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Dealing With Many Species: Improving Methodology For Forming And Assessing Species Complexes

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Dealing with Many Species: Improving Methodology for Forming and Assessing Species
Complexes

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A Dissertation

Presented to

The Faculty of the School of Marine Science

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In Partial Fulfillment

of the Requirements for the Degree of

Doctor of Philosophy

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By

Kristen Liane Omori

August 2021

APPROVAL SHEET

This dissertation is submitted in partial fulfillment of

the requirements for the degree of

Doctor of Philosophy

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ABSTRACT

In the United States, the Magnuson-Stevens Reauthorization Act mandates that all federally fished species must have catch limits, which can be challenging for data-limited species. One approach is to assess and manage a group of species with similar life history characteristics, vulnerability to the fishery, and overlapping geographic distributions in a single management unit, or a complex (i.e., stock or species complex). Using the Gulf of Alaska (GOA) Other Rockfish complex as a case study, the main goals of this dissertation are five-fold: 1) review species complexes in the United States; 2) compare multivariate techniques for assigning species to complexes; 3) group species based on spatial and temporal patterns using a new application of a species distribution model (i.e., Vector Autoregressive Spatio-Temporal model, VAST, model); 4) compare catch advice between existing assessment models used for species complexes with that from the new spatio-temporal modelling (i.e., VAST) application; 5) refine management advice on appropriate species groupings and associated catch limits for this complex.

In *Chapter 1* a review was undertaken of all managed and assessed complexes in the United States, thereby identifying regional differences in management strategies and assessment models used to set catch limits for established complexes. The remaining chapters focused on the GOA Other Rockfish, a group of 27 *Sebastes* species. In *Chapter 2,* a suite of multivariate methods (e.g., cluster analyses and ordination techniques) was developed and applied on an array of datasets (e.g., life history values, fishery-dependent catch, and fishery-independent surveys), to examine how species groupings can vary depending on the methods or data utilized. Results indicated that the species composition for the two main gear types, trawl and longline gear, were different. *Chapter 3* addressed the complex membership using a spatio-temporal species distribution model, which was used to investigate the temporal and spatial relationships among species and compared with groupings based on harvest fractions and life history values. Main results for species groupings were consistent across methods from *Chapter 2* and *3*, suggesting that rockfish belonging to a sub-group of the GOA Other Rockfish (i.e., members of the Demersal Shelf Rockfish) should be removed and managed separately from the Other Rockfish complex throughout the GOA management area. Using the resultant complexes, *Chapter 4* compared two assessment models for the GOA Other Rockfish: the currently used random effects model and a newly, developed spatio-temporal model (VAST). While the results of this research are specific to the GOA Other Rockfish, the lessons and recommendations are applicable to other complexes with similar data availability. Multiple data sources and a variety of methods should be used to identify or verify complex membership, where the best species groupings are those that are consistent across all analyses. Variation in groupings across analytical methods and data inputs can provide further insight into data needs or species that warrant careful monitoring. Additionally, new assessment models for species complexes should be explored and tested to ensure results adequately reflect the status of the complex and provide reasonable harvest limits.

AUTHOR'S NOTE

The chapters that comprise this dissertation were written in manuscript format for scientific publication. Thus, the formatting for each chapter follows the guidelines of the journal to which the manuscript was or will be submitted. At the time of writing, citations for individual chapters are as follows:

Chapter 1:
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Chapter 4:
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Dealing with Many Species: Improving Methodology for Forming and Assessing Species Complexes

CHAPTER 1

Review of assessment and management approaches for species complexes in the United States

