visible in Appendix II.E. The classification tree included Dominant Habitat and Age at Maturity as significant covariates, but Age at Maturity did not show up in the GLMs or GAMs. Interestingly, Dominant Habitat and Mean Habitat Disturbance were not significant in the same models (Appendix II.E). These two factors exhibited moderate correlation (-0.52), with high mean habitat disturbance being associated with coastal habitats. This resulted in competing GAMs and logistic GLMs. Moreover, GAMs and GLMs offered slightly different good models. As almost all continuous covariates in the GAMs displayed essentially linear relationships with the response, we favored the GLMs over the GAMs, but discussed both.

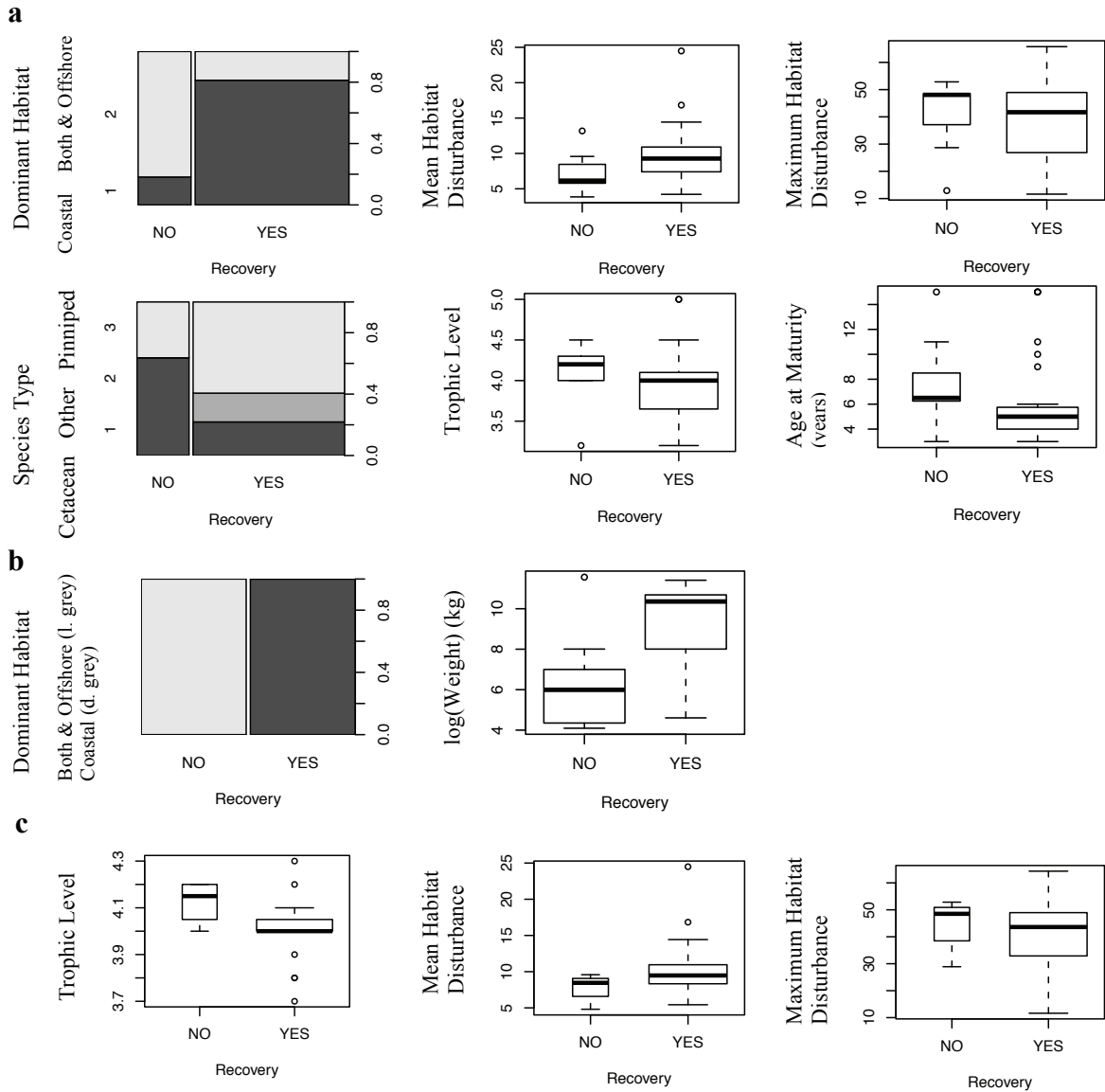


Figure 3.2 Distribution of critical and possibly critical factors for Recovering and Non-recovering populations of marine mammals (a), cetaceans (b), and pinnipeds (c). Appendix II.C contains additional variable plots. Quantitative variables are represented by boxplots, with the box representing the bounds of the upper and lower quartiles containing the median (horizontal line). The whiskers extend to 1.5 times the interquartile range, with outlier points outside the box and whiskers. Categorical data are represented by barplots, displaying the relative proportion of each category level in the data.

Table 3.2 Critical factors from good models for all, cetacean and pinniped populations. Critical factors = green; possible critical factors = yellow; unimportant factors = black. Direction of relationship with Recovery Status is indicated as positive (+), negative (—), or containing multiple directions (e.g. +/—/+). For some smoothed GAM terms). Critical factor significance symbols for p-value: ** < 0.01; * < 0.05, ♦ < 0.10, ♣ > 0.10; √ = included in classification tree model (no p-value given); a term may have more than one symbol depending on its significance in different good models (e.g. ♦ or ♣). More details on results are in Appendix II.E.

Critical Factor	Mean Habitat Disturbance	Maximum Habitat Disturbance	Dominant Habitat	Species Type	Trophic Level	Age at Maturity	Weight (log)
Relationship with Recovery Status	+	—	— (Both & Offshore)	+	— (+/—/+)	—	+
All			√			√	
Classification Tree							
GAM	*		**	♦	♣ (p-value = 0.34)		
GLM	*	*	**	♦			
Critical Factor?	■	■	■	■	■	■	■
Cetaceans			√				♦
Classification Tree							
GLM							
Critical Factor?	■	■	■	■	■	■	■
Pinnipeds			√				
Classification Tree							
GLM	♣	♦ or ♣			♦		
Critical Factor?	■	■	■	■	■	■	■

Both good GAMs contained one smoothed function and one linear, categorical term (Appendix II.E). The first good GAM identified Dominant Habitat as highly significant and negatively related to Recovery Status (p-value = 0.0005, coefficient = -0.33), while Trophic Level, although not significant (p-value = 0.341), exhibited a non-linear relationship (effective degrees of freedom (edf) = 3.73). GAMs do not provide coefficients to describe relationships between covariates and responses (e.g. slope), and smooth function plots instead indicate relationship patterns. Figure 3.3 shows the smoothed function, $s(\text{Trophic_Level})$, as fit in the first model. It indicates that marine mammals with trophic levels of approximately 3.7–4.2 exhibited a negative relationship with Recovery Status, while those at lower or higher trophic levels showed a positive relationship. However, wide confidence bands and the flaring towards higher trophic levels suggest uncertainty about the nonlinear pattern. Although Trophic Level was not significant, it warrants further investigation with larger sample sizes as more data become available.

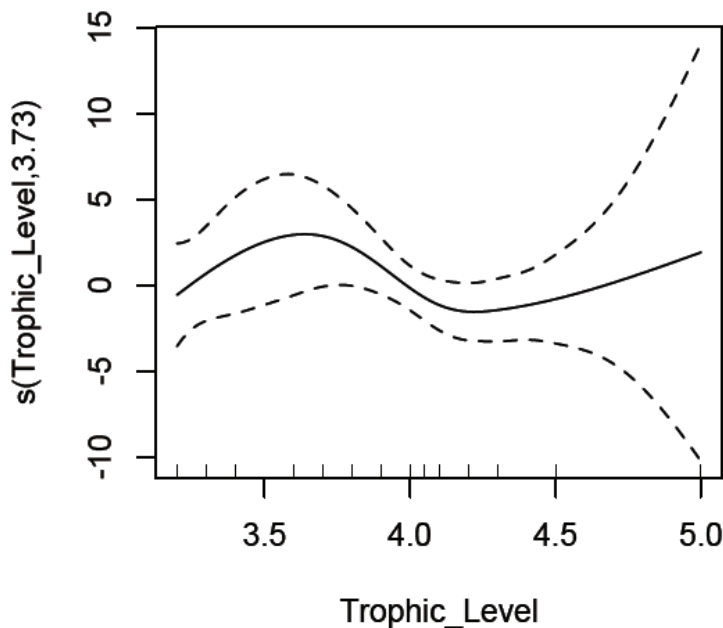


Figure 3.3 Smooth function of trophic level in a good overall marine mammal GAM. Dashed lines indicate confidence bands.

The second good GAM identified Species Type as moderately important, with pinnipeds being positively related to Recovery Status (p-value = 0.114, coefficient = 1.30). The smooth function of Mean Habitat Disturbance was significant (p-value = 0.044), but essentially linear (edf = 0.83), and thus could be sufficiently described by a GLM. The second GAM had a higher AIC (42.34 vs. 36.25), but a lower adjusted R^2 (0.26 vs. 0.48) and deviated more from the assumption of normality than the first GAM.

GLMs appeared more appropriate and less complicated for assessing critical factors to Recovery Status, and we identified two good ones. In the first, Dominant Habitat (coastal and offshore (both) & offshore) was highly significant (p-value = 0.005, coefficient = -2.82) and Species Type (pinniped) was possibly important (p-value = 0.071, coefficient = 1.73). In the second model, both Mean Habitat Disturbance (p-value = 0.014, coefficient = 0.60) and Maximum Habitat Disturbance (p-value = 0.048, coefficient = -0.08) were significant. The first GLM displayed a lower AIC (37.96 vs. 44.52) and a higher approximate R^2 (0.39 vs. 0.21). The first GLM also displayed a better adherence to the assumption of normality in the Normal Q-Q residual plots, and fewer high leverage outliers. In the first model, outlier populations included the Hawaiian monk seal (Hawaii), Steller sea lion (*Eumetopias jubatus*, western Alaska), and subantarctic fur seal (*A. tropicalis*, Marion Island), all of which were Non-recovering pinnipeds. In the second model plot, a distinct break between Recovering and Non-recovering populations contributed to non-normality, with a beluga population (*Delphinapterus leucas*, Cook Inlet) being the most notable outlier (Appendix II.E).

3.3.2 Cetaceans and Pinnipeds

Separate models for cetaceans and pinnipeds, respectively, identified differences in possible critical factors between these two groups. Because small sample sizes limited the degrees of freedom we could not run GAMs over all variables and only considered classification trees and GLMs.

For cetaceans, the classification tree likely gave the most accurate results, indicating a strong relationship between Recovery Status and Dominant Habitat, but GLMs implied Weight was possibly important too. Perfect correlation (-1.00) of Dominant Habitat and Recovery Status

(Figure 3.3b, Appendix II.D) prevented accurate inclusion of the variable in a GLM; each category level must be represented in both levels of the binomial response to accurately analyze categorical variable level significance against a reference level (Wright & London 2009). Consequently, although Dominant Habitat was the most important covariate identified in the classification tree model, it was not significant in the good GLM. In the GLM, Weight (log transformed) was possibly important and positively linked to Recovery Status (p-value = 0.080, coefficient = 0.43). The model adhered well to model assumptions, but had a low approximate R^2 (0.20).

For pinnipeds, the classification tree revealed Mean and Maximum Habitat Disturbance as important factors (Table 3.2, Figure 3.3c), and we found two good GLMs (Appendix II.E). The first contained Mean Habitat Disturbance (p-value = 0.119, coefficient = 0.66) and Trophic Level (p-value = 0.082, coefficient = -9.91), while the second contained Mean Habitat Disturbance (p-value = 0.087, coefficient = 2.28) and Maximum Habitat Disturbance (p-value = 0.125, coefficient = -0.38). They adhered to assumptions of equal variance but deviated from normality in the Normal QQ plots, most notably the lower tails (Appendix II.E). The lower tails were comprised solely of Non-recovering populations, the same outlier pinniped populations noted in the overall marine mammal GLMs above. Deviations from normality were not surprising with the small sample size, and especially small number of Non-recovering populations. Adherence to normality was slightly better in the first model, but the AIC was higher (20.32 vs. 17.06) and the approximate R^2 lower (0.33 vs. 0.48), so we considered both models.

3.4 DISCUSSION

Using multiple modeling approaches, we revealed three main findings related to marine mammal population recoveries. First, we found two statistically significant factors critical for population recovery: Dominant Habitat and Mean Habitat Disturbance. Populations that spent most of their time in coastal habitats and areas of higher mean habitat disturbance exhibited a higher probability of recovering than populations more reliant on offshore and

less disturbed habitats. Although this was a surprising result, it reflects the history of marine mammal exploitation, management and conservation, which started earlier and focused on coastal rather than offshore species. The ongoing effect of these forces continues to be important in determining recovery of marine mammals today. Second, we identified a number of less prominent but possible critical factors including Maximum Habitat Disturbance, Species Type, Age at Maturity, and Trophic Level. Populations with areas of high Maximum Habitat Disturbance within their range showed a lower probability of Recovering. Pinnipeds and earlier maturing species showed a higher probability of Recovering, and there was some weak evidence of a similar pattern for populations with either low or high Trophic Level. Finally, the importance of various critical factors appeared to differ between cetaceans and pinnipeds, with Dominant Habitat and Weight being more important to cetaceans, and Trophic Level, Mean and Maximum Habitat Disturbance for pinnipeds. These results only pertained to a limited dataset of 43 populations from 25 species, which exhibited significantly increasing abundance trends over the last three generations. As more and better abundance data become available, our models can be refined to derive more comprehensive results.

3.4.1 Critical Factors: Dominant Habitat and Mean Habitat Disturbance

Coastal habitats and higher average levels of habitat disturbance are not intuitively linked with population recovery, but historical context can provide insight into this result. Habitat loss and degradation is one of the top threats to species globally (Millenium Ecosystem Assessment 2005), as well as marine species (Kappel 2005) and mammals (Schipper et al. 2008). A growing human population influences coastal waters through coastal development, fishing and resource extraction, aquaculture, disease, and pollution, resulting in more disturbed coastal than offshore areas (Halpern et al. 2008). Moderate correlation between these two variables in our study supported this assertion, yet the correlation was not high enough to exclude one of them from our analysis. Offshore waters may also have areas of high disturbance, for example from shipping, commercial fishing, and climate change (Halpern et al. 2008). We suggest multiple mechanisms influenced the relationships among Dominant Habitat (intrinsic factor), Mean Habitat Disturbance (extrinsic factor) and Recovery Status.

Marine mammals in coastal and more disturbed habitats were generally exploited earlier in history than those in more offshore and less disturbed habitats, but these early depletions may also have allowed for more time for subsequent recovery. Humans have exploited marine mammals throughout history, but largely targeted on-land or nearshore mammals (Hoffman 2005; Hovelsrud et al. 2008; Kasuya 2007; Kock 2007; Lotze 2005; Lotze et al. 2006; Lotze & Milewski 2004; Lyman 1995; Reeves & Smith 2006). Cetacean hunting focused on species that spent substantial time in nearshore areas. Prime targets included gray (*Eschrichtius robustus*), bowhead (*Balaena mysticetus*), right (*Eubalaena* spp.), and humpback whales, and some smaller cetaceans (e.g. harbour porpoises, *Phocoena phocoena*) (Kasuya 2007; Lotze et al. 2006; Reeves et al. 2003; Reeves & Smith 2006). Pinnipeds' were vulnerable to harvests with their haul-out resting behavior and predictable land or ice-based rookeries (Lotze et al. 2006; Lyman 1995), as were coastal sea otters (Sea Otter Recovery Team 2007), polar bears (Hovelsrud et al. 2008), and sirenians (Marsh et al. 2002; Reeves et al. 1996; Silva & Araujo 2001; USFWS 2001).

By the late 1500s, the North Atlantic right whales were the first species to be commercially depleted (Christensen 2006), and over time, many more marine mammal populations became targets of heavy commercial exploitation, mainly in the mid-1700s–1900s. By the early 1900s, many marine mammals were depleted, especially nearshore populations (Reeves & Smith 2006). Technological innovations enabled longer voyages farther out to sea and increased hunting and processing efficiency. Whalers increasingly targeted more pelagic species like large baleen (e.g. blue) whales (Reeves et al. 2003; Reeves & Smith 2006; Schneider & Pearce 2004). In the 20th century, industrialized whaling moved offshore and focused on the southern ocean (Reeves & Smith 2006). Similar nearshore to offshore patterns of exploitation of marine mammals were observed when exploitation began in Antarctic areas (Kock 2007).

The early and strong declines in many coastal populations spurred the introduction of management and conservation measures, as well as some of the first regional and multilateral agreements. For example, Afro-Australian fur seals were amongst the earliest marine

mammals with regional exploitation management in South Africa and Namibia in the late 1800s (Shaughnessy 1999; Wickens & York 1997) and habitat protection via the Wilson Promontory Park in Australia in 1905 (Catrice 1994). Alaskan Parks were established between 1892–1913 to protect terrestrial and coastal species (Bhargava 2005). One notable exception is the Fur Seal Treaty of 1911 (United States, Russia, Great Britain and Japan) protecting largely pelagic northern fur seals (*Callorhinus ursinus*) (Bhargava 2005). The first international management for cetaceans, the Convention for the Regulation of Whaling in 1931 (implemented 1935) banned commercial hunting of nearshore right and bowhead whales (Bhargava 2005). Subsequent protection was extended to other whales, but the earliest and most stringent protection was afforded to nearshore, commercially valuable great whale populations. Substantial protection for larger, more pelagic great whales (with the exception of the sperm whale) only began in the late 1960s–1970s.

From the 1970s onward, an increasing number of conservation measures were introduced with wider protections for more populations across more habitats. Yet management and public emphasis remained on well-known coastal populations. Many commercial hunts ended, although illegal and subsistence hunting continued for many populations. Voluntary international regulations were extended to most species of marine mammals under CITES (CITES, 1973), the Convention on the Conservation of Migratory Species of Wild Animals (CMS, 1979), the Convention on the Conservation of Antarctic Marine Living Resources (1980), and the United Nations Law of the Sea (1983) (Lavigne et al. 1999). In 1986, the International Whaling Commission (IWC) instituted a commercial whaling moratorium protecting all great whales. Although more migratory or offshore species were protected under international agreements like the IWC moratorium, CITES and CMS (Caddy & Agnew 2004; Currie 2007), they still may not have benefited as much as nearshore populations, which are more easily managed under national jurisdictions. An exception to this was the establishment of the largest protected areas in international waters by IWC, banning commercial and aboriginal whale hunting in the South Pacific (1938–1955), Indian (1979) and southern oceans (1994), although the sanctuaries' effectiveness has been criticized (Gerber et al. 2005).

National regulations were also important. The U.S. Marine Mammal Protection Act (MMPA, 1972) (Aron 1988) set a standard for marine mammal protection which was followed by other nations. Under the U.S. Endangered Species Act (ESA, 1973) some of the first marine mammal species listed between 1967–1979 were great whales and nearshore sirenians, marine and sea otters, and monk seals (USFWS 2010). Pinniped management also increased from the 1960s–1970s onward in Canada (Fisheries and Oceans Canada 2008), the UK (UK Government 1970), South Africa and Namibia (David & van Sittert 2008), and Australia (Shaughnessy 1999). At the same time, sea otters were re-introduced to areas where they had been extirpated, with success in almost all locations (Sea Otter Recovery Team 2007). In the 1980s–1990s, co-management between aboriginal groups and government agencies in Canada and the U.S. began (Angliss & Allen 2009; Carretta et al. 2009; Richard & Pike 1993). Some states implemented more marine protected areas, including the National Marine Sanctuaries in the U.S., and some explicitly focused on protecting marine mammals (e.g. the Hawaiian Islands Humpback Whale National Marine Sanctuary (Office of National Marine Sanctuaries 2010)). Regional agreements and groups were established in the 1990s to coordinate research on and conservation of small-bodied and transboundary populations (e.g. the Agreement on the Conservation of Small Cetaceans of the Baltic and North Seas) (Perrin 1999). Of the less commercially valuable smaller cetaceans, offshore beaked whales still have some of the lowest amounts of management (Perrin 1999).

Interestingly neither Management (Exploitation, Trade or Habitat) nor the time period in which it was implemented was a significant critical factor to marine mammal Recovery Status in our models. However, they may still be important to consider for two reasons: (1) a better continuous metric of the implementation time, degree and effectiveness of management may have yielded a better result than the categorical variables used, especially with the limited set of marine mammal populations, and (2) management may have had less effect on marine mammal numbers than economics. First, as management variables were categorical and the temporal component was scaled to generation time, improper designation of category levels or too many variables and levels for the sample size could have affected their significance in the models. A number of populations were on the borderline between two Management Implementation Time categories, and management categories did not take

into account management effectiveness. We chose to use categorical variables for their relatively straightforward application. However a continuous index may have better captured differences in management implementation times, degree and effectiveness while increasing the available degrees of freedom in the models. Hutchings and Reynolds (2004) suggest evaluating the effect of the rapidity of management implementation relative to population collapse. Assessing management variables over absolute time periods (e.g. 1970–1990) may have also given a different perspective. These could be better approached where data over comparable time periods are available, but would have limited the number of comparable populations in our study.

For habitat management, an additional factor may have contributed to the lack of a significant relationship with recovery. Only two populations in our study (harbour seals in the Wadden Sea and grey seals in the Netherlands) had full habitat protection. Cryptic, highly migratory, transboundary or open ocean marine mammals pose difficulties in range protection. Identifying and protecting high use habitat areas has been proposed as a partial solution to this problem (Bailey & Thompson 2009). However, as habitat management was implemented relatively recently for most populations in this study (i.e. recent or mid-past), more time may be needed to see habitat management effects on recovery.

A second possible reason for the lack of significant management variables is the importance of economic drivers, which we did not examine. Market demand for particular products drove commercial hunting of some species, as in the case of exceptionally thick pelts of sea otters. However, larger marine mammals that maximized comparative resources (e.g. oil) for expended effort (CPUE) were preferentially targeted as technology allowed (Lotze et al. 2006; Schneider & Pearce 2004). Thus industrialized whaling targeted species by value and size (e.g. blue (*Balaenoptera musculus*), fin (*B. physalus*) and sei (*B. borealis*) whales) (Reeves et al. 2003; Reeves & Smith 2006; Schneider & Pearce 2004). Strong population depletions resulted in higher capture costs and less return, and eventually even advanced capture technology could not compensate (Schneider & Pearce 2004). Increases in whaling nation GDP and individual incomes made them less reliant on natural resource extraction and more favorable of alternative products, such as petrochemical and vegetable oils (Schneider

& Pearce 2004). Schneider and Pearce (2004) propose these economic factors had an earlier and stronger protective effect on cetacean exploitation than management measures.

Economic drivers still influence pinniped exploitation in Canada. European trade bans spurred regulations on white coat harp (*Pagophilus groenlandicus*) and blueback hooded (*Cystophora cristata*) seal takes in 1983 and completely banned the import of seal products in 2009 (European Commission 2009; Fisheries and Oceans Canada 2003), resulting in drops in pelt prices and quota fulfillment (Fisheries and Oceans Canada 2006). In our study, economic influences were partly included in Trade Management and Implementation Time, however, these were not significant and did not capture non-regulation-based market influences. Inclusion of variables that incorporated price or CPUE and their changes over time could provide insight on the relative influence of economic factors on marine mammal recoveries.

3.4.2 Possible Critical Factors

Several possible critical factors showed some influence on marine mammal recovery. First, while populations in areas with higher Mean Habitat Disturbance were more likely Recovering, high Maximum Habitat Disturbance within their range reduced recovery probability, especially in pinnipeds. This finding is in line with the literature suggesting habitat loss and disturbance are among the greatest threats to many marine species (Halpern et al. 2008). To identify major causes, it could be useful to unpack Halpern et al.'s (2008) cumulative habitat impact score and examine the effect of each disturbance component on recovery. Further investigation of the specific location of Maximum Habitat Disturbance relative to important features in the population's habitat (e.g. nursery areas, rookeries or key foraging grounds) could also offer important insight on population recovery (Bailey & Thompson 2009; Hooker et al. 1999; Kaschner et al. 2006).

Another possible critical factor was Species Type, which provided a rough measure of phylogenetic relatedness and appeared to be linked to life history characteristics. Pinnipeds were more likely Recovering than cetaceans. A likely contributor is pinnipeds' high average growth rate ($r_{\max} = 0.12$ for pinnipeds vs. 0.04 for cetaceans (Wade 1998)). In our models, only Age at Maturity, which is linked to r_{\max} , was identified as a possible critical factor. It

was negatively linked to recovery and moderately to highly correlated with Species Type (-0.664). The pinnipeds included in our study had a lower Age of Maturity (mean = 4.8 years) compared to cetaceans (mean = 10.3 years). The other marine mammals (polar bears, sea otters) matured at ages comparable to the pinnipeds and were all Recovering. Faster maturation typically means faster population growth, which likely contributed to higher probability of recovery in pinnipeds and other marine mammals compared to cetaceans. This may also explain some of the remarkable recoveries exhibited by Northern elephant seal, numerous fur seal (Antarctic (*A. gazella*), Afro-Australian and Guadalupe (*A. townsendi*)), California sea lion (*Zalophus californianus*), and sea otter populations in this study. Fritz and Purvis' (2010) new measure of phylogenetic signal strength and pattern for binary traits (e.g. Recovery Status), *D*, shows promise for representing phylogenetic relatedness in future models.

In our study, Species Type was also highly correlated with the Importance of Social Interactions. However much is still unknown about the importance of social interaction and culture in marine mammals, and how they influence population dynamics. Surprisingly, other life history traits were not significant in our models, possibly due to the specification of the response variable over a three-generation time period. However, even with high correlation between generation time and Species Type (-0.724) and Age at Maturity (0.803) these variables appeared to be possible critical factors. As more and better population abundance data become available, a refined analysis of the relationship between recovery and life history traits would be possible.

Three remaining variables, Direct Exploitation, Bycatch and Habitat Area, were either excluded from our analysis or not critical to recovery. First, Direct Exploitation was excluded due to high correlation with Exploitation Management, yet Exploitation Management was not significant in any models. Previous studies suggested exploitation is the most important threat to marine populations, many of which are still heavily exploited (Hutchings & Reynolds 2004; Roberts & Hawkins 1999), while terrestrial populations tend to be more affected by habitat disturbance (Cardillo et al. 2008, 2005, 2004). Although many marine mammal populations are still directly exploited, this often occurs at much lower levels than

in the past, which perhaps makes them more comparable to terrestrial mammals than other marine species still undergoing intense exploitation (e.g. bony fish, sharks) (Dulvy et al. 2008; Ferretti et al. 2010; Fisher & Owens 2004; Hutchings et al. 2010; Worm et al. 2009). Second, Bycatch has been cited as a critical factor for numerous marine mammal populations, but it was not significant in our models, perhaps being important on a more case-specific basis (see Section 3.4.3). For both Direct Exploitation and Bycatch a more refined analysis incorporating exploitation intensity may be useful. Third, Habitat Area has often been dismissed as a critical factor for marine species because of the high connectivity of marine systems that should minimize habitat fragmentation (Gerber 1998). Our results support this assertion. However, including a depth component might be a useful additional investigation.

3.4.3 Differences between Cetaceans and Pinnipeds

Separate models for cetaceans and pinnipeds revealed some interesting differences between these two groups, despite low sample sizes. For cetaceans, Dominant Habitat and Weight were important with more coastal and larger whales Recovering. The Dominant Habitat has been discussed above, and the effect of depletions by size to maximize economic returns is perhaps best documented for the cetaceans. As large, more valuable species were sequentially depleted, smaller species were increasingly targeted (Reeves & Smith 2006). At the same time, larger species were afforded earlier and better protection (Gerber 1998; Perrin 1999; Reeves et al. 2002). Interestingly, this is the opposite pattern to what we often observe in fisheries, where larger body size is associated with increased decline and non-recovery (Hutchings & Reynolds 2004). This effect of Weight likely disappeared in the overall marine mammal analyses with the addition of the much smaller and faster growing pinnipeds and other mammal species.

The pinniped models revealed Mean and Maximum Habitat Disturbance and Trophic Level as critical factors to recovery. The habitat disturbance effects have been discussed above, however Trophic Level also appeared to be a possible critical factor for pinniped recovery. Overall, recovering probability decreased linearly with increasing trophic level (Figure 3.2), similar to relationships between trophic level and extinction risk (Cardillo et al. 2004; Purvis

et al. 2000). However, the trophic level range among the pinniped populations was quite small (3.7-4.3), which may have minimized its effect in the overall marine mammal models.

Overall, the amount of variation in the data explained by the good pinniped models was only moderate, and Non-recovering populations did not adhere well to the model assumption of normality. Thus, there likely are other important factors influencing pinniped recovery. In a case-by case examination of Non-recovering populations, we found additional possible reasons for lack of recovery, including incidental bycatch and entanglement in marine debris (Hawaiian monk seals, Steller sea lions) (Carretta et al. 2008), competition with commercial fisheries for prey (Hawaiian monk seals, Steller sea lions, northern fur seals) (Carretta et al. 2008), increased predation pressure (Hawaiian monk seals, Steller sea lions) (Carretta et al. 2008), and large scale environmental changes (Steller sea lions) (Carretta et al. 2008). For New Zealand sea lions in the Auckland Islands, bycatch in commercial squid trawl fisheries coincided with important pupping and lactation times from the 1970s onward, and mass mortality events in 1998, 2002 and 2003 affected recovery (New Zealand Department of Conservation 2009). For Hawaiian monk seals, human disturbance on beaches, depletion of terrestrial resting and pupping habitat from coastal erosion, and male mobbing and aggression towards females and young may also hamper population recovery (Carretta et al. 2008).

3.4.4 Caveats

There are three caveats that need to be considered regarding our study. First, we selected populations with the best abundance data available, which resulted in a small sample size and taxonomic as well as geographic data gaps. Small cetaceans, in particular river dolphins and beaked whales, sirenians, and Antarctic phocids were not represented in our sample. These data poor species have more offshore distributions or are cryptic. In many cases they are subject to exploitation for bait or food (numerous dolphins and Amazonian and West African manatees), virtually no management (most beaked whales and river dolphins), and intense habitat disturbance (Clapham & Van Waerebeek 2007; Marsh et al. 2002; Reeves et al. 2003; Reijnders et al. 1993; Reynolds et al. 2009). Abundance data are likely to increase for many species in the next 5–15 years, especially for beaked whales that are increasingly monitored

with respect to acoustic impacts of sonar and oil and gas exploration. However, for species in developing nations where management funds are scarce (LePrestre 2002), data may remain scarce.

Second, this study did not cover all possible critical factors, however, based on our results we suggested additional variables that would provide important insight (e.g. economic factors, individual habitat disturbance components, and continuous indices for management, exploitation and bycatch). Latitude, interspecific interactions, and environmental variables such as SST or El Niño (Gerber & Hilborn 2001) may also be important factors for recovery. Our focus was on general critical factors for recovery across marine mammals, however, more species- or situation-specific studies may be necessary to identify critical factors for individual populations.

Finally, we reemphasize that our definition of “Recovering” does not necessarily mean a recovery to a pre-exploitation abundance level or carrying capacity. The critical factors in this study are related to statistically significant population increases that indicate a population is Recovering. Continued time and action are likely necessary for a number of recovering populations still at low levels, such as the North Atlantic right whale, before they reach designated management recovery goals. Moreover, as better data become available, it would be possible to analyze the critical factors to the rate or magnitude of recovery, not just whether or not populations are increasing.

3.5 CONCLUSION

The patterns and drivers of recovery in formerly exploited marine populations are of increasing interest to science, conservation and management. Using the best available population data with significant abundance trends, we identified intrinsic and extrinsic factors critical to marine mammal recovery that reflect the ongoing importance of the legacy proximity to humans in determining historical exploitation and conservation patterns. Marine mammals in coastal, disturbed areas had a higher probability of recovering compared to

offshore populations. Although the high visibility of these populations has resulted in heavy past exploitation and strong population declines, it also contributed to earlier awareness and conservation. At the same time, many offshore, highly migratory, transboundary and cryptic species have not received much management attention and require more monitoring and assessment, especially in data poor areas. Our results further suggest that earlier maturing populations, pinnipeds (compared to cetaceans), and populations in areas of low maximum habitat disturbance also have a higher probability of recovering. More attention to the overlap of specific habitat disturbances and critical habitat areas would be useful to better inform marine mammal management. The possible importance of trophic level to pinniped recovery suggests a need for focusing on higher trophic level species and more research into how species and trophic interactions influence marine mammal population dynamics. Overall, our results help to broaden and deepen our understanding of the critical factors to marine mammal recovery, and marine species in general, with implications for marine management, conservation, and future research.

CHAPTER 4 CONCLUSION

4.1 SUMMARY

In this thesis, I conducted the first quantitative global assessment of marine mammals at the population level in terms of available data, population trends, recovery and critical factors for recovery. I did this by building a population abundance database with publicly available data, estimating abundance trends with robust statistical methods, and classifying recovery status (Chapter 2). Moreover, I examined the connection between the magnitude of historical population decline and subsequent recovery. I employed a variety of modeling approaches to examine the relationship between hypothesized critical factors (correlates or drivers) and recovery status using those marine mammal populations with definitive trends (Chapter 3). My findings highlighted taxonomic and geographic gaps in population-level abundance data for many marine mammal species. I found that analyzing population trends across time periods scaled to life history (via generation time) allowed for the inclusion of the largest number and variety of marine mammal populations, and robust statistical methods addressed uncertainty in the data. Populations in this study showed a higher proportion of recoveries at a species level (39%) than marine mammal species overall (12%) as reported by the IUCN Red List, but classifications for equivalent species matched well. Recoveries were especially common amongst pinnipeds, other marine mammals, and coastal cetaceans. My results supported previous findings in fish populations that larger declines were related to lower population recoveries (Hutchings 2000, 2001a, b; Hutchings & Reynolds 2004). In addition, I found that coastal species showed higher recovery than offshore species, even though coastal habitats often have higher mean levels of disturbance. This suggests an ongoing influence of the proximity to humans as an important factor for recovery. Accessibility and visibility of marine mammal populations in coastal areas shaped patterns of exploitation, but also of conservation. Several aspects of marine mammal recovery require more examination, including differences in factors critical to pinniped and cetacean recovery. In the following sections, will discuss limitations and recommendations for future research, as well as the

contributions of this thesis to methodologies, recovery and population dynamics, and management.

4.2 LIMITATIONS AND RECOMMENDATIONS FOR FUTURE RESEARCH

I aimed to compare marine mammal population recovery across the largest number of available abundance datasets (Chapter 2) and statistically significant abundance trends (Chapter 3), but this approach had limitations. I used a general definition of recovery (i.e. recovering populations being those showing a statistically significant linear increase in abundance), an analysis time frame scaled to the species' life history, and robust statistical methods to draw general conclusions about recovery status and critical factors to recovery. Using only populations with significant trends increased confidence in the data, but limited sample sizes in Chapter 3, especially in the cetacean and pinniped subgroups.

One could use alternative approaches to assess recovery and its relationship with potential critical factors. For example, one could use the abundance time series robust regression slopes themselves (i.e. rates of population increase or decline, standardized or not), regardless of significance, as continuous response variables (Chapter 3). Essentially this would avoid selecting a level of significance (e.g. p-values) for classifying population trends and recovery status (Chapter 2). These slopes could also advise on the degree of impact of critical factors. In addition, it would be useful to examine trends on the log scale while also adjusting for the species' respective intrinsic rates of growth, r_{\max} . While this scale was investigated as part of preliminary analysis it would be beneficial to revisit for comparative purposes. Given that the data in this study were already standardized to deal with sample size and variance, it is not obvious a priori if these alternative approaches would lead to different conclusions, but they would be insightful nonetheless. Both will be explored imminently. It is my belief that a sensitivity analysis is paramount to ensure the rigor of conclusions, and this work will be reflected in publications.

The conclusions of this study only pertain to the populations in the sample, which underrepresented some taxa and geographical areas, namely beaked whales, river dolphins and sirenians, and marine mammals in equatorial and developing nations. With time, more data will likely become available for certain populations, especially beaked whales impacted by military sonar and sonic testing in the oil and gas industry (Jepson et al. 2003; Taylor et al. 2007) and polar species expected to be impacted by climate change and expanding fisheries (Laidre et al. 2008; Lake et al. 2008; Southwell et al. 2008). However, with cryptic behavior and lack of management and monitoring (Lefebvre et al. 2009; LePrestre 2002; Marsh et al. 2002; Reeves et al. 1996; Reeves et al. 2003; Silva & Araujo 2001; Taylor et al. 2007), sparse or non-existent data will likely continue to be a problem for other marine mammal populations. In many cases continued use of either (1) combinations of quantitative and qualitative analyses or (2) quantitative analysis with less certainty may be necessary to classify population trends. Over time, more data and longer time series should allow for analysis of factors critical to the rate or magnitude of recovery, and not just whether or not populations are increasing. It should also enable analysis of recovery over set time periods (e.g. 1970-1990 or 20 year range), rather than time periods defined by generation time, which we used partly because of inconsistent intervals, time periods and quality of population abundance data.

Other researchers have examined population dynamics and recovery in subgroupings of marine mammals and individual populations (e.g. de Little et al. 2007; Leaper et al. 2006; McMahon et al. 2005). These studies complement my general conclusions about a broad selection of marine mammal populations by addressing situation-specific threats and critical factors. I did not include all possible critical factors to recovery in marine mammals in the analyses due to data limitation and feasibility, and the models only explained a moderate amount of variation in the data. However, I summarized variables that could provide additional insight into recovery in future analyses, including CPUE, economic factors (e.g. market price, harvesting or range state GDP), latitude, specific habitat disturbance type, continuous indices of management, exploitation and bycatch, measures of interspecific interactions, and more direct measures of environmental variables such as SST or El Niño anomalies.

4.3 METHODOLOGICAL CONTRIBUTIONS

This thesis summarized the publicly available marine mammal population data and abundance trends with a fairly high level of confidence. As there are no publicly available global marine mammal population databases, I considerably expanded a database first started by Kristin Kaschner and Line Bang Christensen. I benefited greatly from data sharing with many researchers and I hope to make this database available for future projects to use. I also expanded Kaschner's method for incorporating both quantitative and qualitative error (Kaschner 2004) into quantitative analyses, allowing for better comparison of abundance data of differing qualities through data weighting. Despite criticisms of marine mammal data quality (Taylor et al. 2007), robust linear regression allowed me to combine across datasets and down-weight high influence outliers to increase the likelihood of detecting significant abundance trend signals (Chapter 2) (Wilkinson & Task Force on Statistical Inference 1999; Wright & London 2009). It offered an alternative approach to complex Bayesian or state-space models (e.g. Thomas et al. 2005).

I was also able to uncover statistically significant relationships between hypothesized critical factors and recovery using robust methods (Chapter 3). The use of a variety of models aided in data inspection (classification trees) (Clark & Pregibon 1992; Crawley 2003), allowed for detection of any non-linear relationships (GAMs) (Wood 2006), and permitted simplified analysis of linear model relationships (GLMs) (McCullagh & Nelder 1989). Consideration of a collection of good model results across multiple model types allowed me to consider the biological and statistical relevance of each model (Buckland et al. 1997; Burnham & Anderson 2002; Johnson & Omland 2004) in a simplified approximation of multi-model inference (Burnham & Anderson 2002; Cantoni et al. 2007).

4.4 CONTRIBUTIONS TO RECOVERY AND POPULATION DYNAMICS

This thesis expands understanding of recovery in marine animal populations and mammals in general. Previous initiatives (e.g. IUCN Red List) and studies have focused on identifying

threats and factors contributing to extinction risk and decline in marine mammals. Quantitative studies of mammals typically excluded the marine component (Cardillo et al. 2008, 2005) or did not provide an overview of marine mammals as a whole (e.g. de Little et al. 2007; Leaper et al. 2006; McMahon et al. 2005). Studies on aquatic species focused mainly on fish dynamics (e.g. Garcia et al. 2007; Hutchings 2000, 2001a, b; Hutchings et al. 2010; Hutchings & Reynolds 2004; Musik 1999; Olden et al. 2007; Reynolds et al. 2005). Recovery has received comparatively less focus in population dynamics studies, but interest is increasing. This thesis contributes to understanding of the quality of marine mammal population-level abundance data available for analysis, the proportion of populations that are recovering, the magnitude of recovery relative to historical declines (Chapter 2), and the factors critical to recovery in marine mammal populations (Chapter 3), while identifying important knowledge gaps and areas of future research.

4.5 MANAGEMENT IMPLICATIONS

Although management or management implementation time did not show direct links to population recovery in this study, they are likely indirectly linked and are therefore important to consider. Many marine mammal populations have non-significant or unknown abundance trends, data gaps exist, and numerous populations are still not recovering (Section 4.1, Chapter 2). Thus abundance monitoring and population modeling remain important ventures, especially for more offshore, equatorial, polar and cryptic species. Industrial development and concerns about climate change impacts may motivate increased study and monitoring of some of these species (Section 4.2). However, more international cooperation and attention is needed to manage and protect offshore, highly migratory, transboundary, and cryptic species (especially small cetaceans). These populations may be less effectively regulated in international waters than more nearshore populations, and have been subject to more recent exploitation and less study and protection (Perrin 1999). The identification of high disturbance areas and their relationship to critical habitat features and migration routes is also increasingly important (Bailey & Thompson 2009). Special attention should be paid to populations with large abundance declines as they are likely more susceptible to low

magnitudes of recovery, and their recovery may be less predictable. Pinnipeds may require less protective management than cetaceans, likely due to their earlier maturation and faster life histories in general (Wade 1998). However, case-by-case assessments of threats are valuable, as exceptions certainly exist (e.g. Hawaiian monk seals, New Zealand seal lions, Western Alaskan Steller sea lions and subantarctic fur seals at Marion Island). My results indicate that cetaceans and pinnipeds may require different management foci. Increased protection for offshore populations, and especially smaller-bodied species, may be more important for cetaceans. Protection of populations with areas of especially high disturbance in their range, especially if they are of higher trophic levels, may be more important for pinnipeds. With small sample sizes in this study, more investigation into these differences is required.

More attention may also be needed to the role of not only management, but also its interaction with economic factors in influencing marine mammal population dynamics (Schneider & Pearce 2004). Even after exploitation ends, historical exploitation and conservation patterns, as well as economic trends, appear to influence current patterns of recovery in marine mammals. The economic return of harvesting various marine mammals, market demand, and economic status of the harvesting countries or range states is important to consider (Schneider & Pearce 2004), both in future studies and management planning processes.

Finally, depending on one's management goals for recovery, such as attainment of maximum sustainable yield level (MSYL) or a historical population level, the results of this thesis should be interpreted accordingly. A recovering population may still be at a low level compared to historical population size and continued time and action are likely necessary to reach recovery abundance targets.

4.6 CONCLUSIONS

Of the populations for which I was able to obtain good abundance data, many marine mammal populations (35%) appear to be recovering, especially pinnipeds, coastal cetaceans and other marine mammals. However, population abundance and trend data are still lacking for many populations and species. Larger population declines are connected to smaller, and more variable, recoveries. Moreover, the proximity to humans is an important factor for marine mammal recovery. Earlier exploitation and depletion as well as conservation efforts (and possibly economic stimulus for these actions) likely produced a higher probability of recovery in coastal habitats, despite higher levels of disturbance. As more data become available, research is required into a number of other factors that are possibly important to recovery in marine mammals. It is my hope that this synthesis of marine mammal population data and critical factors to recovery provides useful tools for further study of marine mammal population trends and recoveries and contributes to better management and conservation of marine mammals.

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APPENDIX I.A Abundance Data Sources Information for Study Populations

For each population, denoted by a numeric area code (Population Area ID) and area description, abundance data sources are listed along with the data collection and/or additional analysis methods used to obtain the population abundance estimates. Abundance Confidence ID (ACID) provides an uncertainty rank (1:6, 1=lowest, 6=highest).
CPUE = catch per unit effort

Species common name	Species scientific name	Population Area ID	Population area description	Abundance estimate sources	Abundance data collection & analysis methods (as reported in sources)	ACID
Afro-Australian fur seal	<i>Arctocephalus pusillus</i>	41000	South Africa & Namibia	(Arnould 2002; Arnould et al. 2003; Butterworth et al. 1995; Christensen 2006; David & van Sittert 2008; Shaughnessy 1982)	catch or CPUE, dedicated observer data, Bayesian analysis, hindcasting, unknown	4, 6
Afro-Australian fur seal	<i>Arctocephalus pusillus</i>	92000	Southern Australia	(Arnould et al. 2003; Goldworthy & Shaughnessy 1991; Kirkwood et al. 2005; Pemberton & Gales 2004; Pemberton & Kirkwood 1994; Reijnders et al. 1993; Warneke 1988; Warneke & Shaughnessy 1985)	extrapolation based on pup production, aerial surveys, land-based surveys	2, 3, 4, 6
Antarctic fur seal	<i>Arctocephalus gazella</i>	60000	Antarctica	(Arnould 2002; Christensen 2006; Guinet et al. 1994; Knox 1994; Laws 1984; Payne 1979; Reijnders et al. 1993)	dedicated observer data, unknown	2, 6
Bearded seal	<i>Erignathus barbatus</i>	31302	Bering Sea & Chukchi Sea	(Angliss & Lodge 2002; Bonner 1981; Christensen 2006; Perry et al. 1999)	catch or CPUE, Bayesian analysis, hindcasting, unknown	2, 3, 4
Beluga whale	<i>Delphinapterus leucas</i>	10000	Global	(Christensen 2006; Culik 2002; IWC 2000a)	catch or CPUE, Bayesian analysis, hindcasting, combined total based on literature, unknown	2, 3, 4, 5

Species common name	Species scientific name	Population Area ID	Population area description	Abundance estimate sources	Abundance data collection & analysis methods (as reported in sources)	ACID
Beluga whale	<i>Delphinapterus leucas</i>	11001	Cumberland Sound (Southeast Baffin Island)	(Brodie 1971; COSEWIC 2004; IWC 2000a; Mitchell & Reeves 1981; Sergeant & Brodie 1975)	aerial surveys, on land census, unknown	2, 5, 6
Beluga whale	<i>Delphinapterus leucas</i>	11500	Eastern High Arctic – Baffin Bay	(COSEWIC 2004; Innes & Stewart 2002; Mitchell & Reeves 1981; Richard & Orr 1986)	aerial surveys	2, 3
Beluga whale	<i>Delphinapterus leucas</i>	22112	Eastern Hudson Bay	(Bourdages et al. 2002; Christensen 2006; Reeves & Mitchell 1987)	aerial surveys	4, 6
Beluga whale	<i>Delphinapterus leucas</i>	36004	Cook Inlet, Alaska	(Angliss & Allen 2009)	aerial surveys	2, 3
Beluga whale	<i>Delphinapterus leucas</i>	36005	Bristol Bay, Alaska	(Angliss & Allen 2009; Angliss & Lodge 2002)	aerial surveys, unknown	2, 4, 5
Blue whale	<i>Balaenoptera musculus</i>	12000	Southern Hemisphere	(Christensen 2006; IWC 2000b; Perry et al. 1999)	catch or CPUE, Bayesian analysis, hindcasting, unknown	2, 3, 4, 6
Blue whale	<i>Balaenoptera musculus</i>	20000	North Atlantic	(Christensen 2006; Gambell 1976; Sears 2002)	catch or CPUE, Bayesian analysis, hindcasting, unknown	2, 3, 4
Blue whale	<i>Balaenoptera musculus</i>	30000	North Pacific	(Barlow 1995; Christensen 2006; Clapham et al. 1999; Gambell 1976; Perry et al. 1999; Sears 2002)	catch or CPUE, ship &/or aerial surveys, photo-identification & mark-recapture model, Bayesian analysis, hindcasting, unknown	2, 3, 4, 6
Blue whale	<i>Balaenoptera musculus</i>	60000	Antarctica	(Branch et al. 2004; Branch & Raydemeyer 2003)	ship &/or aerial surveys, Bayesian analysis	2, 3

Species common name	Species scientific name	Population Area ID	Population area description	Abundance estimate sources	Abundance data collection & analysis methods (as reported in sources)	ACID
Bowhead whale	<i>Balaena mysticetus</i>	11000	Arctic Basin	(Christensen 2006; Finley 2001; Hacquebord & Leinenga 1994; Weslawski et al. 2000; Woodby & Botkin 1993)	catch or CPUE, bycatch study, Bayesian analysis, hindcasting	2, 6
Bowhead whale	<i>Balaena mysticetus</i>	22110	Hudson Bay	(Finley 2001; Rugh & Shelden 2002; Woodby & Botkin 1993)	ship &/or aerial surveys, unknown	2, 6
Bowhead whale	<i>Balaena mysticetus</i>	22200	Davis Strait	(Finley 1990, 2001; Mitchell & Reeves 1981; Shelden & Rugh 1995)	combined total based on literature, photo-identification & mark-recapture model, unknown	4, 6
Bowhead whale	<i>Balaena mysticetus</i>	31304	Western Arctic	(Angliss & Outlaw 2008; George et al. 2004; Klinowska 1991; Reeves & Leatherwood 1985; Tillman 1984; Woodby & Botkin 1993)	on land census, acoustic surveys, extrapolation, unknown	2, 3, 4
Bryde's whale	<i>Balaenoptera edeni</i>	12000	Southern Hemisphere	(Christensen 2006; Ohsumi 1981; Tamura & Ohsumi 1999)	catch or CPUE, Bayesian analysis, hindcasting, unknown	2, 6
Bryde's whale	<i>Balaenoptera edeni</i>	32000	Western North Pacific	(Holt 1986; IWC 1997; Kato 2002; Miyashita 1986)	catch or CPUE, ship surveys	2, 5
California sea lion	<i>Zalophus californianus</i>	10000	Global	(Christensen 2006; Heath 2002)	catch or CPUE, on land census, Bayesian analysis, hindcasting, unknown	2, 3, 6