Abstract

One approach to comply with federal mandates that require catch limits for all federally harvested stocks in the United States is to assess and manage multiple stocks, which demonstrate similar biological characteristics or exploitation patterns, as a single stock complex. However, methodology for assigning and assessing species complexes varies widely depending on location, institution, exploitation patterns, and data availability. Thus, we review all managed and assessed stock complexes in the United States, thereby identifying regional differences in management strategies and assessment models used to set catch limits. Approaches for assessing complexes in the United States are typically divided into two categories: deriving harvest limits for each stock individually before producing the total harvest limit and calculating a single harvest limit for the stock aggregation. The assessment models range from using catch scalars based on catch time series to age-structured models depending on the region and data availability. As one of the first reviews of federally managed species complexes in the United States, the results provide guidance to regional fisheries management bodies that could improve how species complexes are treated by identifying alternate methods that might be adapted from similar complexes in other regions. Despite regional differences in data and management needs, a more consistent and generalized approach towards managing species complexes could aid in reducing the scientific burden associated with managing species complexes in the United States.

1.1 Introduction

Marine fisheries provide important food resources and associated livelihoods from the fishing industry (FAO, 2020). But, human population growth has intensified the direct and indirect pressures on marine resources. As a result, it is increasingly important to develop scientific-based assessment and management advice of all directly and indirectly (i.e., non-target) exploited stocks to ensure sustainably managed fisheries. Yet, the majority of the world's fish stocks lacks adequate data for conventional age or length-structured stock assessment methods (referred to as data-limited stocks). Thus, globally, more than 80% of total worldwide marine fish removals come from data-limited species that lack formal assessments (Costello et al., 2012). Similarly, approximately 70% of all managed stocks in the United States are data-limited (Newman et al., 2015). Despite insufficient data for many species, in the United States the Magnuson-Stevens Fishery Conservation and Management Reauthorization Act of 2006 (MSRA; MSRA, 2007) requires annual catch-limits for all federally exploited fish stocks in order to promote sustainable harvest (MSRA, 2007). One approach for dealing with data-limited fisheries that aligns with the federal and international marine policy, is to assess and manage multiple species within a stock complex. A complex is defined as a group of stocks with common life history characteristics, susceptibility to fishing gear, and similar geographic distribution (USOFR, 2009). A stock complex is typically managed as a single functional unit with catch advice provided for the aggregated complex and not for individual species.

Formation of a stock complex can be done for a variety of reasons (USOFR 2009), including data-limitations (e.g., Caribbean angelfish complex; SEDAR, 2009), being a non-target (e.g., bycatch) species, or exploitation by a non-selective gear type necessitating multi-species management advice (e.g., the Bering Sea-Aleutian Islands skate complex; Ormseth, 2020). Another common reason is that species mis-identification may prevent adequate single species assessment and management, because identifying morphologically similar species with overlapping geographic ranges is not possible without careful examination or genetic data (e.g., as is the case for rougheye (*Sebastes aleutianus*) and blackspotted (*S. melanostictus*) rockfishes in the Gulf of Alaska; Shotwell and Hanselman 2019). Inadequate data for individual assessments or lack of funds devoted to species identification is often due to low economic value or limited resources, because it is often not cost-efficient to devote personnel or funds to species of limited economic value. Therefore, the formation of stock complexes can be useful for adhering to the requirements of international and federal mandates requiring catch limits for all exploited species by providing assessments and catch limits for the entire complex instead of on a species-by-species basis. Similarly, identifying and managing stock complexes reduces the number of stock assessments needed, while allowing species that lack adequate data for single-species stock assessments to be quantitatively managed.

In the United States, stock complexes are managed as a single unit in the fishery management plans by the Fishery Management Councils (FMC; i.e., institutions entrusted with managing the fisheries in a given region). The regions and associated FMCs include: Caribbean (CFMC), Gulf of Mexico (GMFMC), Atlantic Highly

Migratory Species (HMS), South Atlantic (SAFMC), Mid-Atlantic (MAFMC), Northeast (NEFMC), Western Pacific (WPFMC), Pacific (PFMC), and North Pacific (NPFMC). Within these complexes are stocks that can be assessed individually or as groups, which results in the annual catch limits (ACLs) being derived for each stock individually before producing the summed complex ACL or calculated simply as a single ACL for the stock aggregation, respectively. However, to date there has been no holistic review of the assessment and management approaches used for stock complexes in the United States. By providing a thorough review of stock complexes in the United States, consistent and divergent patterns across regions can be elucidated, which can help fisheries managers identify and adapt new approaches that may help improve and standardize stock complex assessment methodology. More specifically, stock complexes are reviewed to compare regional differences in: 1) the number of fish stock complex assessments per region in the United States; 2) assessment methods; and 3) approaches to formulating ACLs for fish stock complexes. Therefore, this review addresses the challenges and progress in the assessment of stock complexes across the United States.