Species common name	Species scientific name	Population Area ID	Population area description	Abundance estimate sources	Abundance data collection & analysis methods (as reported in sources)	ACID
California sea lion	<i>Zalophus californianus</i>	31000	Northeast Pacific (California)	(Carretta et al. 2008; Christensen 2006)	catch or CPUE, extrapolation based on pup production, regression analysis, Bayesian analysis, hindcasting ship surveys	2, 4, 5
Common bottlenose dolphin	<i>Tursiops truncatus</i>	17500	Eastern Tropical Pacific	(Gerrodette et al. 2008)		3
Fin whale	<i>Balaenoptera physalus</i>	12000	Southern Hemisphere	(Christensen 2006; Perry et al. 1999)	catch or CPUE, on land census, Bayesian analysis, hindcasting genetic analysis, hindcasting, unknown	2, 3, 4
Fin whale	<i>Balaenoptera physalus</i>	20000	North Atlantic	(IWC 2004; Perry et al. 1999; Roman & Palumbi 2003)	catch or CPUE, on land census, Bayesian analysis, hindcasting	2, 5, 6
Fin whale	<i>Balaenoptera physalus</i>	30000	North Pacific	(Christensen 2006; Perry et al. 1999)	catch or CPUE, on land census, Bayesian analysis, hindcasting land & aerial surveys	2, 3
Florida manatee	<i>Trichechus manatus</i>	22900	Florida (East and West Coasts)	(USFWS 2001)	land & aerial surveys	4
Gray whale	<i>Eschrichtius robustus</i>	31000	Northeast Pacific	(Alter et al. 2007; Butterworth et al. 2002; Henderson 1984; Reilly 1981, 1992; Rugh et al. 2005; Scammon 1874; Swartz et al. 2006; Wade & Perryman 2002)	combined total based on literature, land survey, genetic analysis, unknown	1, 2, 5, 6
Gray whale	<i>Eschrichtius robustus</i>	32000	Northwest Pacific	(Klinowska 1991; Swartz et al. 2006; Vladimirov 1994; Weller et al. 2002)	combined total based on literature, hindcasting, unknown	4, 5

Species common name	Species scientific name	Population Area ID	Population area description	Abundance estimate sources	Abundance data collection & analysis methods (as reported in sources)	ACID
Grey seal	<i>Halichoerus grypus</i>	21000	Great Britain (Combined)	(Beddington et al. 1985; Hiby et al. 1992; Reijnders et al. 1993; Thomas & Harwood 2008)	extrapolation based on pup production, age or stage-based modeling, Bayesian analysis, unknown	2, 6
Grey seal	<i>Halichoerus grypus</i>	21100	Baltic Sea	(Harding & Härkönen 1999; Hiby et al. 2001; ICES 2003; Kokko et al. 1999; Reijnders et al. 1993; Stenman & Helle 1987)	catch or CPUE, bycatch study, hindcasting, age or stage-based modeling	2, 3, 4, 5
Grey seal	<i>Halichoerus grypus</i>	21110	Schleswig-Holstein, Germany	(TSEG 2002, 2009)	ship &/or aerial surveys, unknown	5, 6
Grey seal	<i>Halichoerus grypus</i>	21221	Netherlands	(TSEG 2002, 2009)	ship &/or aerial surveys, unknown	5, 6
Grey seal	<i>Halichoerus grypus</i>	21250	North Sea	(Thomas & Harwood 2008)	extrapolation based on pup production, age or stage-based model, Bayesian analysis	2, 3
Grey seal	<i>Halichoerus grypus</i>	21260	Inner Hebrides, Scotland	(Thomas & Harwood 2008)	extrapolation based on pup production, age or stage-based model, Bayesian analysis	2
Grey seal	<i>Halichoerus grypus</i>	21270	Outer Hebrides, Scotland	(Thomas & Harwood 2008)	extrapolation based on pup production, age or stage-based model, Bayesian analysis	2
Grey seal	<i>Halichoerus grypus</i>	21280	Orkney Islands, Scotland	(Thomas & Harwood 2008)	extrapolation based on pup production, age or stage-based model, Bayesian analysis	1, 2, 3

Species common name	Species scientific name	Population Area ID	Population area description	Abundance estimate sources	Abundance data collection & analysis methods (as reported in sources)	ACID
Grey seal	<i>Halichoerus grypus</i>	21530	Iceland	(Christensen 2006; Hauksson 1987; Reijnders et al. 1993)	catch or CPUE, Bayesian analysis, hindcasting, unknown	2, 3, 6
Grey seal	<i>Halichoerus grypus</i>	22000	Northwest Atlantic – Canada (Combined)	(Anonymous 1986; Thomas et al. 2008; Waring et al. 2005; Waring et al. 2003)	extrapolation based on pup production, age or stage-based model, Bayesian analysis, unknown	2, 4, 6
Grey seal	<i>Halichoerus grypus</i>	22141	Eastern Shore, Nova Scotia	(Thomas et al. 2008)	extrapolation based on pup production, age or stage-based model, Bayesian analysis	2, 3
Grey seal	<i>Halichoerus grypus</i>	22142	Sable Island, Nova Scotia	(Thomas et al. 2008)	extrapolation based on pup production, age or stage-based model, Bayesian analysis	2
Grey seal	<i>Halichoerus grypus</i>	22300	Gulf of St. Lawrence, Canada	(Thomas et al. 2008)	extrapolation based on pup production, age or stage-based model, Bayesian analysis	2
Guadalupe fur seal	<i>Arctocephalus townsendi</i>	17000	Pacific – Guadalupe Island	(Carretta et al. 2008)	on land census	6
Harbour porpoise	<i>Phocoena phocoena</i>	21250	North Sea	(Christensen 2006; Culik 2002; Hammond et al. 2002; Read 1999)	catch or CPUE, dedicated observer programs, on land census, Bayesian analysis, hindcasting	2
Harbour porpoise	<i>Phocoena phocoena</i>	31012	San Francisco – Russian River Stock, California	(Carretta et al. 2008)	aerial & ship surveys	3
Harbour porpoise	<i>Phocoena phocoena</i>	31013	Monterey Bay Stock, California	(Carretta et al. 2008)	aerial & ship surveys	3

Species common name	Species scientific name	Population Area ID	Population area description	Abundance estimate sources	Abundance data collection & analysis methods (as reported in sources)	ACID
Harbour porpoise	<i>Phocoena phocoena</i>	31014	Morro Bay Stock, California	(Carretta et al. 2008)	aerial & ship surveys	3
Harbour seal	<i>Phoca vitulina</i>	21001	England (Combined)	(Lonergan et al. 2007)	aerial surveys, regression analysis	4
Harbour seal	<i>Phoca vitulina</i>	21002	Eastern Scotland	(Lonergan et al. 2007)	aerial surveys, regression analysis	4
Harbour seal	<i>Phoca vitulina</i>	21007	The Wash, England	(Lonergan et al. 2007)	aerial surveys, regression analysis	4
Harbour seal	<i>Phoca vitulina</i>	21211	Wadden Sea	(Reijnders 1992; Reineking 2002)	aerial surveys, hindcasting	4
Harbour seal	<i>Phoca vitulina</i>	21280	Northern Scotland	(Lonergan et al. 2007)	aerial surveys, regression analysis	4
Harbour seal	<i>Phoca vitulina</i>	22122	Grand Manan Island, New Brunswick	(Fowler & Stobo 2005)	aerial survey	4
Harbour seal	<i>Phoca vitulina</i>	31001	Oregon	(Brown et al. 2005)	aerial surveys, deterministic model	2, 4
Harbour seal	<i>Phoca vitulina</i>	31002	Washington (Coast)	(Jeffries et al. 2003)	aerial surveys, deterministic model	2, 4
Harbour seal	<i>Phoca vitulina</i>	31008	Washington (Inland)	(Jeffries et al. 2003)	aerial surveys, deterministic model	2, 4
Harp seal	<i>Pagophilus groenlandicus</i>	20000	West Ice, Eastern Greenland	(ICES 2008)	catch or CPUE, aerial surveys, extrapolation based on pup production, Bayesian analysis, hindcasting, unknown	2, 3, 4
Harp seal	<i>Pagophilus groenlandicus</i>	21520	White Sea, Northwest Russia	(Christensen 2006; Lavigne 2002; Sergeant 1991)	catch or CPUE, aerial surveys, extrapolation based on pup production, Bayesian analysis, hindcasting	2, 3, 4

Species common name	Species scientific name	Population Area ID	Population area description	Abundance estimate sources	Abundance data collection & analysis methods (as reported in sources)	ACID
Harp seal	<i>Pagophilus groenlandicus</i>	22000	Northwest Atlantic	(Bowen & Sergeant 1983; Hammill & Stenson 2005; Hammill & Stenson 2009; Roff & Bowen 1986; Waring et al. 2002; Warren et al. 1997)	catch or CPUE, dedicated observer programs, aerial surveys, extrapolation based on pup production, deterministic model, Bayesian analysis, hindcasting, unknown	2, 3
Hawaiian monk seal	<i>Monachus schauinslandi</i>	50000	Hawaiian Islands	(Carretta et al. 2008; Hiruki & Ragen 1992; Johnson et al. 1982; Reijnders et al. 1993; Rice 1960; Schultz et al. 2009)	land surveys, extrapolation, unknown	4, 6
Hooded seal	<i>Cystophora cristata</i>	21000	Jan Mayen Stock	(Christensen 2006; ICES 1991; Reijnders et al. 1993)	catch or CPUE, on land census, extrapolation based on pup production, Bayesian analysis, hindcasting, unknown	3, 4
Hooded seal	<i>Cystophora cristata</i>	21400	Greenland Sea	(ICES 2008)	aerial surveys, extrapolation based on pup production	2
Hooded seal	<i>Cystophora cristata</i>	22000	Northwest Atlantic Stock	(Christensen 2006; Hammill & Stenson 2006; Reijnders et al. 1993; Waring et al. 2002)	catch or CPUE, dedicated observer programs, aerial surveys, extrapolation based on pup production, Bayesian analysis, hindcasting	2, 3, 4,
Hooded seal	<i>Cystophora cristata</i>	22130	Northwest Atlantic Front	(Hammill & Stenson 2006)	aerial survey, extrapolation based on pup production	2

Species common name	Species scientific name	Population Area ID	Population area description	Abundance estimate sources	Abundance data collection & analysis methods (as reported in sources)	ACID
Hooded seal	<i>Cystophora cristata</i>	22301	Gulf of St. Lawrence	(Hammill et al. 1997; Hammill & Stenson 2006)	aerial survey, extrapolation based on pup production catch or CPUE,	1, 2, 3
Humpback whale	<i>Megaptera novaeangliae</i>	12000	Southern Hemisphere	(Christensen 2006; IWC 1996; Perry et al. 1999; Tamura & Ohsumi 1999)	dedicated observer programs, Bayesian analysis, hindcasting, unknown	2, 3, 4, 6
Humpback whale	<i>Megaptera novaeangliae</i>	20000	North Atlantic	(Christensen 2006; COSEWIC 2003; Mitchell 1973; Perry et al. 1999; Roman & Palumbi 2003; Stevick et al. 2003; Tamura & Ohsumi 1999; Waring et al. 2002; Whitehead 1987; Whitehead & Glass 1985)	catch or CPUE, dedicated observer programs, genetic analysis, extrapolation, Bayesian analysis, hindcasting, unknown	2, 3, 4, 6
Humpback whale	<i>Megaptera novaeangliae</i>	31007	U.S. West Coast	(Angliss & Outlaw 2008; Calambokidis & Barlow 2004; Calambokidis et al. 2001; Carretta et al. 2002)	photo-identification & mark-recapture models, dedicated observer programs, ship surveys	1, 2
Humpback whale	<i>Megaptera novaeangliae</i>	35000	North Pacific	(Calambokidis et al. 2008; Calambokidis et al. 1997; Christensen 2006; Johnson & Wolman 1984)	catch or CPUE, dedicated observer programs, photo-identification & mark-recapture analysis, genetic analysis, extrapolation, Bayesian analysis, hindcasting, unspecified modeling approach, unknown	2, 3, 4, 6

Species common name	Species scientific name	Population Area ID	Population area description	Abundance estimate sources	Abundance data collection & analysis methods (as reported in sources)	ACID
Killer whale	<i>Orcinus orca</i>	31006	Eastern North Pacific – Northern Residents	(Carretta et al. 2008)	photo-identification & mark-recapture analysis	3
Killer whale	<i>Orcinus orca</i>	31007	Eastern North Pacific – Southern Residents	(Carretta et al. 2008; Ford et al. 2000)	photo-identification & mark-recapture analysis	3
Killer whale	<i>Orcinus orca</i>	60000	Southern Hemisphere	(Branch & Butterworth 2001; Christensen 2006; Culik 2002; Kasamatsu et al. 1988)	catch or CPUE, dedicated observer programs, ship surveys, photo-identification & mark-recapture analysis, Bayesian analysis, hindcasting	1, 2
Minke whale (Common)	<i>Balaenoptera acutorostrata</i>	21000	Northeast Atlantic	(Skaug et al. 2004; Tamura & Ohsumi 2000a)	photo-identification, extrapolation, unknown	2, 4
Narwhal	<i>Monodon monoceros</i>	22115	Hudson Bay	(Christensen 2006; COSEWIC 2005)	catch or CPUE, aerial surveys, Bayesian analysis, hindcasting	2, 3
Narwhal	<i>Monodon monoceros</i>	21400	Baffin Bay	(Christensen 2006; COSEWIC 2005)	catch or CPUE, aerial surveys, Bayesian analysis, hindcasting	2, 3
New Zealand sea lion	<i>Phocarctos hookeri</i>	70007	Auckland Islands, NZ	(New Zealand Department of Conservation 2009)	unknown	6
New Zealand sea lion	<i>Phocarctos hookeri</i>	70008	Sandy Bay, Enderby Island (Auckland Islands), NZ	(Childerhouse & Gales 1998)	photo-identification & mark-recapture study, unknown	4, 6

Species common name	Species scientific name	Population Area ID	Population area description	Abundance estimate sources	Abundance data collection & analysis methods (as reported in sources)	ACID
North Atlantic right whale	<i>Eubalaena glacialis</i>	22000	Northwest Atlantic	(Christensen 2006; Reeves et al. 1992; Tamura & Ohsumi 2000a; Waring et al. 2007; Waring et al. 2002)	catch or CPUE, aerial surveys, photo-identification & mark-recapture analysis, extrapolation, combined total based on literature, Bayesian analysis, hindcasting	3, 4
Northern elephant seal	<i>Mirounga angustirostris</i>	10000	Global	(Hindell 2002; Reijnders et al. 1993; Stewart et al. 1994; Trites et al. 1997)	combined total based on literature, extrapolated, unknown	3, 6
Northern elephant seal	<i>Mirounga angustirostris</i>	31009	Channel Islands, California	(Carretta et al. 2002)	unknown	6
Northern elephant seal	<i>Mirounga angustirostris</i>	31010	Central California	(Carretta et al. 2002)	unknown	6
Northern elephant seal	<i>Mirounga angustirostris</i>	31011	California (Total)	(Carretta et al. 2002; Stewart et al. 1994)	dedicated observer programs, unknown	2, 6
Northern fur seal	<i>Callorhinus ursinus</i>	10000	Global	(Christensen 2006; Reijnders et al. 1993; Trites et al. 1997)	catch or CPUE, combined total based on literature, Bayesian analysis, hindcasting, unknown	4, 6
Northern fur seal	<i>Callorhinus ursinus</i>	17500	Eastern Pacific Stock	(Angliss & Lodge 2002; Angliss & Outlaw 2008; Carretta et al. 2002)	unknown	4, 6
Northern fur seal	<i>Callorhinus ursinus</i>	31003	Pribilof Islands, Alaska	(Anonymous 2004; Christensen 2006; COSEWIC 2006; Roppel & Davey 1965; Sinclair 1994a, b; Towell & Ream 2006)	catch or CPUE, aerial surveys, extrapolation based on pup production, Bayesian analysis, hindcasting, unknown	3, 4, 6

Species common name	Species scientific name	Population Area ID	Population area description	Abundance estimate sources	Abundance data collection & analysis methods (as reported in sources)	ACID
Northern fur seal	<i>Callorhinus ursinus</i>	31004	San Miguel Island, California	(Reijnders et al. 1993; Sinclair 1994a, b; Testa 2007, 2008)	extrapolation based on pup production, unknown	4, 6
Pantropical spotted dolphin	<i>Stenella attenuata</i>	17500	Eastern Tropical Pacific - Offshore (Combined)	(Gerrodette et al. 2008; Smith 1983)	catch or CPUE, bycatch study, ship surveys, extrapolation, hindcasting	4
Pantropical spotted dolphin	<i>Stenella attenuata</i>	17501	Eastern Tropical Pacific – Coastal Stock	(Gerrodette et al. 2008)	ship surveys	3
Pantropical spotted dolphin	<i>Stenella attenuata</i>	31000	Eastern Tropical Pacific – Northern Offshore Stock	(Gerrodette & Forcada 2005; Gerrodette et al. 2008)	ship surveys	2, 3
Pantropical spotted dolphin	<i>Stenella attenuata</i>	32400	Japanese Waters	(Christensen 2006; Miyashita 1993a, b)	catch or CPUE, ship surveys, Bayesian analysis, hindcasting	2
Pantropical Spotted dolphin	<i>Stenella attenuata</i>	52000	Eastern Tropical Pacific – Western/Southern Stock	(Gerrodette et al. 2008)	ship surveys	3
Polar bear	<i>Ursus maritimus</i>	22113	Manitoba, Canada	(Stirling et al. 2004)	aerial surveys	4
Polar bear	<i>Ursus maritimus</i>	22114	Ontario, Canada	(Stirling et al. 2004)	aerial surveys	4
Polar bear	<i>Ursus maritimus</i>	22115	Western Hudson Bay, Churchill & Cape Tatnam Study Area (Manitoba, Canada)	(Lunn et al. 1997)	photo-identification & mark-recapture study	1, 2

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Ribbon seal	<i>Histiophoca fasciata</i>	10000	Global	(Angliss & Lodge 2002; Christensen 2006)	catch or CPUE, combined estimate based on literature, Bayesian analysis, hindcasting, unknown	3, 4, 6
Ribbon seal	<i>Histiophoca fasciata</i>	31100	Bering Sea	(Angliss & Lodge 2002; Boveng et al. 2008; Burns 1994; Fedoseev 2002)	aerial surveys, extrapolation, unknown	3, 4, 6
Ribbon seal	<i>Histiophoca fasciata</i>	31101	Bering Sea & Sea of Okhotsk	(Boveng et al. 2008; Reijnders et al. 1993)	aerial surveys, extrapolation, unknown	2, 4, 6
Ribbon seal	<i>Histiophoca fasciata</i>	31102	Western Bering Sea	(Boveng et al. 2008; Fedoseev 2002)	aerial surveys, unknown	3, 4
Ribbon seal	<i>Histiophoca fasciata</i>	31103	Western Bering Sea & Sea of Okhotsk	(Boveng et al. 2008)	aerial surveys	3, 4
Ribbon seal	<i>Histiophoca fasciata</i>	32200	Sea of Okhotsk	(Boveng et al. 2008; Fedoseev 2002; Mizuno et al. 2002)	aerial surveys, extrapolation, unknown	4, 6
Ringed seal	<i>Pusa hispida</i>	10000	Global	(Christensen 2006; Frost & Lowry 1981; Reijnders et al. 1993; Trites et al. 1997)	catch or CPUE, combined estimate based on literature, Bayesian analysis, hindcasting, unknown	2, 4, 6
Ringed seal	<i>Pusa hispida</i>	21100	Baltic Sea	(Frost & Lowry 1981; Harding & Härkönen 1999; Härkönen et al. 1998; Kokko et al. 1999; Reijnders et al. 1993)	catch or CPUE, aerial surveys, age or stage-based modeling, hindcasting, unknown	3, 4
Risso's dolphin	<i>Grampus griseus</i>	17500	Eastern Tropical Pacific	(Gerrodette et al. 2008)	ship surveys	3
Rough-toothed dolphin	<i>Steno bredanensis</i>	17500	Eastern Tropical Pacific	(Gerrodette et al. 2008)	ship surveys	3

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Sea otter	<i>Enhydra lutris</i>	30000	North Pacific	(Johnson 1982; Kenyon 1969; Sea Otter Recovery Team 2007)	unknown	4, 6
Sea otter	<i>Enhydra lutris</i>	31002	Washington	(USFWS 2008b)	aerial, land & ship surveys, unspecified modeling approach, unknown	2, 4, 6
Sea otter	<i>Enhydra lutris</i>	31005	British Columbia	(Estes 1990; Nichol et al. 2005; Sea Otter Recovery Team 2007; Watson 1993)	aerial & ship surveys, unknown	4, 6
Sea otter	<i>Enhydra lutris</i>	31011	California	(Bryant 1916; Laidre et al. 2001; USFWS 2008c)	aerial & land surveys, unknown	4, 6
Sea otter	<i>Enhydra lutris</i>	31100	Bering Island, Russia	(Bodkin et al. 1995)	aerial surveys, unknown	4, 5
Sea otter	<i>Enhydra lutris</i>	36001	Prince William Sound, Alaska	(Bodkin et al. 1995; Bodkin & Monson 2003)	aerial & land surveys, unknown	4
Sea otter	<i>Enhydra lutris</i>	38000	Aleutian Archipelago	(Burn et al. 2003; Doroff et al. 2003; Estes et al. 2005)	aerial & ship surveys, unknown	2, 4
Sea otter	<i>Enhydra lutris</i>	41000	Southeast Alaska	(USFWS 2008a)	unknown	6
Sei whale	<i>Balaenoptera borealis</i>	10000	Global	(Christensen 2006; Trites et al. 1997)	catch or CPUE, combined total based on literature, Bayesian analysis, hindcasting	2, 3, 4
Sei whale	<i>Balaenoptera borealis</i>	12000	Southern Hemisphere	(Christensen 2006; Gambell 1985; Horwood 2002; Klinowska 1991; Perry et al. 1999; Tamura & Ohsumi 2000b)	catch or CPUE, ship surveys, extrapolation, Bayesian analysis, hindcasting, unknown	2, 3, 4, 6
Sei whale	<i>Balaenoptera borealis</i>	20000	North Atlantic	(Christensen 2006; Perry et al. 1999; Tamura & Ohsumi 2000a)	catch or CPUE, Bayesian analysis, hindcasting	3, 4

Species common name	Species scientific name	Population Area ID	Population area description	Abundance estimate sources	Abundance data collection & analysis methods (as reported in sources)	ACID
Sei whale	<i>Balaenoptera borealis</i>	30000	North Pacific	(Carretta et al. 2001, 2003; Christensen 2006; Tillman 1977)	catch or CPUE, Bayesian analysis, hindcasting, unknown	2, 3, 6
Short-beaked common dolphin	<i>Delphinus delphis</i>	17500	Eastern Tropical Pacific	(Christensen 2006; Gerrodette et al. 2008)	catch or CPUE, ship surveys, Bayesian analysis, hindcasting	2, 3
Short-finned pilot whale	<i>Globicephala macrorhynchus</i>	32000	Japanese Waters	(Christensen 2006; Miyashita 1993a)	catch or CPUE, ship surveys, Bayesian analysis, hindcasting	2, 3
South American sea lion	<i>Otaria flavescens</i>	42000	Northern Patagonia	(Christensen 2006; Dans et al. 2004)	catch or CPUE, Bayesian analysis, hindcasting, unknown	2, 3, 6
Southern elephant seal	<i>Mirounga leonina</i>	10000	Global	(Christensen 2006; McMahon et al. 2005)	catch or CPUE, Bayesian analysis, hindcasting, unknown	3, 6
Southern elephant seal	<i>Mirounga leonina</i>	60003	Marion Island	(McMahon et al. 2005)	unknown	6
Southern elephant seal	<i>Mirounga leonina</i>	60004	Gough Island	(Bester et al. 2001)	unknown	6
Southern elephant seal	<i>Mirounga leonina</i>	60005	Isles Crozet & Possession Island	(Guinet et al. 1999)	unknown	6
Southern elephant seal	<i>Mirounga leonina</i>	60006	Macquarie Island	(Australian Government Department of the Environment and Heritage 2004; McMahon et al. 2005)	unknown	4, 6
Southern elephant seal	<i>Mirounga leonina</i>	60007	South Georgia	(Boyd et al. 1996; McMahon et al. 2005)	unknown	6
Southern elephant seal	<i>Mirounga leonina</i>	60008	Falkland Island	(Boyd et al. 1996; McMahon et al. 2005)	unknown	6

Species common name	Species scientific name	Population Area ID	Population area description	Abundance estimate sources	Abundance data collection & analysis methods (as reported in sources)	ACID
Southern elephant seal	<i>Mirounga leonina</i>	60009	Kerguelen Isles	(Guinet et al. 1999)	unknown	6
Southern elephant seal	<i>Mirounga leonina</i>	60010	Heard Island	(Australian Government Department of the Environment and Heritage 2004; Slip & Burton 1999)	unknown	6
Southern elephant seal	<i>Mirounga leonina</i>	60011	Peninsula Valdes	(Lewis et al. 1998)	unknown	6
Southern elephant seal	<i>Mirounga leonina</i>	60012	South Shetland Island	(Laws 1994)	unknown	6
Southern elephant seal	<i>Mirounga leonina</i>	60013	South Orkney Island	(Laws 1994)	unknown	6
Southern right whale	<i>Eubalaena australis</i>	12000	Southern Hemisphere	(Baker & Clapham 2004; Cummings 1985; IWC 2001; Perry et al. 1999)	photo-identification & mark-recapture analysis, Bayesian analysis, hindcasting, unknown	3, 5, 6
Southern right whale	<i>Eubalaena australis</i>	70006	New Zealand	(Jackson et al. 2009)	photo-identification & mark-recapture analysis, genetic analysis, Bayesian analysis, hindcasting	1, 2, 5
Sperm whale	<i>Physeter macrocephalus</i>	10000	Global	(Rice 1989; Trites et al. 1997; Whitehead 2002)	total based on literature, extrapolation	2, 3, 4
Sperm whale	<i>Physeter macrocephalus</i>	12001	Southern Hemisphere (South of 60 Degrees South)	(Branch & Butterworth 2001; Perry et al. 1999)	ship surveys, extrapolation	2, 3
Spinner dolphin	<i>Stenella longirostris</i>	17000	Eastern Tropical Pacific – Whitebelly Subspecies	(Gerrodette et al. 2008; Smith 1983)	bycatch studies, ship surveys, extrapolation, unknown	4

Species common name	Species scientific name	Population Area ID	Population area description	Abundance estimate sources	Abundance data collection & analysis methods (as reported in sources)	ACID
Spinner dolphin	<i>Stenella longirostris</i>	17500	Eastern Tropical Pacific – Eastern Subspecies	(Gerrodette & Forcada 2005; Gerrodette et al. 2008; Smith 1983; Wade & Gerrodette 1993)	bycatch studies, aerial & ship surveys, extrapolation, regression analysis, unknown	2, 3, 4
Steller sea lion	<i>Eumetopias jubatus</i>	10000	Global	(Carretta et al. 2008; Christensen 2006)	catch or CPUE, aerial surveys, Bayesian analysis, hindcasting	2, 3
Steller sea lion	<i>Eumetopias jubatus</i>	31005	British Columbia	(Fisheries and Oceans Canada 2008; Reijnders et al. 1993)	aerial surveys, unknown	4, 6
Steller sea lion	<i>Eumetopias jubatus</i>	36002	Eastern Alaska Stock (Includes SE AK, BC, WA, OR, CA)	(Angliss & Outlaw 2008; Christensen 2006)	catch or CPUE, aerial & ship surveys, Bayesian analysis, hindcasting	3, 4
Steller sea lion	<i>Eumetopias jubatus</i>	36003	Western Alaska Stock	(Angliss & Outlaw 2008; Fritz et al. 2008; Trites & Larkin 1992)	aerial, ship & land based surveys, unknown	3, 4, 6
Striped dolphin	<i>Stenella coeruleoalba</i>	17500	Eastern Tropical Pacific	(Gerrodette et al. 2008)	ship surveys	3
Sub-antarctic fur seal	<i>Arctocephalus tropicalis</i>	60003	Marion Island	(Hofmeyr et al. 1997; Hofmeyr et al. 2006)	land surveys, photo-identification & mark-recapture analysis	4
Sub-antarctic fur seal	<i>Arctocephalus tropicalis</i>	60004	Gough Island	(Bonner 1981; Reijnders et al. 1993)	unknown	6
Walrus	<i>Odobenus rosmarus</i>	31302	Chukchi Sea & Bering Sea	(Christensen 2006; Fay et al. 1989; Reijnders et al. 1993)	catch or CPUE, aerial surveys, extrapolation, Bayesian analysis, hindcasting	2, 3, 4
Walrus	<i>Odobenus rosmarus</i>	35000	Alaska - Russia	(Fay et al. 1997; Kastelein 2002)	aerial surveys, unknown	4, 6

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APPENDIX I.B Abundance Confidence ID (ACID) System – Explanation and Verification

II.B.1 Explanation

We used a modified version of an Abundance Confidence ID (ACID) rating system developed by Kaschner (2004) to incorporate both qualitative (e.g. method of data collection, reliability) and, where available, quantitative (e.g. SE, CI) information into the weighting of each abundance observation in the database. This system was developed by (Kaschner 2004), and allows for error information to be incorporated and compared between abundance estimates with and without quantitative statements of error. Quantitative statements ranked higher than qualitative statements of error (Kaschner 2004).

Since ACID is an amalgam of both Quantitative and Qualitative information, we used Table II.B.1. and the following rules to determine the ACID for each abundance observation.

- In assessing qualitative data quality, we considered the data collection or estimation method, and assigned an ACID accordingly (see Table II.B.2.).
- We ranked the ACID of each data point based on the both the Quantitative and Qualitative error information available.
- When the two categories suggest differing ACIDs, we took the average of the two as the ACID.
- In cases where a mean abundance was generated from a range of values (e.g. 2000-3000 whales), and the statistics, including the CV were generated in a similar way, an additional quantitative category ranking of 4 was adding to the averaging of the ACID (i.e. the ACID became an average of three numbers).

Table II.B.1. Abundance Confidence ID (ACID) Criteria Categories (based on Kaschner, 2004). More information on assigning Qualitative Error is contained in Table II.B.2

ACID	Label	Quantitative Error	Qualitative Error
1	very high	$CV < 0.2$	<ul style="list-style-type: none"> - Dedicated survey with known survey area (map or clearly defined area) and information about uncertainties - Photo-identification, mark-recapture analysis or dedicated acoustic survey - Modeling methods
2	high	$0.2 < CV < 0.5$	<ul style="list-style-type: none"> - Dedicated survey without definite area description or map and information about uncertainties - Photo-identification, mark-recapture analysis or dedicated acoustic survey - Dedicated observer program, dedicated aerial/ship/land-based survey or pup-count extrapolation - Modeling methods
3	medium	$CV > 0.5$	<ul style="list-style-type: none"> - Survey without area description or time period, but giving a range (e.g. minimum to maximum estimates) - Photo-identification, mark-recapture analysis or dedicated acoustic survey without range - Dedicated observer program, dedicated aerial/ship/land-based survey or pup-count extrapolation - Opportunistic survey, bycatch study, catch-per-unit effort, stranding, genetic diversity analysis, bone remains, extrapolation, or total based on literature - Modeling methods

ACID	Label	Quantitative Error	Qualitative Error
4	low	Large min/max range OR range provided and mean abundance estimate needs to be estimated	<ul style="list-style-type: none"> - Very general estimate, no specific time period or area, no uncertainties (mostly secondary references) - General global estimates - Dedicated observer program, dedicated aerial/ship/land-based survey or pup-count extrapolation - Opportunistic survey, bycatch study, catch-per-unit effort, stranding, genetic diversity analysis, bone remains, extrapolation, or total based on literature - Modeling methods
5	very low	No real range provided or “guess-estimate” OR inferred from other species	<ul style="list-style-type: none"> - Outdated general estimates - Single points estimate with no error, but with sampling method stated - Opportunistic survey, bycatch study, catch-per-unit effort, stranding, genetic diversity analysis, bone remains, extrapolation, or total based on literature - Modeling methods
6	“guess-timate”	Nothing	<ul style="list-style-type: none"> - Guesstimate or inferred from other species - Single abundance estimates with no range - No survey method recorded

Table II.B.2. Abundance Data Collection or Estimation Methods Used In Deriving Qualitative Error Rank (based on Kaschner, 2004). The method or technique used to generate an abundance estimate is often species and situation-specific, depending on species behavior, ease and appropriateness of sampling through different methods, population size/range, funding and cost-effectiveness. On a scale of 1-6, 1 is highest (best) rank, while 6 is the lowest (worst).

Sampling Method	Comments	References	Qualitative Error Rank
Photo-identification or mark-recapture analysis	Useful and accurate for small populations where all individuals are accounted for and have identifiable distinguishing markers (e.g. distinct fin shape or markings, as seen in resident killer whales) and have an equal probability of being captured and re-captured (e.g. migrating humpback whales).	(Berta et al. 2006) (Forney & Wade 2006) (Seber 1992) (Whitehead et al. 2000)	1 – 3 (depending on other error information provided)
Dedicated observer program, dedicated aerial/ship/land-based survey, acoustic survey or pup-count extrapolation	Standard methods for assessing marine mammal abundances, and can be especially useful when consistently performed measurements are collected over time. Acoustic methods are especially useful for populations that are hard to observe, may occur over vast areas and communicate acoustically (e.g. sei and blue whales).	(Berta et al. 2006) (Buckland & York 2002) (Forney & Wade 2006) (Seber 1992) (Širović et al. 2009) (Skalski et al. 2005) (Whitehead et al. 2000)	2 – 4 (depending on other error information provided)

Sampling Method	Comments	References	Qualitative Error Rank
Opportunistic survey, bycatch study, catch-per-unit effort, stranding, genetic diversity analysis, bone remains, extrapolation, or total based on literature	Likely more difficult to obtain accurate abundance estimates over time from these methods, and historical population estimates may have high uncertainty.	(Forney & Wade 2006) (Roman & Palumbi 2003)	3 – 5 (depending on other error information provided)
Modeling techniques	Different techniques may be more or less appropriate and accurate for estimating abundance of a population, depending on the situation and sample data available.	(Baker & Clapham 2004) (Skalski et al. 2005) (S.T. Buckland et al. 2007)	1 – 6 (can be any level depending on appropriateness of model for species and data available (situation specific) and resulting quantitative error estimation)
No stated method	NA	NA	6

II.B.2 Verification for Weighting Regressions

We tested whether the ACID system was an appropriate weighting scheme and comparable to weighting by SE, and it did adhere well to the available SE data. We examined the population data for the populations that did have SE information associated with their data points (n = 53 populations). We ran robust linear regressions on the scaled data, and compared the results of the regressions using two different weighting systems: (1) SE and (2) ACID. We then assess whether the regressions agreed in terms of (1) the trend information (i.e. Increasing, Stable, Decreasing or Unknown as denoted by the slope) and (2) whether the results were significant or not. We found similar signals in the ACID and SE regressions 77% of the time (Table II.B.3.). Thus, we surmised that the ACID weighting system yields a good representation of quantitative error information in the weighting of abundance data points in a regression for trend determination.

Table II.B.3. Comparisons of scaled population abundance trend results (i.e. Increasing, Decreasing, Stable or Unknown) for different types of regression for marine mammal populations with standard error information (n=53) using combinations of two types of weighting: (1) SE and (2) ACID. “Agree” and “Do Not Agree” denote whether all compared regression method trend results agree or not.

Populations	Agree	Do Not Agree	Total
N	41	12	53
%	77	23	100

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APPENDIX I.C Overview of Population Time Series: Area Descriptions, Generation Times, Time Spans, and Data Types

This Excel data table is an electronic appendix to be found at the Dalhousie University DalSpace repository at the following link: <http://dalspace.library.dal.ca/>

APPENDIX I.D R Statistical Software Code for Analyzing Marine Mammal Population Abundance Trends

```
##### LOAD DATA

setwd#locates working directory
setwd("~/Documents/Dalhousie/MMDatabase_ammagera_2009/Species_Queries/")
#sets working directory

##### RENAME DATA FOR USE IN FUNCTION

data0 <- read.csv("Gray_whale_Query_10may10.csv")
# load species .csv file with population abundance data; load separately for each species

##### SET UP DATAFRAME & REMOVE NA

data1 <- as.data.frame(data0) # create a data frame to manipulate columns
data1_2 <- subset(data1, !is.na(data1$AbundMean))
# remove values for which mean abundance value not available
data2 <- subset(data1_2, !is.na(data1_2$YearRead))
# remove values for which year value not available

# SPECIFY INFORMATION FOR EACH SPECIES

Species <- "gray_whale_scaled" # label -> character string name
Pop_int <- c(31000, 32000) # vector of populations of interest, indicated by Area_ID
GenT <- 22.9 # year
Species_com <- "Gray Whale"
Stype <- "Cetacean"
Dtype <- "Regular_scaled"

##### SET UP AN EMPTY MATRIX TO STORE REGRESSION RESULTS
# AND THEN DELIVER RESULTS TO IT
# EACH TIME A SET OF REGRESSIONS IS PERFORMED FOR A POPULATION
# calls reg.rev1() command listed later
# run four types of regression: (1) linear (lm), (2) weighted linear (lm_w),
# (3) robust (lmRob), (4) weighted robust (lmRob_w)
# 36 rows of results = 4 types of regression over 9 time periods for each population

library(MASS) # weighted regression command included in here
library(robust) # for lmRob() function

pick.pops <- function(data2, Species, Pop_int, GenT)
{
results_mat<-NULL
```

```

MinY <- c()
MaxY <- c()
Area_Des <- c()
iter <- 0
for (i in Pop_int){
iter <- iter + 1
data3 <- subset(data2, data2$AREAID==i) # organize by population Area ID
res1 <- reg.rev1(data3, Species, i, GenT, paste(Species,"_",i,"_",sep=""))
results_mat <- rbind(results_mat,res1)
# for each species, multiple population results are added in sequential order

# column labels for output data matrix
Spp_Common_Name <- rep(Species_com, 36*length(Pop_int))
Species_Type <- rep(Stype, 36*length(Pop_int))
Area_ID <- rep(Pop_int, each=36)
Area_Des[iter] <- as.character(data3$AreaDes)
GenTime <- rep(GenT, 36*length(Pop_int))
print(as.numeric(tapply(data3$YearRead, data3$AREAID, min)))
MinY[iter] <- as.numeric(tapply(data3$YearRead, data3$AREAID, min))
MaxY[iter] <- as.numeric(tapply(data3$YearRead, data3$AREAID, max))
Data_Type <- rep(Dtype, 36*length(Pop_int))
}

Area_Des <- rep(Area_Des, each=36)
MinYearPop <- rep(MinY, each=36)
MaxYearPop <- rep(MaxY, each=36)
TimePeriod_Reg <- rep(rep(1:9, each=4), length(Pop_int))
RegType <- rep(c("lm", "lm_w", "lmRob", "lmRob_w"), (9*length(Pop_int)))

results <- data.frame(Spp_Common_Name, Species_Type, Area_ID, Area_Des, GenTime,
MinYearPop, MaxYearPop, Data_Type, TimePeriod_Reg, RegType, results_mat)
return(results)
}

##### FUNCTION FOR RUNNING REGRESSIONS OF SCALED DATA → reg.rev1
# calls function regressions4, which is specified later
# runs regressions over nine time periods (tp1:tp9), specified below
# generates columns of NAs in matrix if data are insufficient to perform robust regression

reg.rev1 <- function(data3, Species, Pop_int, GenT, pdf_prefix){
  years <- data3$YearRead
  maxyear <- max(years)
  minyear <- min(years)
  years_diff <- maxyear-minyear

```

```

# 9 time periods for regressions

# tp1 --> all data
time_per1 <- years >= minyear & years <= maxyear
if ((sum(time_per1) > 2) & (length(unique(years[time_per1])) > 2))
{
  y1 <- (data3$AbundMean[time_per1] -
mean(data3$AbundMean[time_per1]))/(sqrt(var(data3$AbundMean[time_per1]))/sqrt(length
(data3$AbundMean[time_per1])))
  x1 <- (data3$YearRead[time_per1] -
mean(data3$YearRead[time_per1]))/(sqrt(var(data3$YearRead[time_per1]))/sqrt(length(data
3$YearRead[time_per1])))
  tp1_res <- regressions4(y1, x1, 1/(data3$AbundLCID[time_per1]^2),
paste(pdf_prefix,"tp1",sep=""))}
else {tp1_res <- matrix(NA,4,8)}

# tp2 --> from min abundance to present
yr_min_abund <- min(years[data3$AbundMean == min(data3$AbundMean)])
time_per2 <- years >= yr_min_abund & years <= maxyear
if ((sum(time_per2)>2) & (length(unique(years[time_per2])) > 2))
{
  y1 <- (data3$AbundMean[time_per2] -
mean(data3$AbundMean[time_per2]))/(sqrt(var(data3$AbundMean[time_per2]))/sqrt(length
(data3$AbundMean[time_per2])))
  x1 <- (data3$YearRead[time_per2] -
mean(data3$YearRead[time_per2]))/(sqrt(var(data3$YearRead[time_per2]))
/sqrt(length(data3$YearRead[time_per2])))
  tp2_res <- regressions4(y1, x1, 1/(data3$AbundLCID[time_per2]^2),
paste(pdf_prefix,"tp2",sep=""))}
else {tp2_res <- matrix(NA,4,8)}

# tp3 --> 3 generations --> present
three_gen <- maxyear - (3*GenT)
time_per3 <- years >= three_gen & years <= maxyear
if ((sum(time_per3) > 2) & (length(unique(years[time_per3])) > 2))
{
  y1 <- (data3$AbundMean[time_per3] -
mean(data3$AbundMean[time_per3]))/(sqrt(var(data3$AbundMean[time_per3]))/sqrt(length
(data3$AbundMean[time_per3])))
  x1 <- (data3$YearRead[time_per3] -
mean(data3$YearRead[time_per3]))/(sqrt(var(data3$YearRead[time_per3]))/sqrt(length(data
3$YearRead[time_per3])))
  tp3_res <- regressions4(y1 ,x1, 1/(data3$AbundLCID[time_per3]^2),
paste(pdf_prefix,"tp3",sep=""))}
else {tp3_res <- matrix(NA,4,8)}

# tp4 --> 1990--> present
time_per4 <- years >= 1990 & years <= maxyear
if ((sum(time_per4) > 2 & length(unique(years[time_per4])) > 2))

```

```

{
  y1 <- (data3$AbundMean[time_per4] -
mean(data3$AbundMean[time_per4]))/(sqrt(var(data3$AbundMean[time_per4]))/sqrt(length
(data3$AbundMean[time_per4])))
  x1 <- (data3$YearRead[time_per4] -
mean(data3$YearRead[time_per4]))/(sqrt(var(data3$YearRead[time_per4]))/sqrt(length(data
3$YearRead[time_per4])))
  tp4_res <- regressions4(y1, x1, 1/(data3$AbundLCID[time_per4]^2),
paste(pdf_prefix,"tp4",sep=""))}
else {tp4_res <- matrix(NA,4,8)}

# tp5 --> 1970 --> 1990
time_per5 <- years >= 1970 & years <= 1990
if ((sum(time_per5) > 2 & length(unique(years[time_per5])) > 2))
{
  y1 <- (data3$AbundMean[time_per5] -
mean(data3$AbundMean[time_per5]))/(sqrt(var(data3$AbundMean[time_per5]))/sqrt(length
(data3$AbundMean[time_per5])))
  x1 <- (data3$YearRead[time_per5]-
mean(data3$YearRead[time_per5]))/(sqrt(var(data3$YearRead[time_per5]))/sqrt(length(data
3$YearRead[time_per5])))
  tp5_res <- regressions4(y1, x1, 1/(data3$AbundLCID[time_per5]^2),
paste(pdf_prefix,"tp5",sep=""))}
else {tp5_res <- matrix(NA,4,8)}

# tp6 --> 1950 --> 1970
time_per6 <- years>=1950 & years<=1970
if ((sum(time_per6) > 2 & length(unique(years[time_per6])) > 2))
{
  y1 <- (data3$AbundMean[time_per6] -
mean(data3$AbundMean[time_per6]))/(sqrt(var(data3$AbundMean[time_per6]))/sqrt(length
(data3$AbundMean[time_per6])))
  x1 <- (data3$YearRead[time_per6] -
mean(data3$YearRead[time_per6]))/(sqrt(var(data3$YearRead[time_per6]))/sqrt(length(data
3$YearRead[time_per6])))
  tp6_res <- regressions4(y1, x1, 1/(data3$AbundLCID[time_per6]^2),
paste(pdf_prefix,"tp6",sep=""))}
else {tp6_res <- matrix(NA,4,8)}

# tp7 --> 1900 --> 1950
time_per7 <- years >= 1900 & years <= 1950
if((sum(time_per7) > 2 & length(unique(years[time_per7])) > 2))
{
  y1 <- (data3$AbundMean[time_per7] -
mean(data3$AbundMean[time_per7]))/(sqrt(var(data3$AbundMean[time_per7]))/sqrt(length
(data3$AbundMean[time_per7])))
  x1 <- (data3$YearRead[time_per7] -
mean(data3$YearRead[time_per7]))/(sqrt(var(data3$YearRead[time_per7]))/sqrt(length(data
3$YearRead[time_per7])))
  tp7_res <- regressions4(y1, x1, 1/(data3$AbundLCID[time_per7]^2),

```

```

paste(pdf_prefix,"tp7",sep=""))}
  else {tp7_res <- matrix(NA,4,8)}

# tp8 --> beginning of data --> 1970
  time_per8 <- years >= minyear & years <= 1970
  if((sum(time_per8) > 2) & (length(unique(years[time_per8])) > 2))
  {
    y1 <- (data3$AbundMean[time_per8] -
mean(data3$AbundMean[time_per8]))/(sqrt(var(data3$AbundMean[time_per8]))/sqrt(length
(data3$AbundMean[time_per8])))
    x1 <- (data3$YearRead[time_per8] -
mean(data3$YearRead[time_per8]))/(sqrt(var(data3$YearRead[time_per8]))/sqrt(length(data
3$YearRead[time_per8])))
    tp8_res <- regressions4(y1, x1 , 1/(data3$AbundLCID[time_per8]^2),
paste(pdf_prefix,"tp8",sep=""))}
  else {tp8_res <- matrix(NA,4,8)}

# tp9 --> beginning of data --> 1990
  time_per9 <- years >= minyear & years <= 1990
  if((sum(time_per9)>2) & (length(unique(years[time_per9]))>2))
  {
    y1 <- (data3$AbundMean[time_per9]-
mean(data3$AbundMean[time_per9]))/(sqrt(var(data3$AbundMean[time_per9]))/sqrt(length
(data3$AbundMean[time_per9])))
    x1 <- (data3$YearRead[time_per9]-
mean(data3$YearRead[time_per9]))/(sqrt(var(data3$YearRead[time_per9]))/sqrt(length(data
3$YearRead[time_per9])))
    tp9_res <- regressions4(y1, x1, 1/(data3$AbundLCID[time_per9]^2),
paste(pdf_prefix,"tp9",sep=""))}
  else {tp9_res <- matrix(NA,4,8)}

overall_summary_tp <- rbind(tp1_res, tp2_res, tp3_res, tp4_res, tp5_res, tp6_res, tp7_res,
tp8_res, tp9_res) # results bound together & returned for each population
return(overall_summary_tp)
}

##### FUNCTION FOR PERFORMING FOUR REGRESSIONS ON EACH
# POPULATION → regressions4
# performs four regressions over each time period (i.e. 9 time periods total) for each
population
# regressions4 is the function for actually performing the four regressions in each time period
for each population
# weights = Abundance Confidence ID (ACID)

regressions4 <- function (y, x, weight, pdf_file)
{
  print(x)
  print(y)
  print(pdf_file)

```

```

reg <- lm(y ~ x)
reg_w <- lm(y ~ x, weights = weight)
rreg <- lmRob(y ~ x)
rreg_w <- lmRob(y ~ x, weights = weight)
results_mat <- matrix(0,4,8)
dimnames(results_mat) <- list(NULL, c("coeff_est", "SE", "tval", "pval", "Rsq",
"Intercept", "Mest_bias_pval", "LSeest_bias_pval")) # column labels

# linear regression
results_mat[1,] <- c(summary(reg)$coef[2,], summary(reg)$r.squared,
summary(reg)$coef[1,1], NA, NA)
# vector with 8 elements
# coef[2,] gives 1st 4 values, coef[1,1] gives intercept, no values for last 2

# weighted linear regression
results_mat[2,] <- c(summary(reg_w)$coef[2,], summary(reg_w)$r.squared,
summary(reg_w)$coef[1,1], NA, NA)

# robust linear regression
results_mat[3,] <- c(summary(rreg)$coef[2,], summary(rreg)$r.squared,
summary(rreg)$coef[1,1], summary(rreg)$biasTest[1,2], summary(rreg)$biasTest[2,2])
# last two columns give bias test pvals for Mest and LSeest

# weighted robust linear regression
results_mat[4,] <- c(summary(rreg_w)$coef[2,], summary(rreg_w)$r.squared,
summary(rreg_w)$coef[1,1], summary(rreg_w)$biasTest[1,2],
summary(rreg_w)$biasTest[2,2])

# save residual plots
pdf(pdf_file)
par(mfrow=c(2,2))
plot(reg)
plot(reg_w)
plot.lmRob(rreg, which.plots=c(5,2,6,7))
plot.lmRob(rreg_w, which.plots=c(5,2,6,7))
dev.off()
return(results_mat) # return regression results matrix
}

##### RUN ALL FUNCTIONS

spp_regdata <- pick.pops(data2, Species, Pop_int, GenT)

write.csv(spp_regdata, file=paste(Species, "_", "table", ".csv", sep="")) # save matrix to a .csv

##### END