1.2 Methods

A database of federally managed species in the United States was analyzed to identify the number of stock complexes being managed within each region along with key characteristics determining why the stock complex approach was utilized (e.g., data limitations). Similarly, the type of assessment methodology was then determined and described. Comparisons across complexes and regions were made to identify key drivers of stock complex management in the United States and common methods utilized. The

Gulf of Alaska Other rockfish complex is explored in detail as a case study, because this complex provides an exemplar for stock complex management that is then analyzed in detail in subsequent chapters.

1.2.1   *Data sources and comparison metrics*

Federal fishery management plans (FMPs) were reviewed to obtain designated management complexes, then compared to stocks listed in the Stock SMART (Status, Management, Assessments and Resource Trends; https://www.st.nmfs.noaa.gov/stocksmart) database to ensure consistency across listings. Ecosystem component species (i.e., stocks not caught in the fisheries, not subject to overfishing, nor would being overfished be likely, but are considered to be an important part of the ecosystem) are excluded from the list of complexes, because these species are not required to have formal stock assessments or catch limits. The management complexes are further classified by type of management strategies utilized: indicator species (single-species stock assessments for one or a few key species only), individual (single-species assessments for each stock in the complex), unassessed, complex (2+ aggregated stocks assessed as a single unit), or indicator and complex (combination of using indicator species and a complex). For all managed stock complexes, the number of species, indicator species (if applicable), and reason for managing as a complex were recorded. Assessments for fish stock complexes containing 2+ stocks are reviewed (i.e., complexes containing only multiple stocks of the same species and assessments for invertebrate complexes are not addressed here). Because many data-limited stocks are not assessed annually, the most recent, full (i.e., complete) assessments are used with the

years ranging from 2017 to mid-2021. Accepted assessments for stock complexes are ones that use an estimation model approach, which has been accepted by the associated regional Science and Statistical Committee (SSC; i.e., the review body entrusted with verifying the appropriateness and robustness of all United States federal stock assessments; MSRA, 2007). If assessments were rejected or ACLs were formed based on fractions of past catch (i.e., catch scalars), the management strategy was marked as 'unassessed'.

The following information from each assessed fish complex stock assessment was also recorded: number of species, indicator species (if applicable), reason for managing as a complex, assessment model, harvest strategy, and data-level assignment (if applicable). Furthermore, assessment models were classified based on data needs, data-availability, and type of harvest control rule utilized. Because each fisheries management region has its own data-level assignments for assessed stocks, there is no consistent data-level assignment available. For example, the PFMC assigns stocks in categories from 1 (data-rich) to 3 (data-poor), whereas the NPFMC designates stocks into tiers ranging from 1 (data-rich) to 6 (data-poor). Thus, for this review, assessment model categorizations were redefined from 1 to 4, where: "1" designates a data-rich statistical age- or length-structured model "2" represents a data-moderate model that that can estimate maximum sustainable yield (MSY) values, but without age or lengths (e.g., production models); "3" was a data-limited estimation model that produces biomass estimates, but uses MSY proxies; and "4" was reserved for data-poor methods that use historical catch-based approaches to set catch limits (i.e., falls into the "unassessed" category and used catch scalars). Finally, because a managed complex consisted of

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multiple stocks managed under a single ACL, stocks belonging to a given complex may have different levels of available data. Therefore, there were multiple data-level tiers and two assessment model categorizations were provided. The first assessment model category for the assessed complex is based on the majority of category assignments (i.e., model level 'majority'). The second assessment model category assignment was based on the lowest category value (i.e., the least data-rich level or 'lowest' model level).