```


APPENDIX I.E Marine Mammal Abundance Trends for 127 Marine Mammal Species Listed by the IUCN (2008)

This Excel data table is an electronic appendix to be found at the Dalhousie University DalSpace repository at the following link: <http://dalspace.library.dal.ca/>

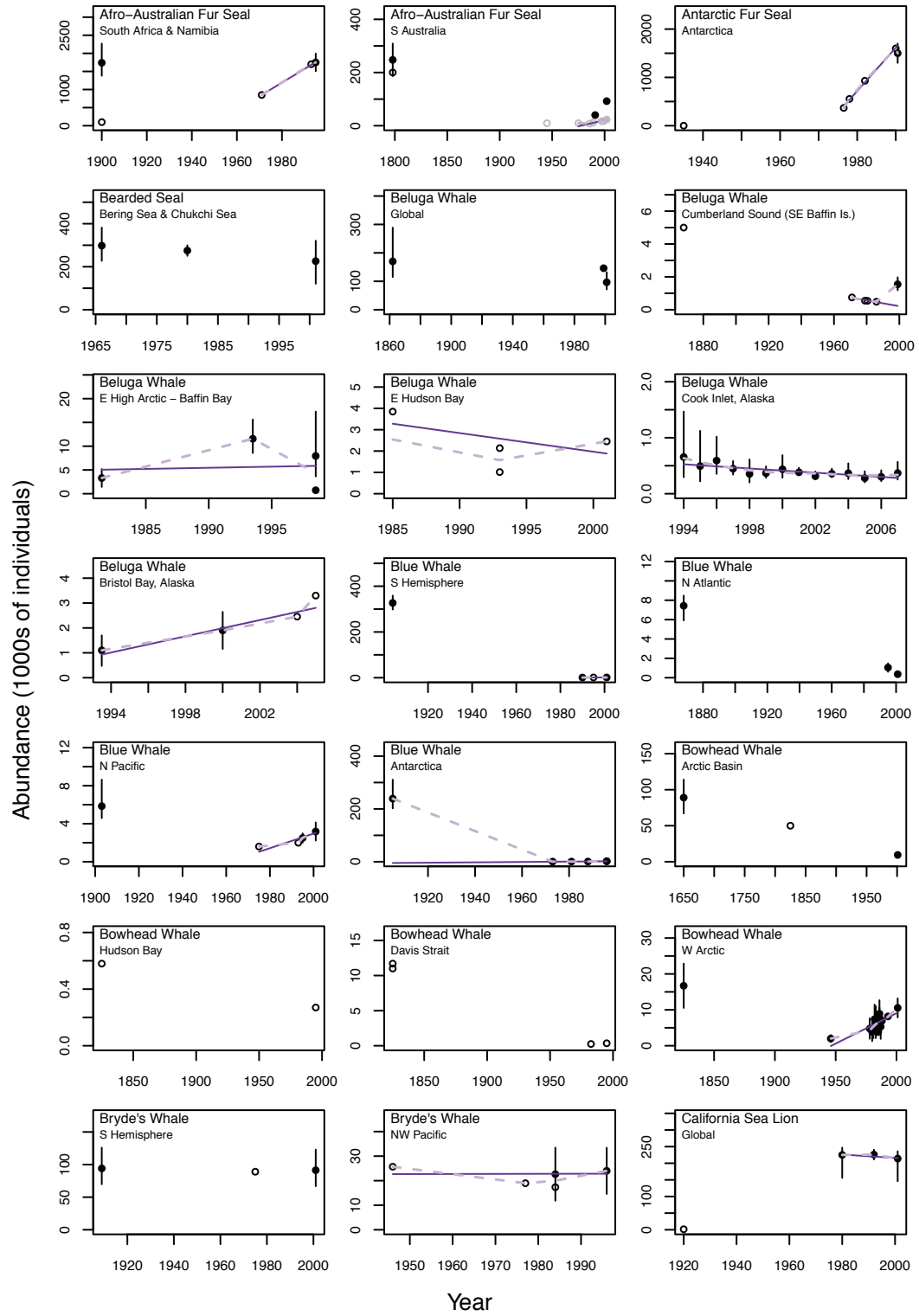
APPENDIX I.F Marine Mammal Populations (n=47) with Historical, Minimum and Recent Population Estimates and Their Percent Decline and Recovery With Respect to Historical Population Level

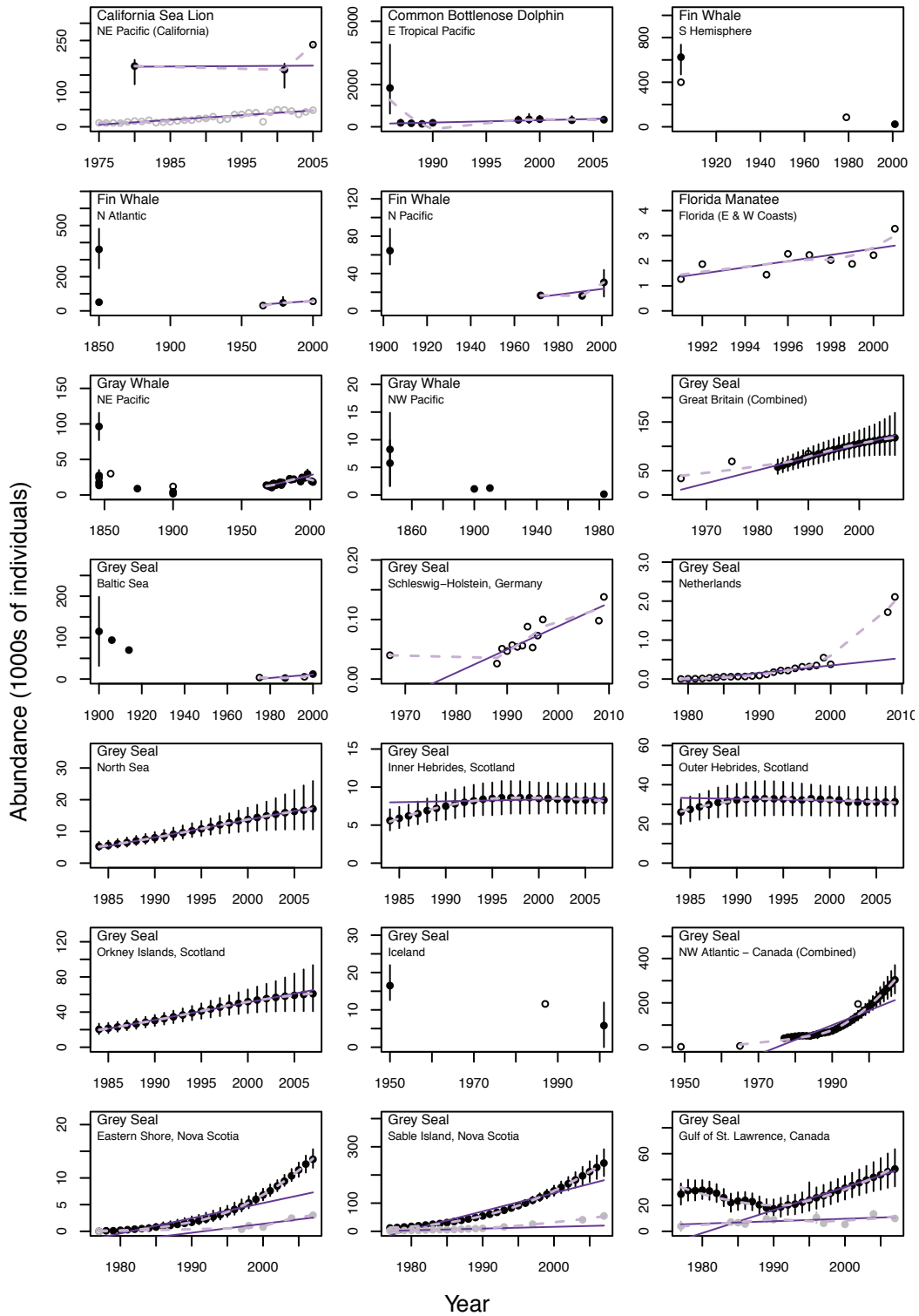
This Excel data table is an electronic appendix to be found at the Dalhousie University DalSpace repository at the following link: <http://dalspace.library.dal.ca/>

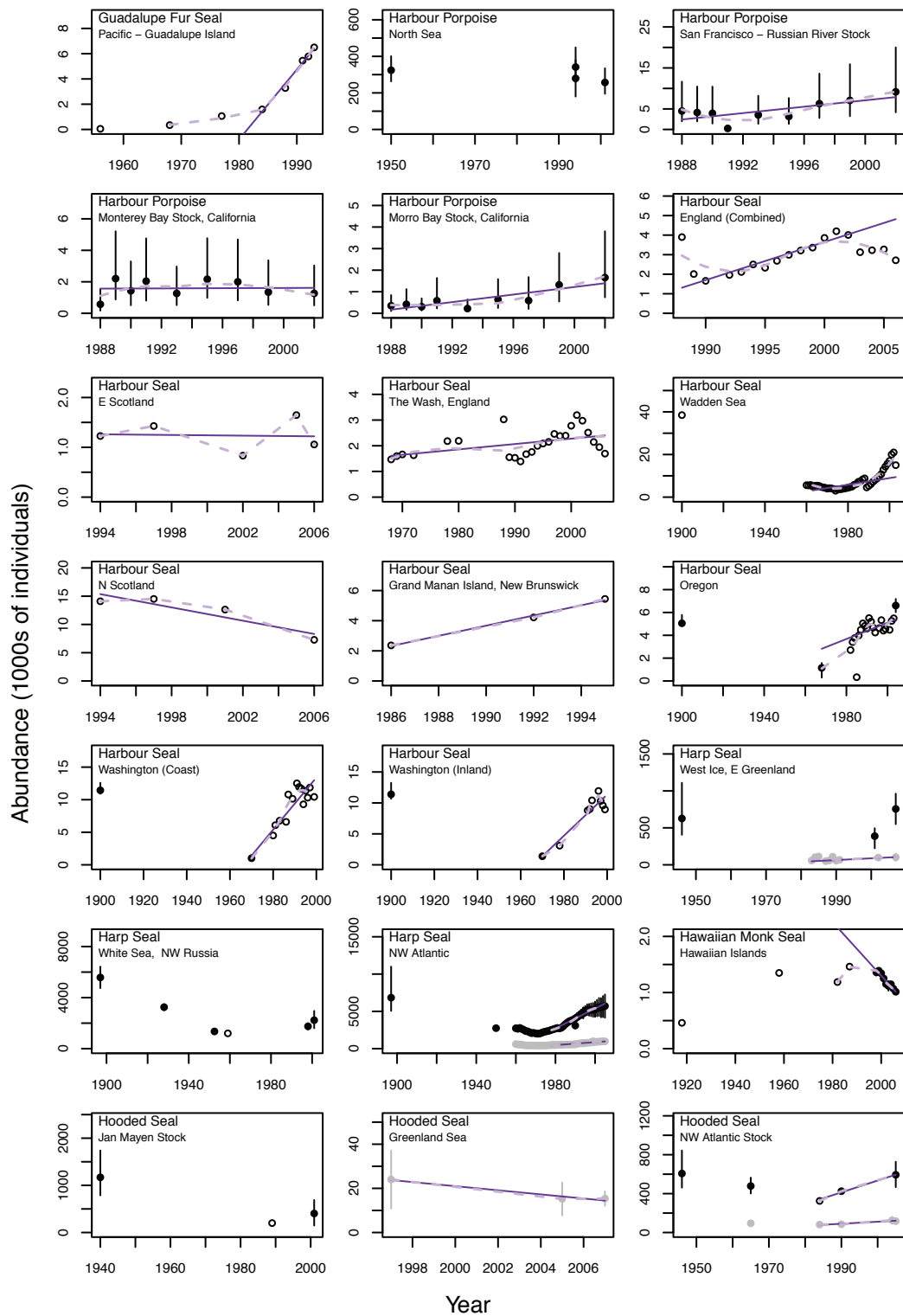
APPENDIX I.G Marine Mammal Population Abundances Over Time and Trends Over Three Generations (n = 157 with duplicates, n = 143 without duplicate regular and pup count data)

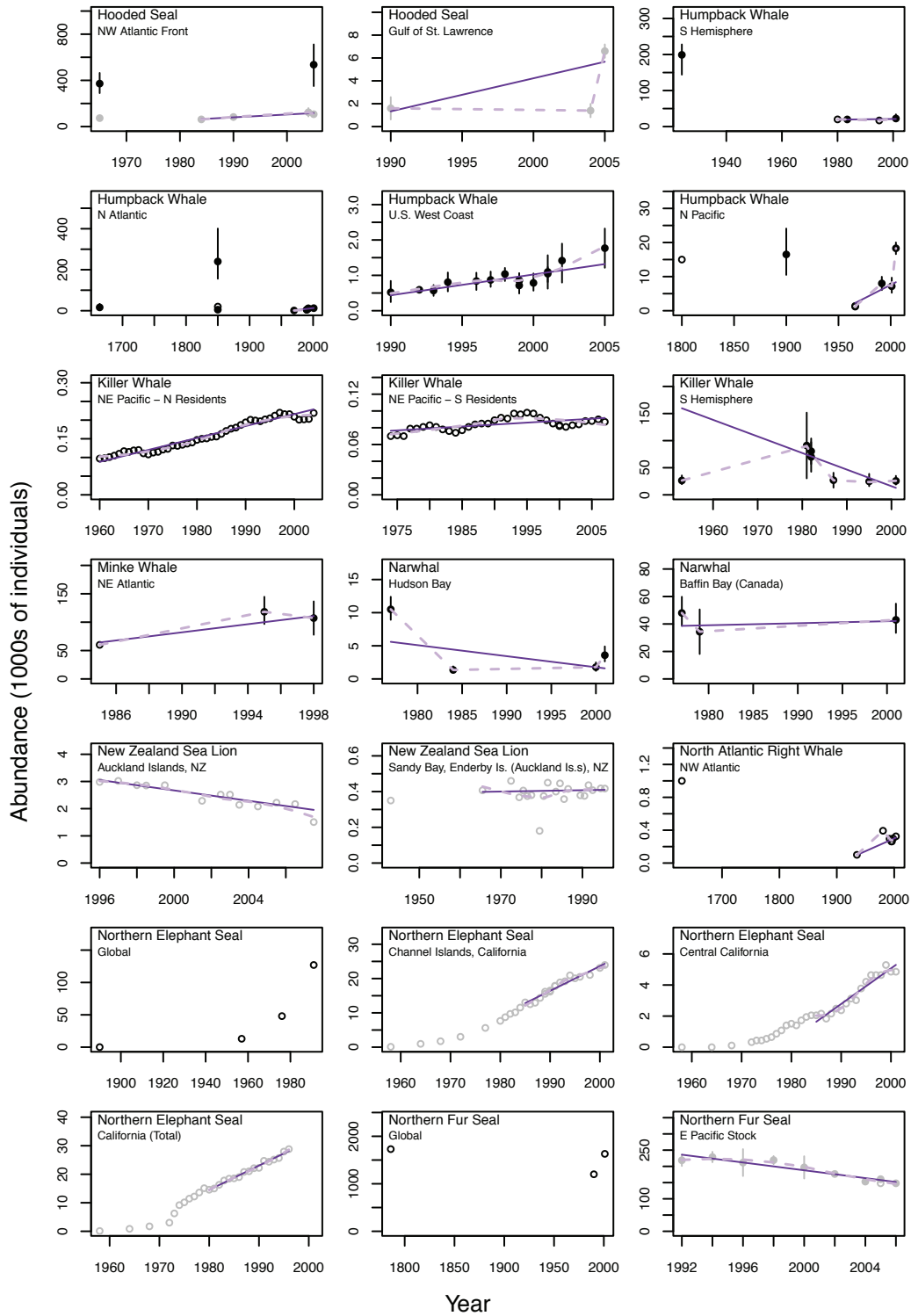
Plots legend:

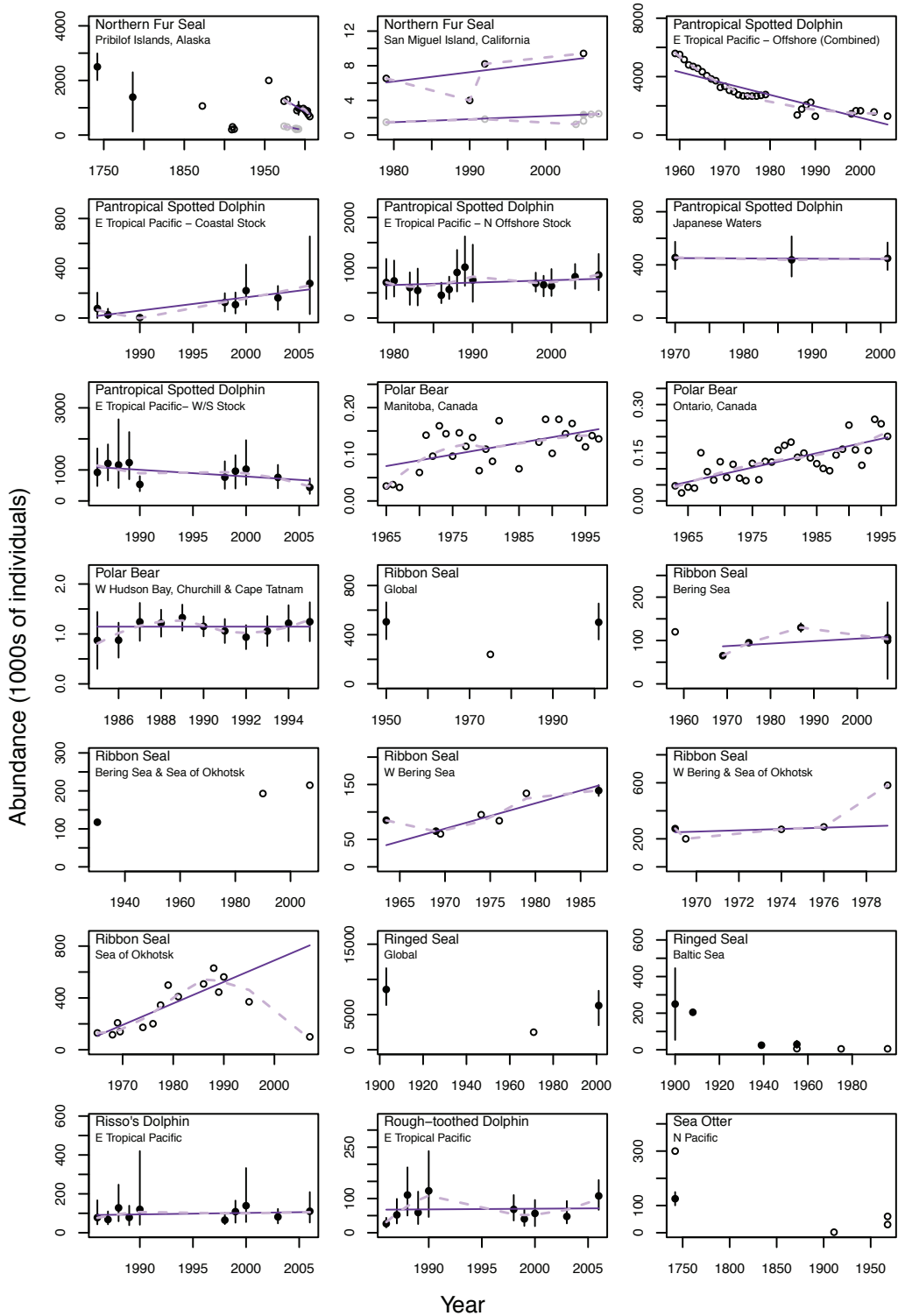
- Species and population areas are described in the left hand corner of each plot.
- Solid purple lines = robust linear regression weighted by Abundance Confidence ID (ACID)
- Dashed light purple lines = Loess curve (and additive model).
- Solid points = abundance data with quantitative error information (95% confidence interval bars)
- Empty points = abundance data with no stated quantitative error information
- Black points = regular data that was collected from the entire population.
- Grey points = pup count data

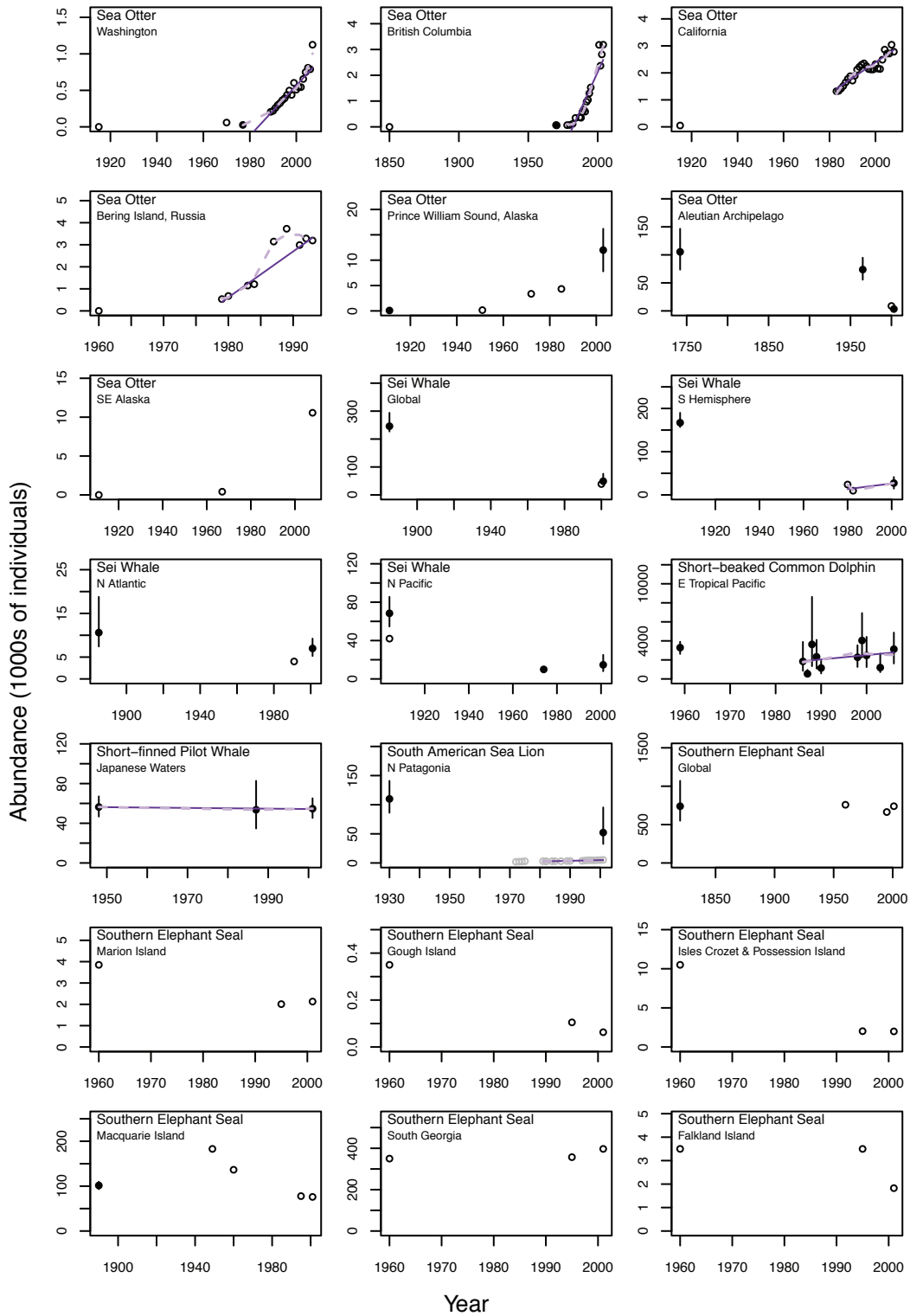


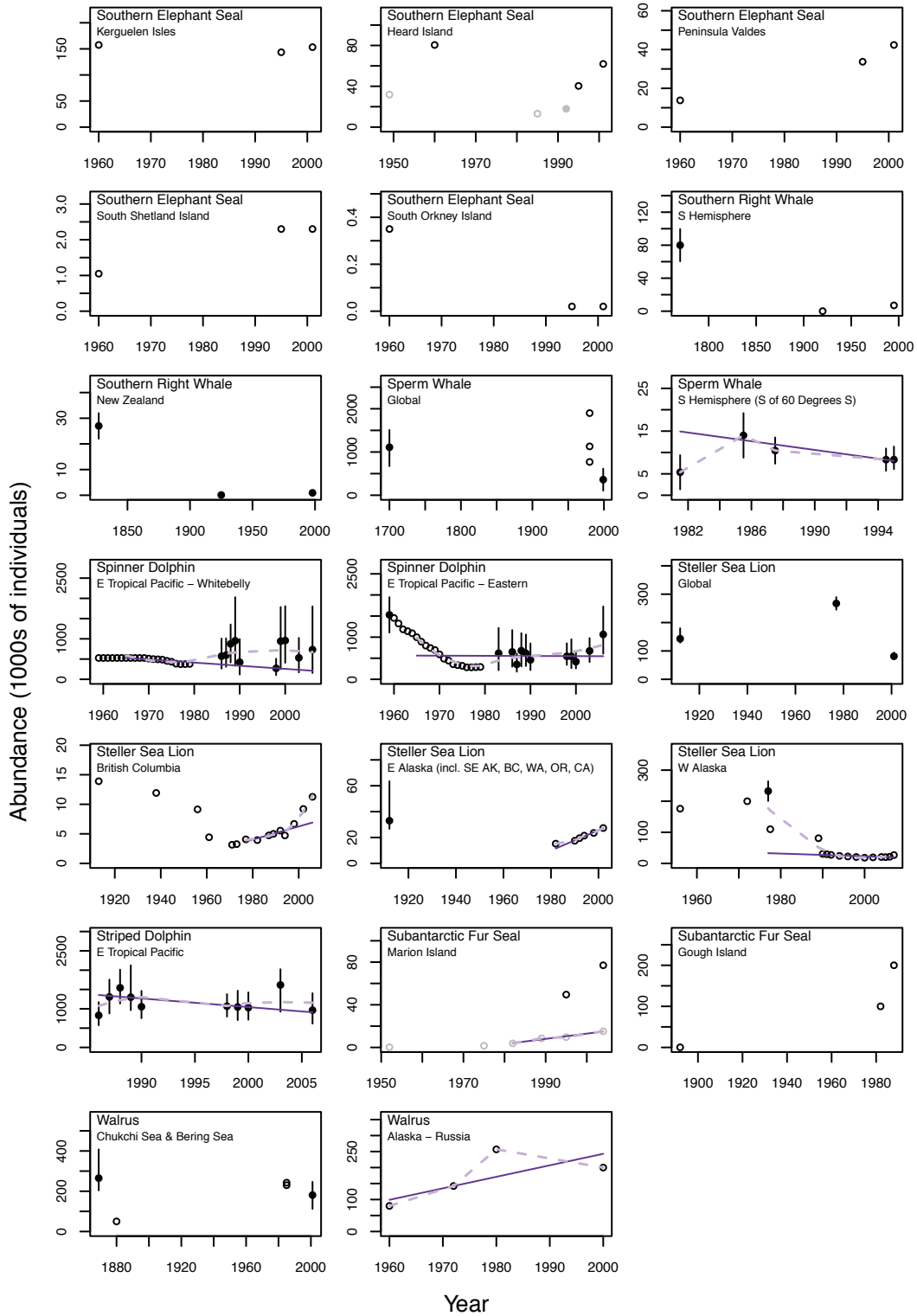










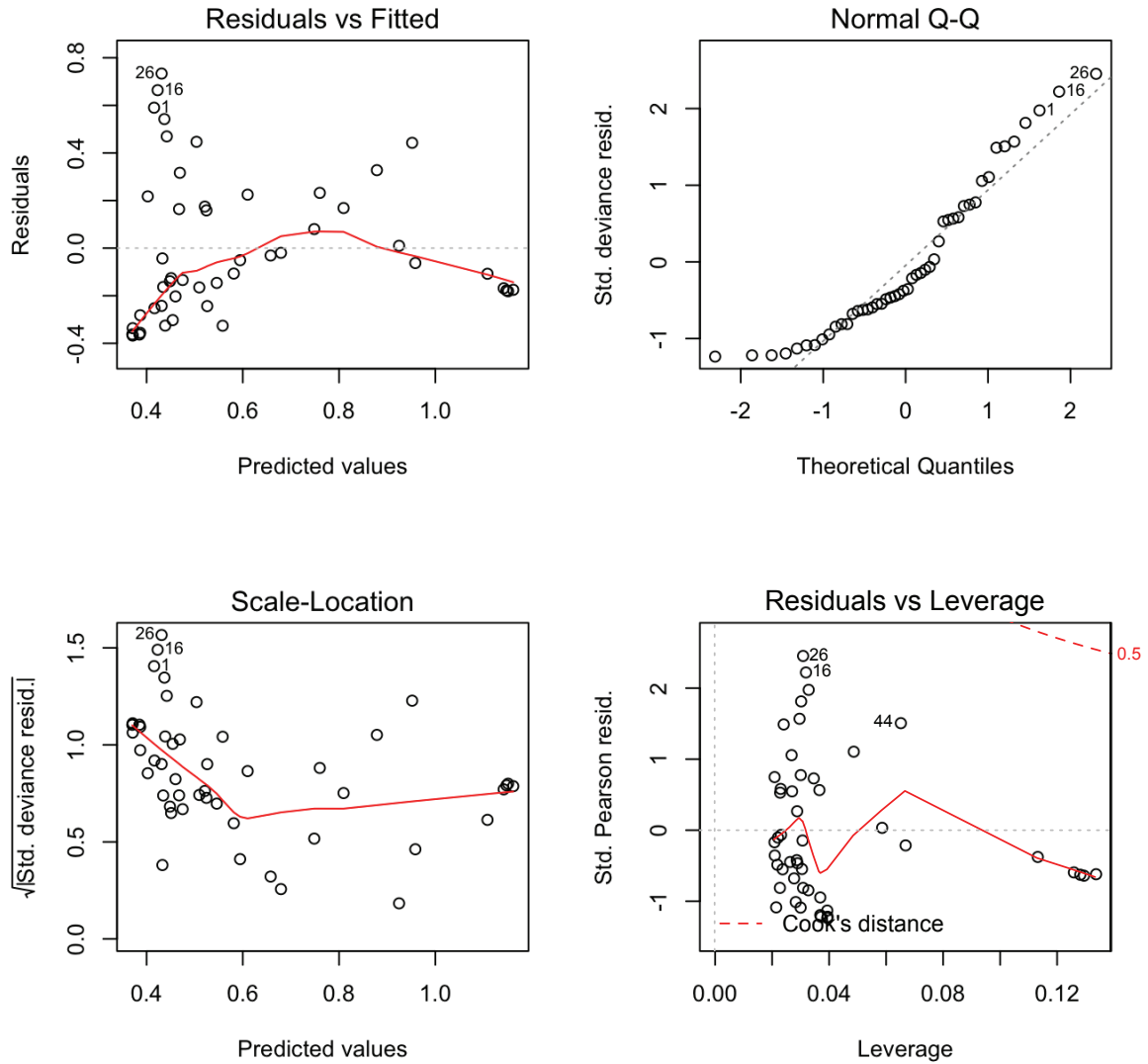


APPENDIX I.H Results from Scaled Robust Linear Regressions, Weighted by Abundance Confidence ID (ACID), Over Three Generation Times of Marine Mammal Population Abundance Data (157 populations)

This Excel data table is an electronic appendix to be found at the Dalhousie University DalSpace repository at the following link: <http://dalspace.library.dal.ca/>

APPENDIX I.I Residual Plots for GLM (Quasi Family, Identity Link) of the Relationship Between Marine Mammal Population (n = 47) Abundance Recovery and Decline Relative to Historical Population Estimates

Numbered points indicate largest outliers in each plot.



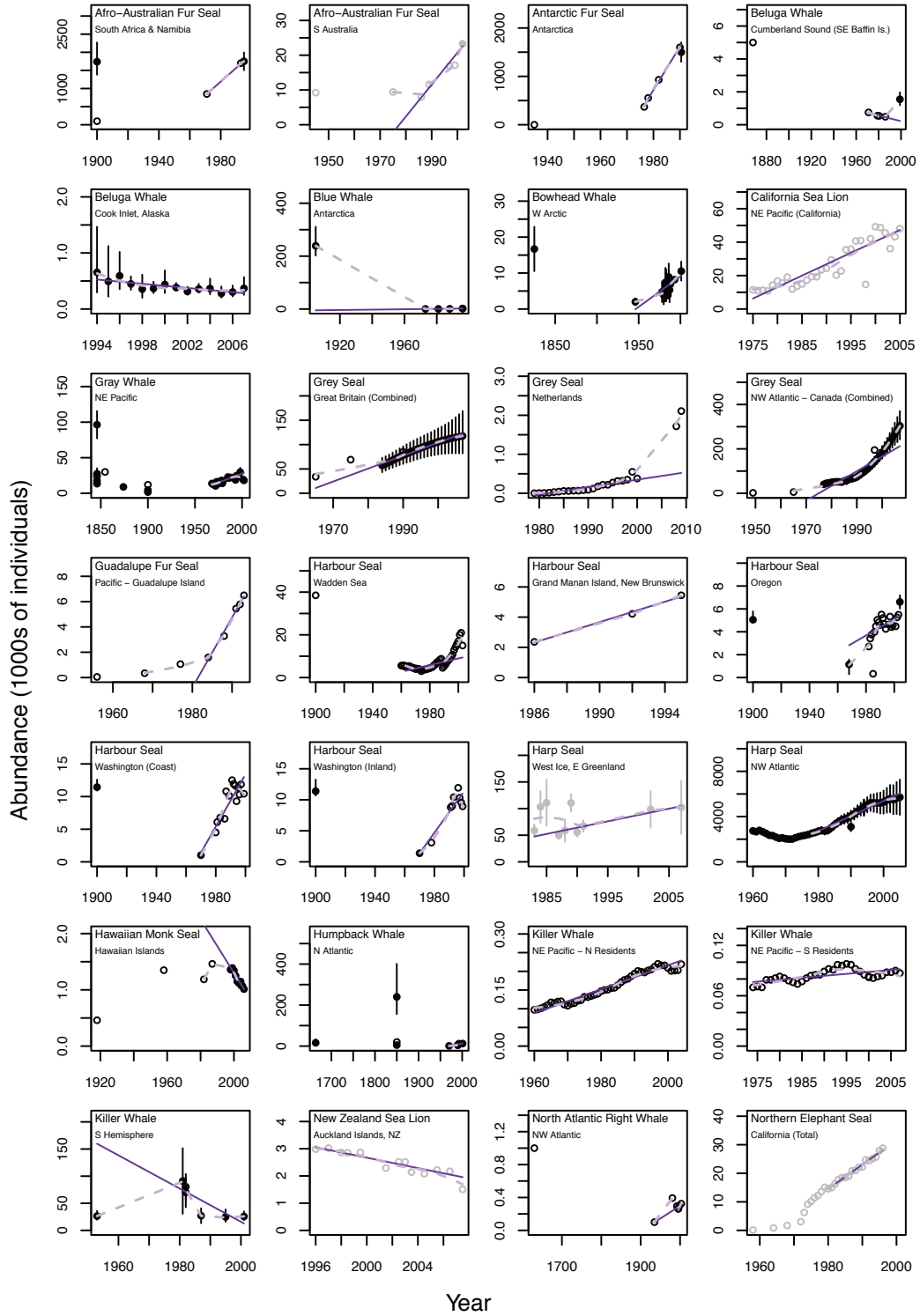
APPENDIX II.A Data and Sources for Hypothesized Critical Factors to Marine Mammal Abundance Recovery

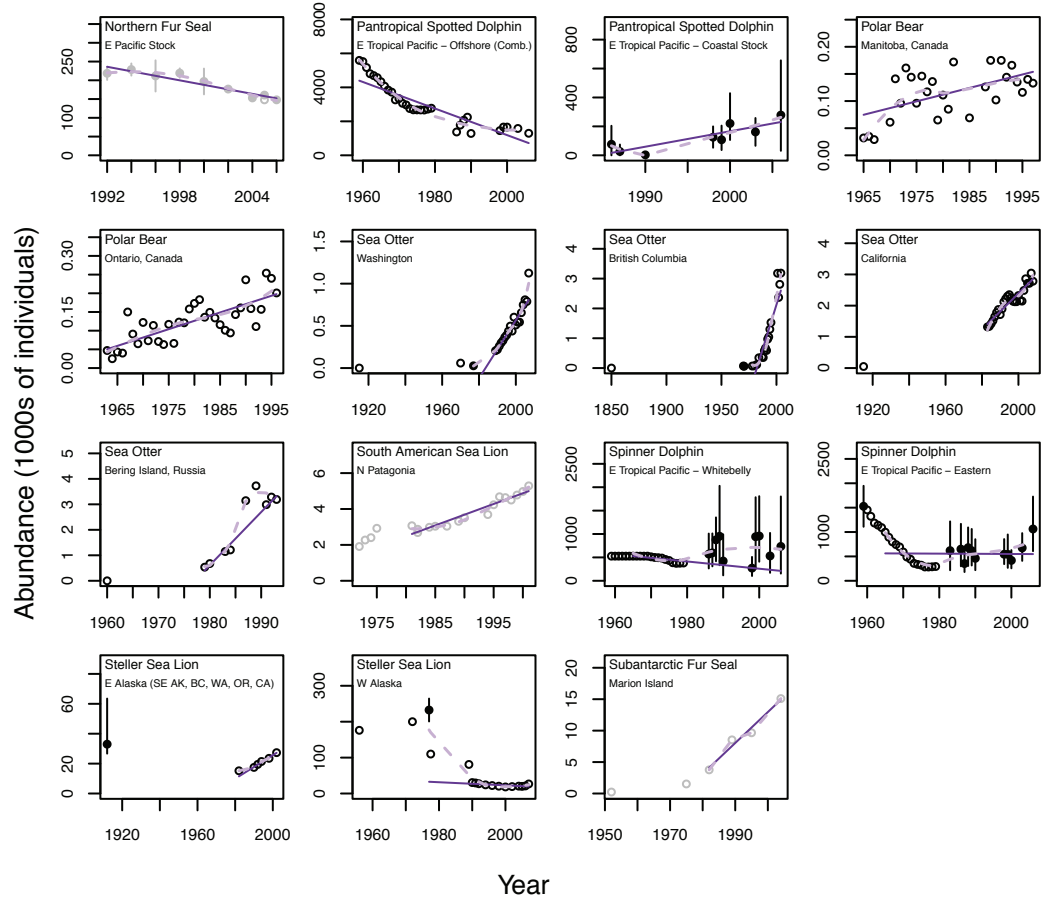
This Excel data table is an electronic appendix to be found at the Dalhousie University DalSpace repository at the following link: <http://dalspace.library.dal.ca/>

APPENDIX II.B Marine Mammal Population Abundances Over Time and Trends Over Three Generations (n = 43)

Plots legend:

- Species and population areas are described in the left hand corner of each plot.
- Solid purple lines = robust linear regression weighted by Abundance Confidence ID (ACID)
- Dashed light purple lines = Loess curve (and additive model).
- Solid points = abundance data with quantitative error information (95% confidence interval bars)
- Empty points = abundance data with no stated quantitative error information
- Black points = regular data that were collected from the entire population.
- Grey points = pup count data





APPENDIX II.C R Code for Exploratory Data Analysis, Classification Trees, GAMs, and GLMs

```
##### LOAD DATA
```

```
setwd # locate working directory  
setwd("~/file_path_name/") # set working directory
```

```
##### SELECT DATA SET TO USE IN ANALYSIS
```

```
data0 <- read.csv("CritFac_ALL_p05.csv")  
#data0 <- read.csv("CritFac_CET_p05.csv")  
#data0 <- read.csv("CritFac_PINN_p05.csv")  
#data0 <- read.csv("CritFac_OTHER_p05.csv")
```

```
data1 <- as.data.frame(data0) # create a dataframe to manipulate columns
```

```
##### EXPLORATORY DATA ANALYSIS
```

```
##### CORRELATIONS
```

```
library(stats) # for cor()
```

```
cor(cbind(as.factor(data1$Recovery), as.numeric(data1$Length_med_F),  
as.numeric(log(data1$Weight_med_F)), as.numeric(data1$Age_mat_yrs_F),  
as.numeric(data1$Gestation_Time), as.numeric(data1$Interbirth_Interval),  
as.factor(data1$Mgt_Exploitation_Ord), as.factor(data1$Mgt_Exploitation_Time),  
as.factor(data1$Direct_Exploitation), as.factor(data1$Bycatch),  
as.factor(data1$Mgt_Habitat_Ord), as.factor(data1$Mgt_Habitat_Ord_2),  
as.factor(data1$Mgt_Habitat_Time), as.factor(data1$Mgt_Trade_Ord),  
as.factor(data1$Mgt_Trade_Time), as.numeric(data1$Hab_Dist_Max_Index),  
as.numeric(data1$Hab_Dist_Index), as.factor(data1$Soc_Imp_Ord),  
as.factor(data1$Habitat_Type_Ord), as.factor(data1$Habitat_Dom_Ord),  
as.factor(data1$Habitat_Dom_Ord2), as.numeric(data1$Hab_Area_km2),  
as.numeric(log(data1$Hab_Area_km2)), as.numeric(data1$Trophic_Level),  
as.factor(data1$Species_Type_Num)), method="spearman")
```

```
##### PLOT INDEPENDENT VARIABLES AGAINST RESPONSE
```

```
library(graphics) # for boxplot & barplots
```

```
pdf(file = "Recovery_plotvars_ALL_p05.pdf")  
par(mfrow=c(3,3)) # set up graphics window for plots  
plot(as.factor(data1$Recovery), data1$Weight_med_F, xlab = "Recovery", ylab =
```

```

"Weight_med_F", cex= 0.8, varwidth=TRUE)
plot (as.factor(data1$Recovery), log(data1$Weight_med_F), xlab = "Recovery", ylab =
"Log_Weight_med_F", cex= 0.8, varwidth=TRUE)
plot (as.factor(data1$Recovery), data1$Length_med_F, xlab = "Recovery", ylab =
"Length_med_F", cex= 0.8, varwidth=TRUE)
#plot (as.factor(data1$Recovery), data1$Max_weight, xlab = "Recovery", ylab =
"Max_weight", cex= 0.8, varwidth=TRUE)
#plot (as.factor(data1$Recovery), data1$Max_length, xlab = "Recovery", ylab =
"Max_length", cex= 0.8, varwidth=TRUE)
plot (as.factor(data1$Recovery), data1$Age_mat_yrs_F, xlab = "Recovery", ylab =
"Age_mat_yrs_F", cex= 0.8, varwidth=TRUE)
#plot (as.factor(data1$Recovery), data1$Max_Age_yrs, xlab = "Recovery", ylab =
"Max_Age_yrs", cex= 0.8, varwidth=TRUE)
plot (as.factor(data1$Recovery), data1$Gestation_Time, xlab = "Recovery", ylab =
"Gestation_Time", cex= 0.8, varwidth=TRUE)
plot (as.factor(data1$Recovery), data1$Interbirth_Interval, xlab = "Recovery", ylab =
"Interbirth_Interval", cex= 0.8, varwidth=TRUE)
plot (as.factor(data1$Recovery), as.factor(data1$Mgt_Exploitation_Ord), xlab = "Recovery",
ylab = "Mgt_Exploitation_Ord", cex= 0.8, varwidth=TRUE)
plot (as.factor(data1$Recovery), as.factor(data1$Mgt_Exploitation_Time), xlab =
"Recovery", ylab = "Mgt_Exploitation_Time", cex= 0.8, varwidth=TRUE)
plot (as.factor(data1$Recovery), as.factor(data1$Direct_Exploitation), xlab = "Recovery",
ylab = "Direct_Exploitation", cex= 0.8, varwidth=TRUE)
plot (as.factor(data1$Recovery), as.factor(data1$Bycatch), xlab = "Recovery", ylab =
"Bycatch", cex= 0.8, varwidth=TRUE)
plot (as.factor(data1$Recovery), as.factor(data1$Mgt_Habitat_Ord), xlab = "Recovery", ylab =
"Mgt_Habitat_Ord", cex= 0.8, varwidth=TRUE)
plot (as.factor(data1$Recovery), as.factor(data1$Mgt_Habitat_Time), xlab = "Recovery",
ylab = "Mgt_Habitat_Time", cex= 0.8, varwidth=TRUE)
plot (as.factor(data1$Recovery), as.factor(data1$Mgt_Trade_Ord), xlab = "Recovery", ylab =
"Mgt_Trade_Ord", cex= 0.8, varwidth=TRUE)
plot (as.factor(data1$Recovery), as.factor(data1$Mgt_Trade_Time), xlab = "Recovery", ylab =
"Mgt_Trade_Time", cex= 0.8, varwidth=TRUE)
plot (as.factor(data1$Recovery), data1$Hab_Dist_Max_Index, xlab = "Recovery", ylab =
"Hab_Dist_Max_Index", cex= 0.8, varwidth=TRUE)
plot (as.factor(data1$Recovery), data1$Hab_Dist_Index, xlab = "Recovery", ylab =
"Hab_Dist_Index", cex= 0.8, varwidth=TRUE)
plot (as.factor(data1$Recovery), as.factor(data1$Soc_Imp_Ord), xlab = "Recovery", ylab =
"Soc_Imp_Ord", cex= 0.8, varwidth=TRUE)
plot (as.factor(data1$Recovery), as.factor(data1$Habitat_Type_Ord), xlab = "Recovery",
ylab = "Habitat_Type_Ord", cex= 0.8, varwidth=TRUE)
plot (as.factor(data1$Recovery), as.factor(data1$Habitat_Dom_Ord), xlab = "Recovery",
ylab = "Habitat_Dom_Ord", cex= 0.8, varwidth=TRUE)
plot (as.factor(data1$Recovery), as.factor(data1$Habitat_Dom_Ord2), xlab = "Recovery",
ylab = "Habitat_Dom_Ord2", cex= 0.8, varwidth=TRUE)
plot (as.factor(data1$Recovery), as.numeric(data1$Hab_Area_km2), xlab = "Recovery", ylab

```

```

= "Hab_Area_km2", cex= 0.8, varwidth=TRUE)
plot (as.factor(data1$Recovery), as.numeric(log(data1$Hab_Area_km2)), xlab = "Recovery",
ylab = "Log_Hab_Area_km2", cex= 0.8, varwidth=TRUE)
plot (as.factor(data1$Recovery), as.numeric(data1$Trophic_Level), xlab = "Recovery", ylab
= "Trophic_Level", cex= 0.8, varwidth=TRUE)
plot (as.factor(data1$Recovery), as.factor(data1$Species_Type_Num), xlab = "Recovery",
ylab = "Species_Type_Num", cex= 0.8, varwidth=TRUE)
dev.off()# turn off graphics device

```

CLASSIFICATION TREES

INITIAL CLASSIFICATION TREE MODEL

```
library(tree)
```

```

tree_mod <- tree(as.factor(Recovery)~ as.numeric(log(data1$Weight_med_F)) +
as.numeric(data1$Age_mat_yrs_F) + as.numeric(data1$Gestation_Time) +
as.factor(data1$Mgt_Exploitation_Ord) + as.factor(data1$Mgt_Exploitation_Time) +
as.factor(data1$Bycatch) + as.factor(data1$Mgt_Habitat_Ord) +
as.factor(data1$Mgt_Habitat_Time) + as.factor(data1$Mgt_Trade_Ord) +
as.factor(data1$Mgt_Trade_Time) + as.numeric(data1$Hab_Dist_Max_Index) +
as.numeric(data1$Hab_Dist_Index) + as.factor(data1$Habitat_Type_Ord) +
as.factor(data1$Habitat_Dom_Ord2)+ as.numeric(log(data1$Hab_Area_km2)) +
as.numeric(data1$Trophic_Level) + as.factor(data1$Species_Type_Num), data = data1)# add
in different variables; add RECOVERY column into table
summary(tree_mod)
pdf(file = "Regressiontree_ALL_p05.pdf") # store tree diagram as pdf file with this title
plot(tree_mod)
text(tree_mod, cex=0.6) # add labels to plot
dev.off() # turn off graphics device

```

PRUNED CLASSIFICATION TREE MODEL

```

cv_tree_mod<- cv.tree(tree_mod, method="misclass") # identifies optimal number of model
nodes and variables
plot(cv_tree_mod)

ptree<- prune.tree(tree_mod, best=3) # best = # of nodes in best model (by cross validation)
summary(ptree) # summary of reduced model outputs
pdf(file = "Classificationtree_p05_PRUNED.pdf")
plot(ptree)
text(ptree, cex=0.6) # add labels to plot
dev.off() # turn off graphics device

```

GAMS

```

library(mgcv)

gam_mod_w <- gam(as.factor(Recovery_N) ~ s(log(Weight_med_F), bs="ts") +
s(Age_mat_yrs_F, bs="ts") + s(Gestation_Time, bs="ts") + as.factor(Mgt_Exploitation_Ord)
+ as.factor(Mgt_Exploitation_Time) + as.factor(Bycatch) + as.factor(Mgt_Habitat_Ord) +
as.factor(Mgt_Habitat_Time) + as.factor(Mgt_Trade_Ord) + as.factor(Mgt_Trade_Time) +
s(Hab_Dist_Index, bs="ts") + s(Hab_Dist_Max_Index, bs="ts") +
as.factor(Habitat_Type_Ord) + as.factor(Habitat_Dom_Ord2) + s(log(Hab_Area_km2),
bs="ts") + s(Trophic_Level, bs="ts") + as.factor(Species_Type_Num), family =
binomial(link = logit), data = data1)
summary(gam_mod_w) # model output summary
AIC(gam_mod_w)
gam.check(gam_mod_w) # residual plots
plot(gam_mod_w) # plot smooth terms

# remove highly non-significant or shrunken variables as necessary and re-run model until a
good model or set of models is chosen; confirm by starting with only highly significant
variables and add re-fitting model with different combinations of variables (i.e. backward and
forward selection)

##### GLMS

glm_mod_full <- glm(Recovery~ as.numeric(log(data1$Weight_med_F)) +
as.numeric(data1$Age_mat_yrs_F) + as.numeric(data1$Gestation_Time) +
as.factor(data1$Mgt_Exploitation_Ord) + as.factor(data1$Mgt_Exploitation_Time) +
as.factor(data1$Bycatch) + as.factor(data1$Mgt_Habitat_Ord) +
as.factor(data1$Mgt_Habitat_Time) + as.factor(data1$Mgt_Trade_Ord) +
as.factor(data1$Mgt_Trade_Time) + as.numeric(data1$Hab_Dist_Max_Index) +
as.numeric(data1$Hab_Dist_Index) + as.factor(data1$Habitat_Type_Ord) +
as.factor(data1$Habitat_Dom_Ord2) + as.numeric(log(data1$Hab_Area_km2)) +
as.numeric(data1$Trophic_Level) + as.factor(data1$Species_Type_Num), family =
binomial(link=logit), data = data1)
summary(glm_mod_full) # model output summary
par(mfrow=c(2,2)) # set up 2x2 graphics window for residual plots
plot(glm_mod_full) # plot 4 residual plots

# remove variables as necessary and re-run model until a good model (or set of models) is
chosen; confirm by starting with only highly significant variables and add re-fitting model
with different combinations of variables (i.e. backward and forward selection)

##### END #####

```

APPENDIX II.D Distribution of Data Over Independent Variables In Relation to Response (Recovery Status) for All Marine Mammals (a), Cetaceans (b), Pinnipeds (c), and Other (d) Data

Quantitative variables are represented by boxplots, with the box representing the bounds of the upper and lower quartiles, containing the median (horizontal line). The whiskers extend to 1.5 times the interquartile range, with outlier points outside the box and whiskers. Categorical data are represented by barplots, displaying the relative proportion of each category level in the data.