1.2.2 *Gulf of Alaska Other Rockfish complex background*

The Gulf of Alaska (GOA) Other Rockfish complex comprises 27 *Sebastes* species in the GOA management region. In general, rockfish species are characterized by their late maturity and high longevity and they bear live young (Love et al., 2002). However, there is a wide range of life history values within the rockfish complex (see Chapter 2 for life history values and references). The length and age at 50% maturity range from 150 - 450 mm and 2.5 - 22 years, respectively, and the maximum age of maturity ranges from 26 – 117. The maximum average length, defined here as von Bertalanffy asymptotic length, L_∞, ranges from 304 – 810 mm. Given the slow growth and long-lived attributes for rockfish, the estimated natural mortality (*M*) is low, 0.04 – 0.06 yr-1. Unfortunately, most life history studies examining maximum age, age at maturity and associated lengths were completed in lower latitudes than the Gulf of Alaska. Studies have shown differential growth rates in different latitudes (e.g., splitnose rockfish [*S. diploproa*]; Gertseva et al., 2010); thus, life history characteristics presented here are likely to contain a moderate degree of uncertainty.

In rockfish, fertilization of the egg, embryonic development, and hatching occur internally, and studies have shown that some energy during development is transferred directly from mother to embryo (Love et al., 2002). This reproductive strategy is defined as viviparous instead of ovoviviparous (i.e., where energy arises solely from yolk sacs). This strategy of internal development and hatching of the eggs increases the survival of the eggs by almost four times compared to external fertilization and development in the water column (Bechtol, 1998). Estimated fecundity for GOA rockfish species ranges from 1,700 to close to 2 million (Love et al., 2002). Older females produce more offspring than younger females, while annual fecundity, the number of broods, and reproductive season vary by year and region for each *Sebastes* species (Love et al., 2002; Beyer et al., 2015). However, multiple broods may be less likely in the northern latitudes (Love et al., 2002).

In addition to having an array of life history characteristics, the Other Rockfish species vary in their distribution and habitat selection. Most of these species are at their northern distribution limits, spanning from off the coast of Southern California to Alaska (Love et al., 2002). Harlequin rockfish (*S. variegatus*) is the only species that is found primarily in the northern waters from British Columbia to Alaska (Tribuzio and Echave, 2019). Typically, rockfish are found at depths ranging from 100 - 275 m (Love et al., 2002), but can be found in depths up to 800 m. Some rockfish species undergo an ontogenetic shift, where the juveniles commonly occupy shallower depths feeding on plankton, then adults move to deeper depths over a variety of substrate types (Love et al., 2002). Adults occupy a wide range of habitat types including high relief rocks, reefs or crevices, low relief rocky bottoms, mudflats, vegetative areas, and mixed habitat

(Johnson et al., 2003; Conrath et al., 2019). Individuals of some species are more solitary, whereas others tend to aggregate in large mixed-species schools (Johnson et al., 2003).

1.3 Results

In total, there are 117 stock complexes managed in United States federal waters across all regions, 75% of which are fish stock complexes and 25% are composed of invertebrates (e.g., octopus, crustaceans, and corals; Table 1). While the individual invertebrate species belonging to complexes could not be tabulated due to the innumerable coral species, there are around 388 individual fish species that are assigned to managed stock complexes. The exact number of fish species remains unknown, because a few complexes are assigned by family groups (e.g., *Gempylidae* in the Western Pacific region). The CFMC manages the most fish complexes with 35, while the NPFMC manages the second highest number of fish complexes with 17 (Table 1). All species belonging to complexes are caught in multispecies fisheries, where the majority are not directly targeted. Stocks in fish complexes frequently are fished recreationally and, in some regions (i.e., Caribbean and Western Pacific), are caught in subsistence fisheries. In addition to being caught in a multi-species and often in multi-gear fisheries, stocks belonging to complexes largely lack sufficient data to assess as a single-species stock. There are a few complexes that are assessed and managed as a complex due to mis-identification (e.g., rougheye and blackspotted rockfish in the North Pacific fisheries; Spencer et al., 2020; Shotwell and Hanselman 2019) or for which genetic analyses have only recently been conducted that clearly delineate what was previously assumed to be a single stock into two distinct species (e.g., Blue [*Sebastes mystinus*] and Deacon