Potential critical factors:

Length_med_female = length, mean or median, female (m)

log(Weight_med_female) = weight, mean or median, female (log transformed) (m)

Age_mat_years_F = age at maturity, female (years)

Gestation_Time = gestation time (months)

Interbirth_Interval = interbirth interval (years)

Mgt_Exploitation_Ord = exploitation management; 1= None, 2 = Partial, 3 = Full

Mgt_Exploitation_Time = exploitation management implementation time; 1= Recent, 2 = Mid, 3= Distance past, 4= NA;

Direction_Exploitation = whether the population is directly exploited; 0 = No, 1 = Yes

Bycatch = whether the population is caught as bycatch; 0 = No, 1= Yes

Mgt_Habitat_Ord = habitat management; 1= None, 2 = Partial, 3 = Full

Mgt_Habitat_Time = habitat management implementation time; 1= recent, 2 = mid, 3= distance past, 4= NA;

Mgt_Trade_Ord = trade management; 1= None, 2 = Partial, 3 = Full

Mgt_Trade_Time = trade management implementation time; 1= Recent, 2 = Mid, 3= Distance past, 4= NA;

Hab_Dist_Max_Index = habitat disturbance (maximum)

Hab_Dist_Index = habitat disturbance (mean)

log(Hab_Area_km2) = habitat area (log transformed) (km squared)

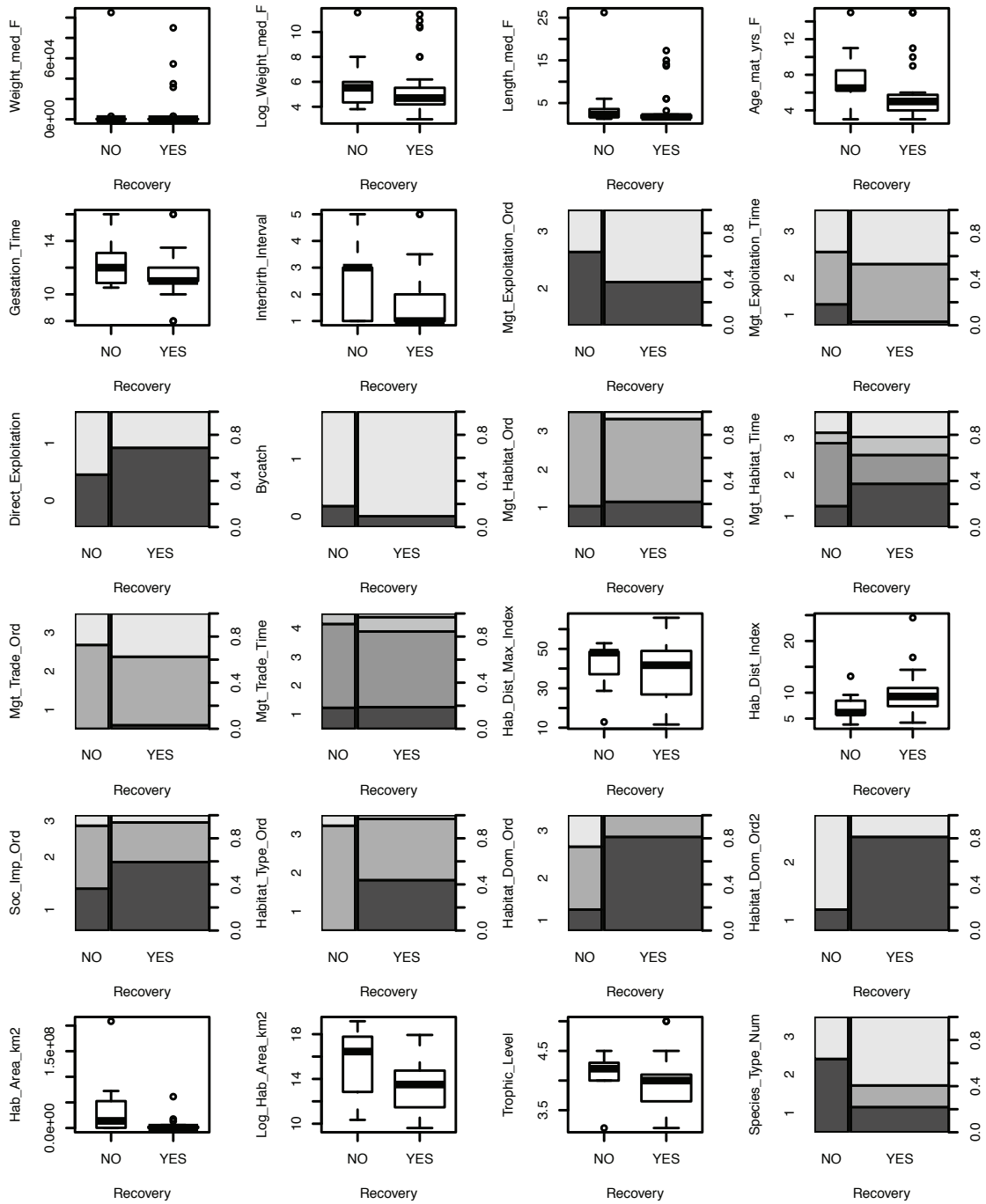
Soc_Imp_Ord = importance of social interaction; 1= Low, 2 = Medium, 3 = High

Habitat_Dom_Ord2 = dominant habitat type; 1=coastal, 2 = both and offshore

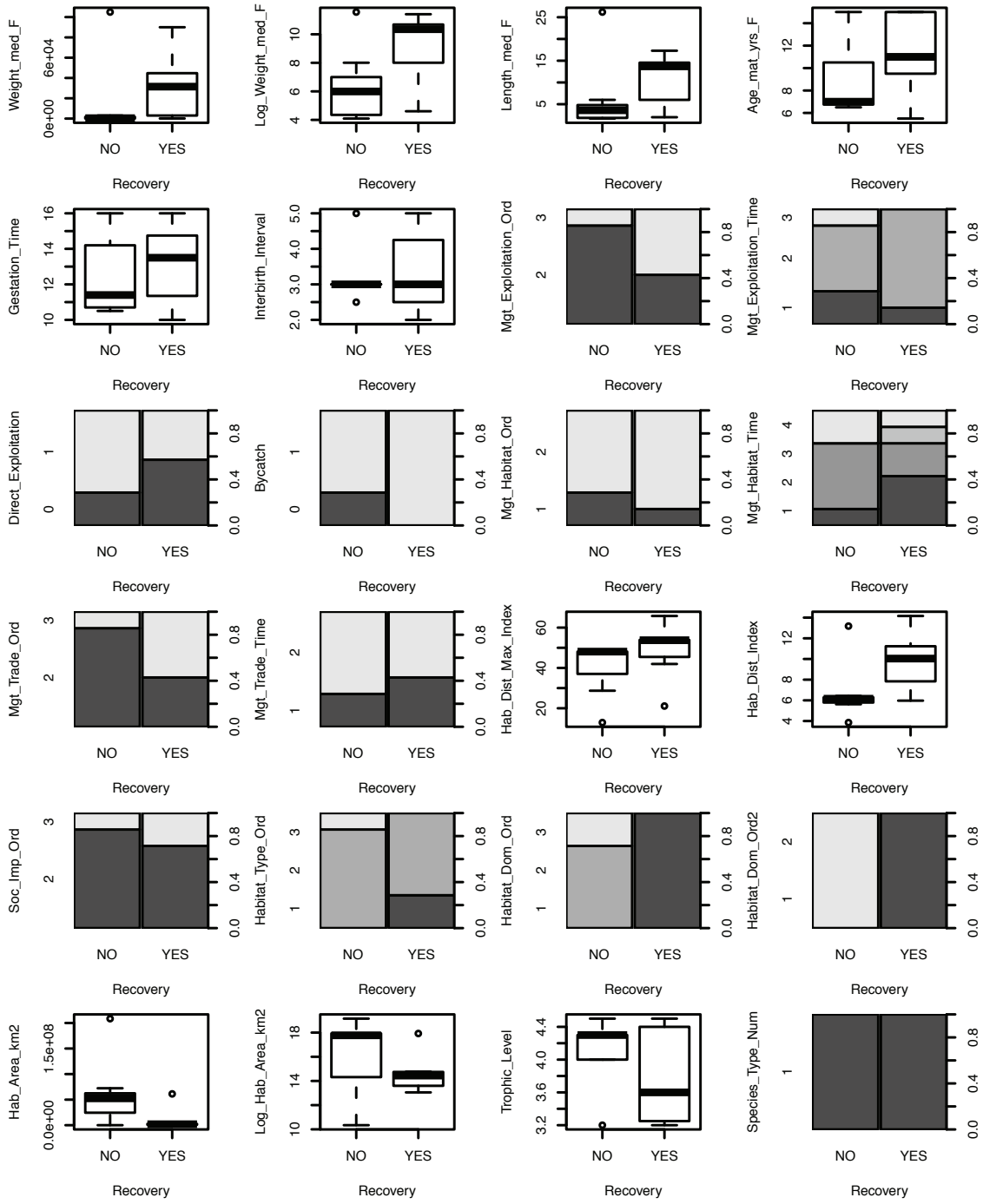
Trophic_Level = trophic level

Species_Type_Num = marine mammal species type; 1= cetacean, 2= other, 3 = pinniped.

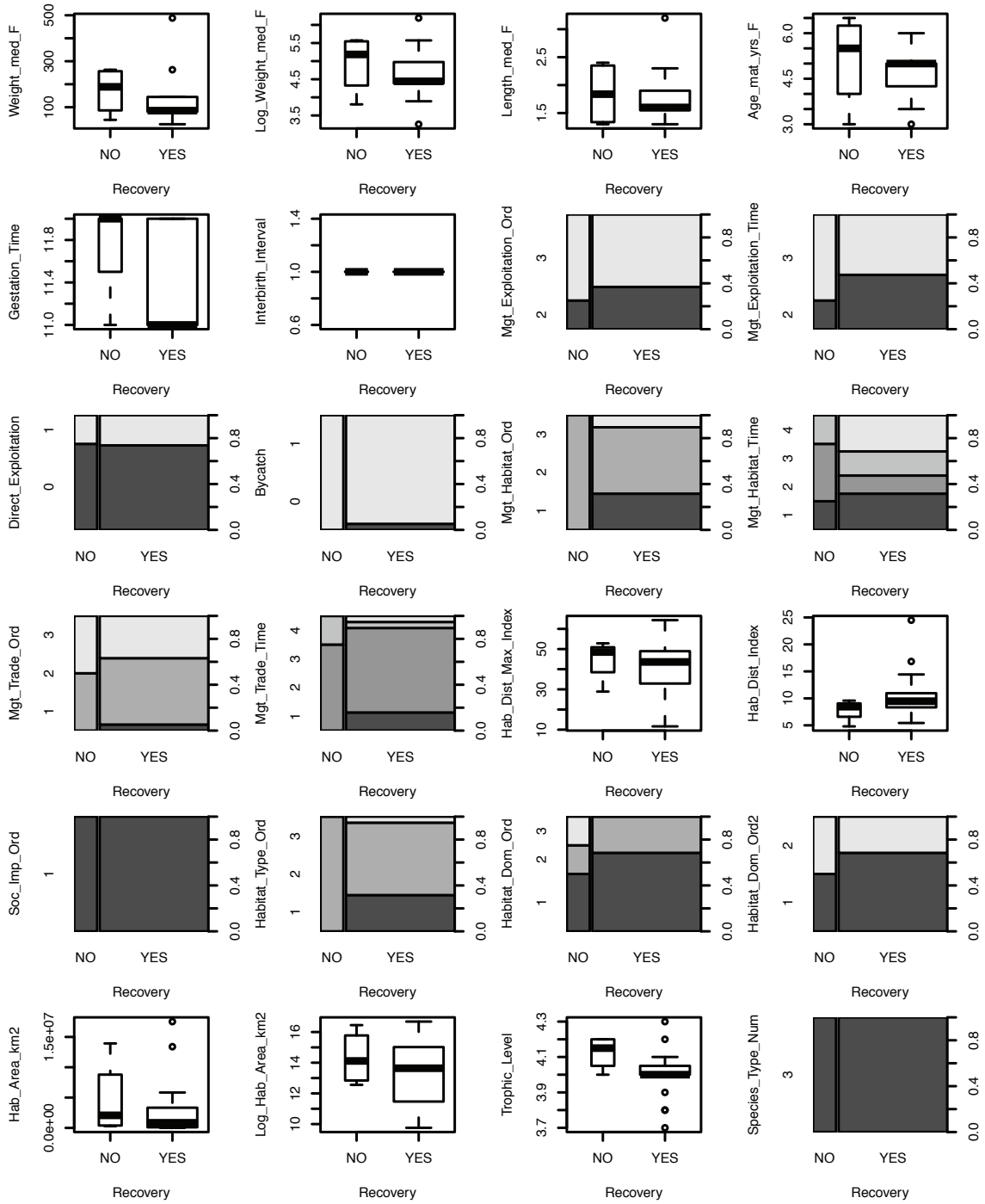
a. All Marine Mammals



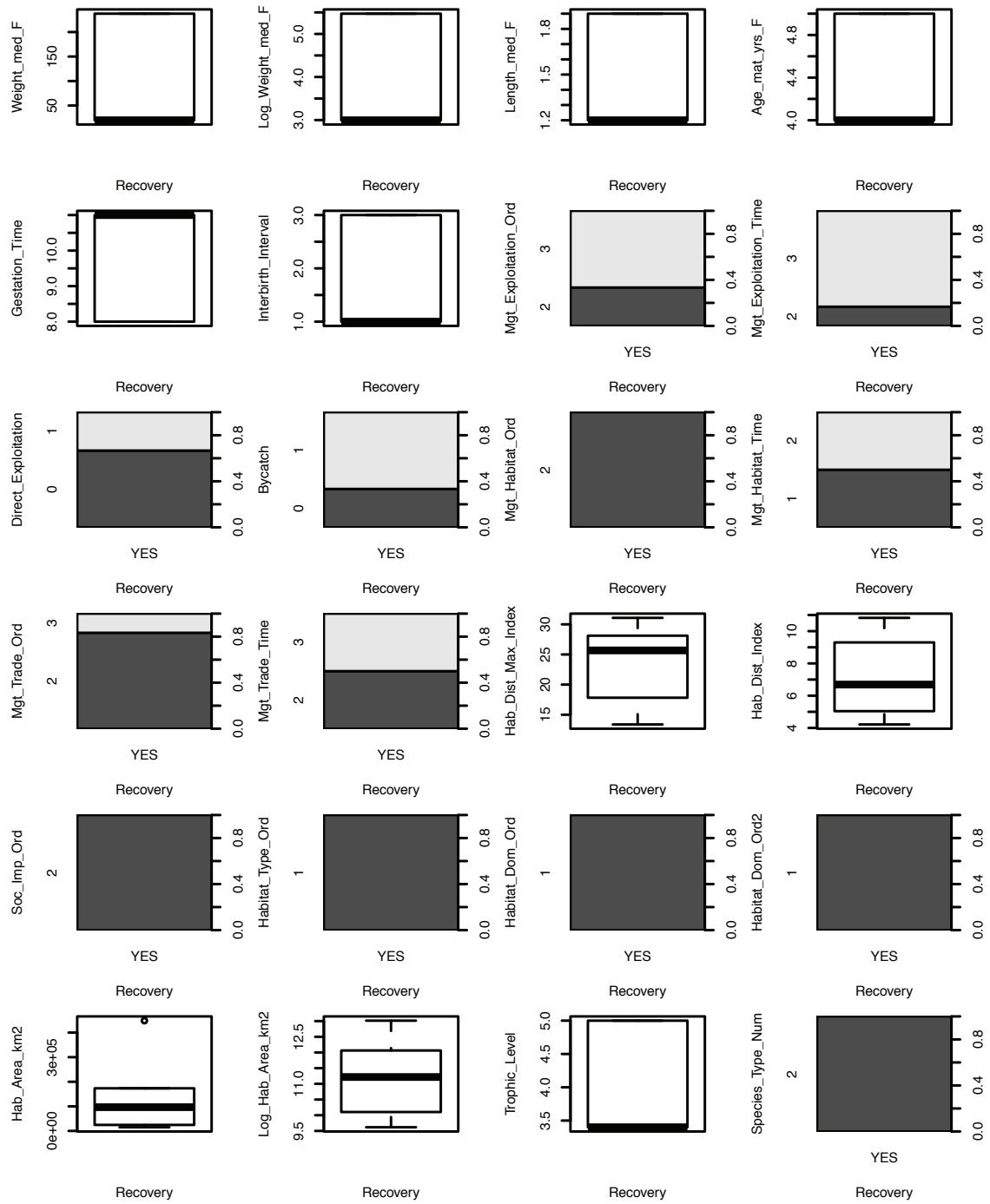
b. Cetaceans



c. Pinnipeds



d. Other



APPENDIX II. E Model Output

Table III.E.1 Output from Models Using All Population, Cetacean and Pinniped Data

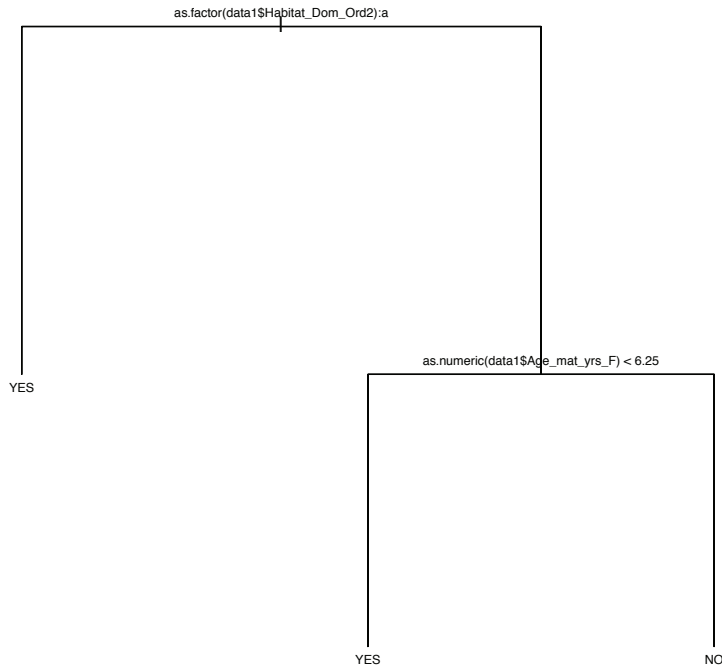
Dataset	Model Type	Model Output	AIC & Variance/Deviance																																			
All	Classification tree	Hab_Dom_Ord2 Age_mat_yrs_F Misclassification error rate: 0.09302	AIC: na Residual mean deviance: 0.5852																																			
All	GAM	Family: binomial, Link function: logit Formula: as.factor(Recovery_N) ~ as.factor(Habitat_Dom_Ord2) + s(Trophic_Level, bs="ts") Parametric coefficients: <table border="0"> <tr> <td></td> <td>Estimate</td> <td>Std. Error</td> <td>z value</td> <td>Pr(> z)</td> </tr> <tr> <td>(Intercept)</td> <td>2.9682</td> <td>0.8461</td> <td>3.508</td> <td>0.000452***</td> </tr> <tr> <td>Habitat_Dom_Ord2 (2)</td> <td>-3.2655</td> <td>1.0264</td> <td>-3.182</td> <td>0.001465 **</td> </tr> </table> Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1 Approximate significance of smooth terms: <table border="0"> <tr> <td></td> <td>edf</td> <td>Ref.df</td> <td>Chi.sq</td> <td>p-value</td> </tr> <tr> <td>s(Trophic_Level)</td> <td>3.734</td> <td>4.611</td> <td>5.213</td> <td>0.341</td> </tr> </table> UBRE score = -0.1571 Scale est. = 1 n = 43		Estimate	Std. Error	z value	Pr(> z)	(Intercept)	2.9682	0.8461	3.508	0.000452***	Habitat_Dom_Ord2 (2)	-3.2655	1.0264	-3.182	0.001465 **		edf	Ref.df	Chi.sq	p-value	s(Trophic_Level)	3.734	4.611	5.213	0.341	AIC: 36.245 R-sq.(adj) = 0.482 Deviance explained = 49.3%										
	Estimate	Std. Error	z value	Pr(> z)																																		
(Intercept)	2.9682	0.8461	3.508	0.000452***																																		
Habitat_Dom_Ord2 (2)	-3.2655	1.0264	-3.182	0.001465 **																																		
	edf	Ref.df	Chi.sq	p-value																																		
s(Trophic_Level)	3.734	4.611	5.213	0.341																																		
All	GAM	Family: binomial, Link function: logit Formula: as.factor(Recovery_N) ~ s(Hab_Dist_Index, bs="ts") + as.factor(Species_Type_Num) Parametric coefficients: <table border="0"> <tr> <td></td> <td>Estimate</td> <td>Std. Error</td> <td>z value</td> <td>Pr(> z)</td> </tr> <tr> <td>(Intercept)</td> <td>2.873e-01</td> <td>6.125e-01</td> <td>0.469</td> <td>0.639</td> </tr> <tr> <td>Species_Type_Num(2)</td> <td>1.374e+02</td> <td>2.740e+07</td> <td>5.01e-06</td> <td>1.00</td> </tr> <tr> <td>Species_Type_Num(3)</td> <td>1.300e+00</td> <td>8.233e-01</td> <td>1.578</td> <td>0.114</td> </tr> </table> Approximate significance of smooth terms: <table border="0"> <tr> <td></td> <td>edf</td> <td>Ref.df</td> <td>Chi.sq</td> <td>p-value</td> </tr> <tr> <td>s(Hab_Dist_Index)</td> <td>0.8328</td> <td>0.985</td> <td>4.01</td> <td>0.0442 *</td> </tr> </table> Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1 UBRE score = -0.015454 Scale est. = 1 n = 43		Estimate	Std. Error	z value	Pr(> z)	(Intercept)	2.873e-01	6.125e-01	0.469	0.639	Species_Type_Num(2)	1.374e+02	2.740e+07	5.01e-06	1.00	Species_Type_Num(3)	1.300e+00	8.233e-01	1.578	0.114		edf	Ref.df	Chi.sq	p-value	s(Hab_Dist_Index)	0.8328	0.985	4.01	0.0442 *	AIC: 42.335 R-sq.(adj) = 0.263 Deviance explained = 29.1%					
	Estimate	Std. Error	z value	Pr(> z)																																		
(Intercept)	2.873e-01	6.125e-01	0.469	0.639																																		
Species_Type_Num(2)	1.374e+02	2.740e+07	5.01e-06	1.00																																		
Species_Type_Num(3)	1.300e+00	8.233e-01	1.578	0.114																																		
	edf	Ref.df	Chi.sq	p-value																																		
s(Hab_Dist_Index)	0.8328	0.985	4.01	0.0442 *																																		
All	GLM	Call: glm(formula = Recovery ~ as.factor(data1\$Habitat_Dom_Ord2) + as.factor(data1\$Species_Type_Num), family = binomial, data = data1) Deviance Residuals: <table border="0"> <tr> <td>Min</td> <td>1Q</td> <td>Median</td> <td>3Q</td> <td>Max</td> </tr> <tr> <td>-2.5207</td> <td>-0.3305</td> <td>0.2919</td> <td>0.6612</td> <td>1.0467</td> </tr> </table> Coefficients: <table border="0"> <tr> <td></td> <td>Estimate</td> <td>Std. Error</td> <td>z value</td> <td>Pr(> z)</td> </tr> <tr> <td>(Intercept)</td> <td>1.4094</td> <td>0.8367</td> <td>1.685</td> <td>0.09207 .</td> </tr> <tr> <td>Habitat_Dom_Ord2(2)</td> <td>-2.8188</td> <td>0.9946</td> <td>-2.834</td> <td>0.00459 **</td> </tr> <tr> <td>Species_Type_Num (2)</td> <td>17.1566</td> <td>2662.8562</td> <td>0.006</td> <td>0.99486</td> </tr> <tr> <td>Species_Type_Num (3)</td> <td>1.7249</td> <td>0.9561</td> <td>1.804</td> <td>0.07123 .</td> </tr> </table> --- Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1 (Dispersion parameter for binomial family taken to be 1) Null deviance: 48.902 on 42 degrees of freedom Residual deviance: 29.962 on 39 degrees of freedom Number of Fisher Scoring iterations: 17	Min	1Q	Median	3Q	Max	-2.5207	-0.3305	0.2919	0.6612	1.0467		Estimate	Std. Error	z value	Pr(> z)	(Intercept)	1.4094	0.8367	1.685	0.09207 .	Habitat_Dom_Ord2(2)	-2.8188	0.9946	-2.834	0.00459 **	Species_Type_Num (2)	17.1566	2662.8562	0.006	0.99486	Species_Type_Num (3)	1.7249	0.9561	1.804	0.07123 .	AIC: 37.962 R-sq. approx. = 0.387
Min	1Q	Median	3Q	Max																																		
-2.5207	-0.3305	0.2919	0.6612	1.0467																																		
	Estimate	Std. Error	z value	Pr(> z)																																		
(Intercept)	1.4094	0.8367	1.685	0.09207 .																																		
Habitat_Dom_Ord2(2)	-2.8188	0.9946	-2.834	0.00459 **																																		
Species_Type_Num (2)	17.1566	2662.8562	0.006	0.99486																																		
Species_Type_Num (3)	1.7249	0.9561	1.804	0.07123 .																																		

Dataset	Model Type	Model Output	AIC & Variance/Deviance																														
All	GLM	<p>Call: glm(formula = Recovery ~ as.numeric(Hab_Dist_Max_Index) + as.numeric(Hab_Dist_Index), family = binomial, data = data1)</p> <p>Deviance Residuals:</p> <table> <tr> <td>Min</td> <td>1Q</td> <td>Median</td> <td>3Q</td> <td>Max</td> </tr> <tr> <td>-3.1732</td> <td>-0.4260</td> <td>0.4138</td> <td>0.7090</td> <td>1.2003</td> </tr> </table> <p>Coefficients:</p> <table> <tr> <td></td> <td>Estimate</td> <td>Std. Error</td> <td>z value</td> <td>Pr(> z)</td> </tr> <tr> <td>(Intercept)</td> <td>-0.71294</td> <td>1.46784</td> <td>-0.486</td> <td>0.6272</td> </tr> <tr> <td>Hab_Dist_Max_Index</td> <td>-0.07639</td> <td>0.03871</td> <td>-1.973</td> <td>0.0485 *</td> </tr> <tr> <td>Hab_Dist_Index</td> <td>0.60168</td> <td>0.24595</td> <td>2.446</td> <td>0.0144 *</td> </tr> </table> <p>Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1</p> <p>(Dispersion parameter for binomial family taken to be 1)</p> <p>Null deviance: 48.902 on 42 degrees of freedom</p> <p>Residual deviance: 38.520 on 40 degrees of freedom</p> <p>Number of Fisher Scoring iterations: 6</p>	Min	1Q	Median	3Q	Max	-3.1732	-0.4260	0.4138	0.7090	1.2003		Estimate	Std. Error	z value	Pr(> z)	(Intercept)	-0.71294	1.46784	-0.486	0.6272	Hab_Dist_Max_Index	-0.07639	0.03871	-1.973	0.0485 *	Hab_Dist_Index	0.60168	0.24595	2.446	0.0144 *	<p>AIC: 44.52</p> <p>R-sq. approx. = 0.212</p>
Min	1Q	Median	3Q	Max																													
-3.1732	-0.4260	0.4138	0.7090	1.2003																													
	Estimate	Std. Error	z value	Pr(> z)																													
(Intercept)	-0.71294	1.46784	-0.486	0.6272																													
Hab_Dist_Max_Index	-0.07639	0.03871	-1.973	0.0485 *																													
Hab_Dist_Index	0.60168	0.24595	2.446	0.0144 *																													
Cetacean	Classification tree	<p>Hab_Dom_Ord2</p> <p>Misclassification error rate: 0</p>	<p>AIC: na</p> <p>Residual mean deviance: 0</p>																														
Cetacean	GLM	<p>Call: glm(formula = Recovery ~ as.numeric(log(data1\$Weight_med_F)), family = binomial, data = data1)</p> <p>Deviance Residuals:</p> <table> <tr> <td>Min</td> <td>1Q</td> <td>Median</td> <td>3Q</td> <td>Max</td> </tr> <tr> <td>-1.914382</td> <td>-0.833554</td> <td>-0.005069</td> <td>0.741452</td> <td>1.771508</td> </tr> </table> <p>Coefficients:</p> <table> <tr> <td></td> <td>Estimate</td> <td>Std. Error</td> <td>z value</td> <td>Pr(> z)</td> </tr> <tr> <td>(Intercept)</td> <td>-3.3174</td> <td>1.9909</td> <td>-1.666</td> <td>0.0957 .</td> </tr> <tr> <td>log(Weight_med_F)</td> <td>0.4303</td> <td>0.2462</td> <td>1.748</td> <td>0.0804 .</td> </tr> </table> <p>Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1</p> <p>(Dispersion parameter for binomial family taken to be 1)</p> <p>Null deviance: 19.408 on 13 degrees of freedom</p> <p>Residual deviance: 15.551 on 12 degrees of freedom</p> <p>Number of Fisher Scoring iterations: 4</p>	Min	1Q	Median	3Q	Max	-1.914382	-0.833554	-0.005069	0.741452	1.771508		Estimate	Std. Error	z value	Pr(> z)	(Intercept)	-3.3174	1.9909	-1.666	0.0957 .	log(Weight_med_F)	0.4303	0.2462	1.748	0.0804 .	<p>AIC: 19.551</p> <p>R-sq. approx. = 0.199</p>					
Min	1Q	Median	3Q	Max																													
-1.914382	-0.833554	-0.005069	0.741452	1.771508																													
	Estimate	Std. Error	z value	Pr(> z)																													
(Intercept)	-3.3174	1.9909	-1.666	0.0957 .																													
log(Weight_med_F)	0.4303	0.2462	1.748	0.0804 .																													
Pinniped	Classification tree	<p>Hab_Dist_Index</p> <p>Hab_Dist_Max_Index</p> <p>Misclassification error rate: 0.1304</p>	<p>AIC: na</p> <p>Residual mean deviance: 0.6505</p>																														

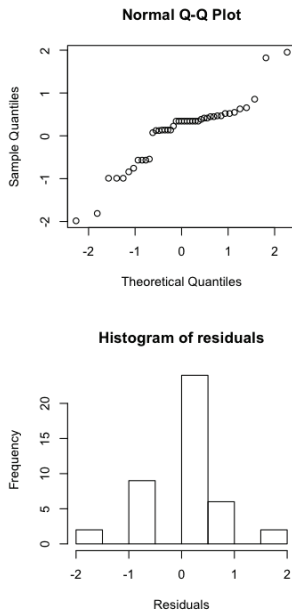
Dataset	Model Type	Model Output	AIC & Variance/Deviance																									
Pinniped	GLM	<p>Call: glm(formula = Recovery ~ as.numeric(Hab_Dist_Index) + as.numeric(Trophic_Level), family = binomial, data = data1)</p> <p>Deviance Residuals:</p> <table> <tr> <td>Min</td> <td>1Q</td> <td>Median</td> <td>3Q</td> <td>Max</td> </tr> <tr> <td>-1.99537</td> <td>0.04984</td> <td>0.22026</td> <td>0.46550</td> <td>1.41522</td> </tr> </table> <p>Coefficients: Estimate Std. Error z value Pr(> z)</p> <table> <tr> <td>(Intercept)</td> <td>36.1324</td> <td>22.1905</td> <td>1.628</td> <td>0.1035</td> </tr> <tr> <td>Hab_Dist_Index</td> <td>0.6623</td> <td>0.4242</td> <td>1.561</td> <td>0.1185</td> </tr> <tr> <td>Trophic_Level</td> <td>-9.9101</td> <td>5.7021</td> <td>-1.738</td> <td>0.0822</td> </tr> </table> <p>Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1</p> <p>(Dispersion parameter for binomial family taken to be 1)</p> <p>Null deviance: 21.254 on 22 degrees of freedom</p> <p>Residual deviance: 14.321 on 20 degrees of freedom</p> <p>Number of Fisher Scoring iterations: 7</p>	Min	1Q	Median	3Q	Max	-1.99537	0.04984	0.22026	0.46550	1.41522	(Intercept)	36.1324	22.1905	1.628	0.1035	Hab_Dist_Index	0.6623	0.4242	1.561	0.1185	Trophic_Level	-9.9101	5.7021	-1.738	0.0822	<p>AIC: 20.321</p> <p>R-sq. approx. = 0.326</p>
Min	1Q	Median	3Q	Max																								
-1.99537	0.04984	0.22026	0.46550	1.41522																								
(Intercept)	36.1324	22.1905	1.628	0.1035																								
Hab_Dist_Index	0.6623	0.4242	1.561	0.1185																								
Trophic_Level	-9.9101	5.7021	-1.738	0.0822																								
Pinniped	GLM	<p>Call: glm(formula = Recovery ~ as.numeric(data1\$Hab_Dist_Max_Index) + as.numeric(data1\$Hab_Dist_Index), family = binomial, data = data1)</p> <p>Deviance Residuals:</p> <table> <tr> <td>Min</td> <td>1Q</td> <td>Median</td> <td>3Q</td> <td>Max</td> </tr> <tr> <td>-2.243235</td> <td>0.001316</td> <td>0.036045</td> <td>0.383247</td> <td>1.061316</td> </tr> </table> <p>Coefficients: Estimate Std. Error z value Pr(> z)</p> <table> <tr> <td>(Intercept)</td> <td>-1.2064</td> <td>3.7853</td> <td>-0.319</td> <td>0.750</td> </tr> <tr> <td>Hab_Dist_Max_Index</td> <td>-0.3775</td> <td>0.2461</td> <td>-1.534</td> <td>0.125</td> </tr> <tr> <td>Hab_Dist_Index</td> <td>2.2753</td> <td>1.3292</td> <td>1.712</td> <td>0.087</td> </tr> </table> <p>---</p> <p>Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1</p> <p>(Dispersion parameter for binomial family taken to be 1)</p> <p>Null deviance: 21.254 on 22 degrees of freedom</p> <p>Residual deviance: 11.056 on 20 degrees of freedom</p> <p>Number of Fisher Scoring iterations: 8</p>	Min	1Q	Median	3Q	Max	-2.243235	0.001316	0.036045	0.383247	1.061316	(Intercept)	-1.2064	3.7853	-0.319	0.750	Hab_Dist_Max_Index	-0.3775	0.2461	-1.534	0.125	Hab_Dist_Index	2.2753	1.3292	1.712	0.087	<p>AIC: 17.056</p> <p>R-sq. approx. = 0.480</p>
Min	1Q	Median	3Q	Max																								
-2.243235	0.001316	0.036045	0.383247	1.061316																								
(Intercept)	-1.2064	3.7853	-0.319	0.750																								
Hab_Dist_Max_Index	-0.3775	0.2461	-1.534	0.125																								
Hab_Dist_Index	2.2753	1.3292	1.712	0.087																								

Figure III.E.1 All Marine Mammals: Classification Tree (a), GAM Residual Plots for Dominant Habitat GAM (b.i) and Associated Smoothed Terms (b.ii) and Habitat Disturbance GAM (b.iii) and Associated Smoothed Terms (b.iv), Residual Plots for Dominant Habitat GLM (c.i) and Habitat Disturbance GLM (c.ii). Habitati_Dom_Ord2 = Dominant Habitat, Age_mat_yrs_F = female age of maturity (years), Hab_Dist_Index = Mean Habitat Disturbance.

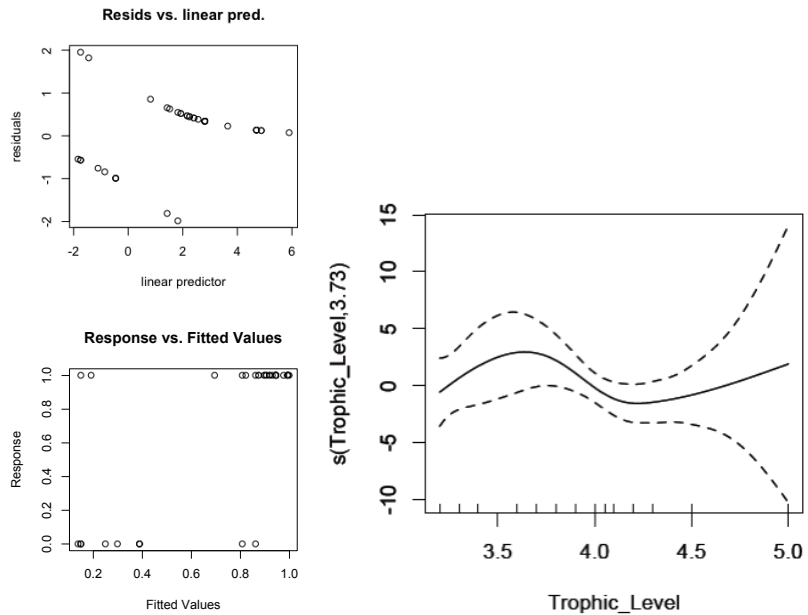
a



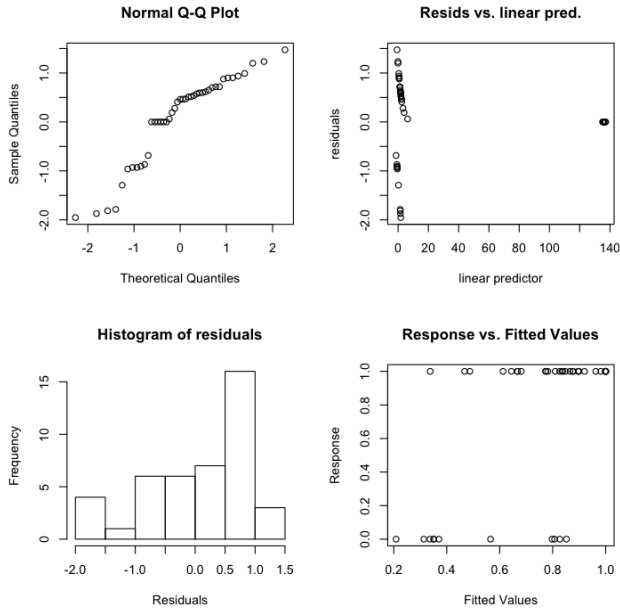
b.i



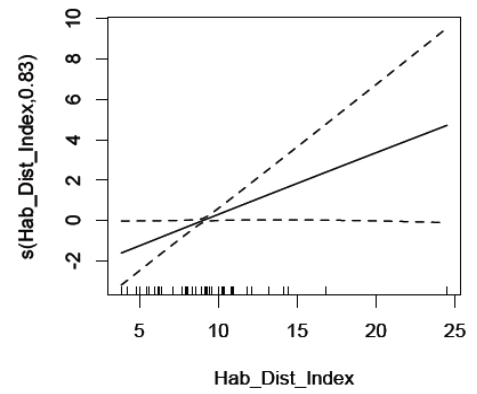
b.ii



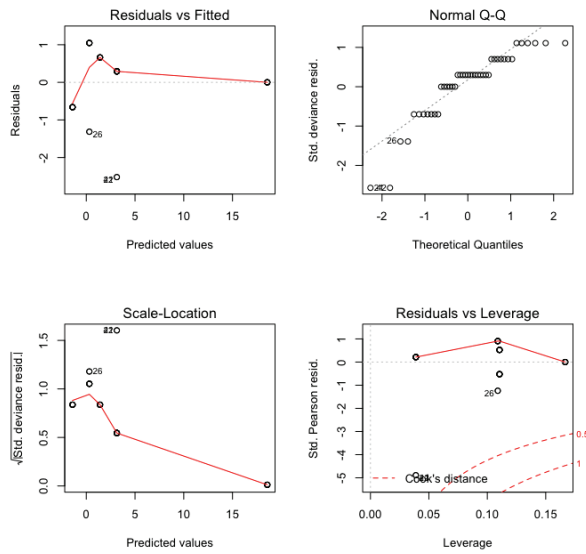
b.iii



b.iv



c.i



c.ii

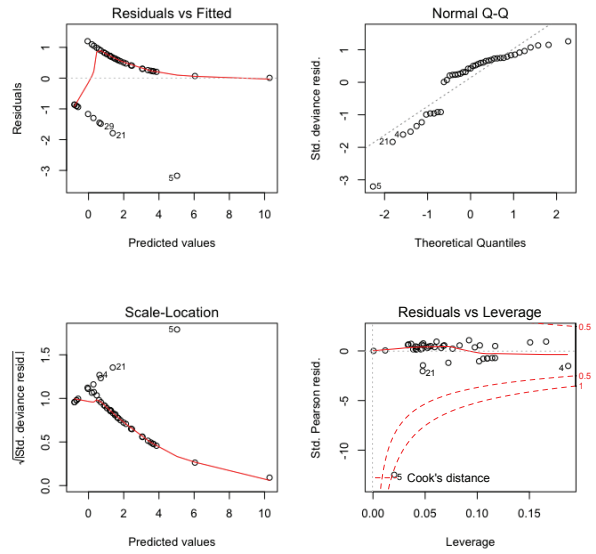


Figure III.E.2 Cetaceans Classification Tree (a) and GLM Residual Plots (b).
 Habitat_Dom_Ord2 = Dominant Habitat.

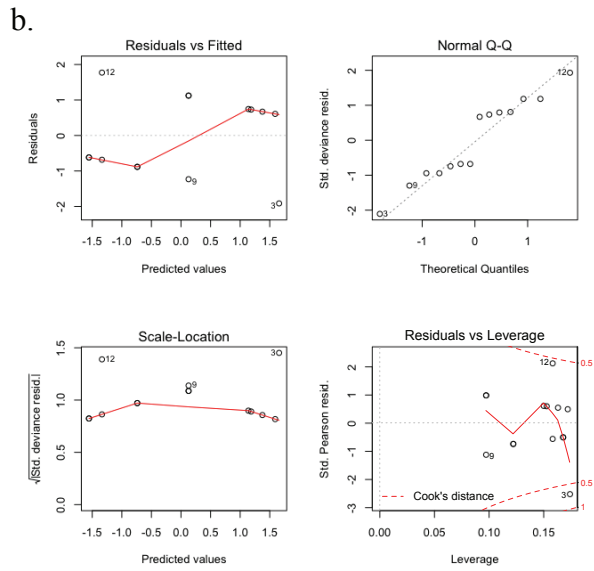
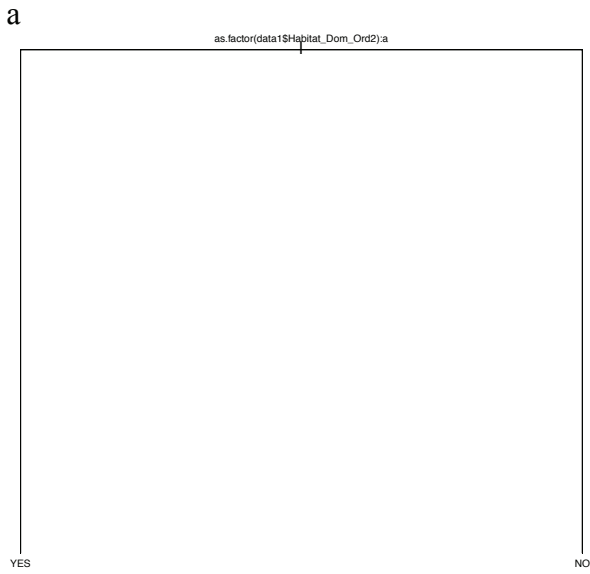
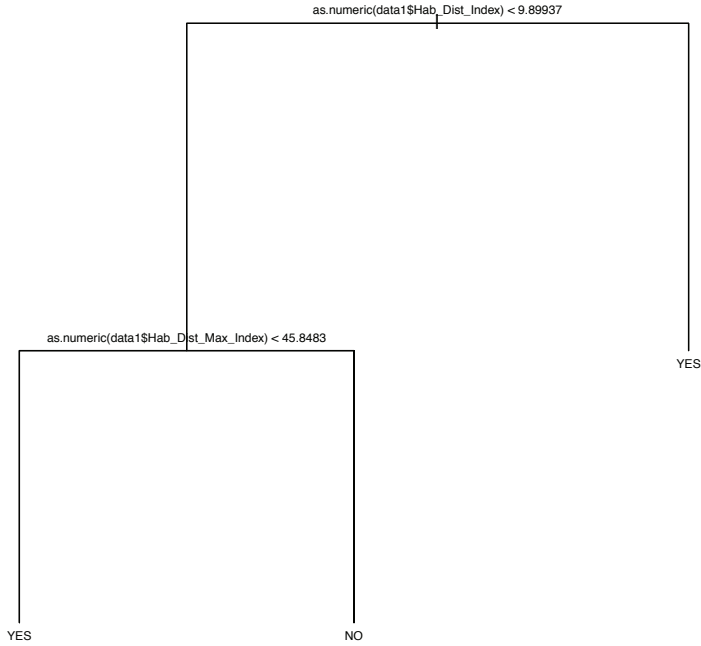
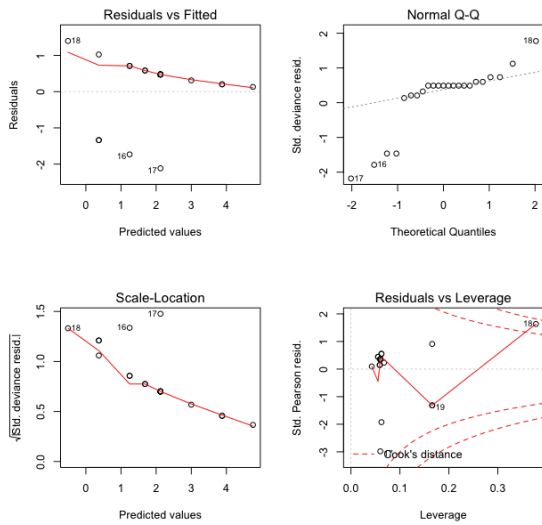


Figure III.E.3 Pinniped Classification Tree (a), GLM Residual Plots for Trophic Level GLM (b.i) and Habitat Disturbance GLM (b.ii). Hab_Dist_Index = Mean Habitat Disturbance, Hab_Dist_Max_Index = Maximum Habitat Disturbance.

a



b.i



b.ii