[*Sebastes deaconus*] rockfish in the Pacific Coast fisheries). As of 2021, the NEFMC and MAFMC are the only regions that do not manage any stock complexes.

The majority (68%) of stock complexes are considered to be unassessed (i.e., do not have quantitative stock assessments or stock assessments were not accepted by the associated SSC). For example, all complexes in the South Atlantic region are currently considered to be unassessed, mainly due to insufficient data to assess many non-target species (Table 1). Compared to other regions, the PFMC and NPFMC more frequently used indicator species, when deemed appropriate, to determine the status of the stock complex, which helps to reduce the number of individual assessments required. When indicator species are used, ACLs are based either solely on the estimated abundance of the indicator species or jointly using both the indicator species and the total catch of the complex (Table 1; Fig. 1). Typically, when ACLs are set using only indicator species, the indicator species comprises the majority of the catch of the complex (e.g., Northern sole [*Lepidopsetta polyxystra*] in the Bering Sea- Aleutian Islands Rock Sole complex).

Each FMC has a unique set of models that are typically used to assess the fish complexes managed in the region. With the exception of one complex, the CFMC, GMFMC, HMS, and SAFMC rely on catch scalars based on the available time series of catch to calculate ACLs, which are not classified as accepted stock assessments (i.e., model level 4; Table 1). The WPFMC, which manages all the Pacific Islands fisheries, only have four accepted stock assessments for complexes (Table 1). These four complexes consist of 'bottomfish' (i.e., groundfish) caught in multi-species fisheries. The associated assessments depend mostly on fishery catch, because the Pacific Islands Fisheries Science Center (PIFSC), which provides scientific advice for these species,

does not have the infrastructure, personnel, or financial resources to perform fishery-independent surveys for the remote islands around which these species tend to aggregate. The four PIFSC species complexes are assessed using Bayesian surplus production models, a data-moderate method (model level 2). The NPFMC and PFMC have the largest suite of stock assessment models for fish complexes. As noted, the PFMC assesses complexes based on individual indicator species when appropriate (Fig. 1). For the stocks with sufficient data that are assessed as smaller subunits of the complex (e.g., Blue and Deacon rockfish for Minor Nearshore Rockfish Complexes in the Northern and Southern regions of the West Coast), a data-rich, statistical catch-at-age model is used (model level 1; i.e., Stock Synthesis 3 [SS3]; Methot and Wetzel, 2013). Unassessed fish complexes in the Pacific region use depletion-based stock reduction analysis (XDB-SRA; Dick and MacCall, 2011; Cope et al., 2015) or extended simple stock synthesis (exSSS; Cope et al., 2015) when sufficient catch histories or survey data are available to set ACLs (i.e., model level 3 stocks because it sets ACLs based on estimated depletion values). Finally, the NPFMC manages their complexes using SS3 for the data-rich (model level 1) complexes, a random effects model (SAWG, 2013) for the data-limited complexes (model level 3), and using catch scalars based on fishery catch for the data-poor stock complexes (model level 4) to calculate ACLs. Frequently, species within fish complexes in the North Pacific region, similar to the Pacific region, are further divided into subunits and assessed using methods appropriate for the available data at the subunit level before summing the ACLs. For example, Alaska skate (*Bathyraja parmifera*) is used as an indicator species for the Bering Sea and Aleutian Islands Skate complex and is assessed

using SS3 (model level 1), while the other remaining species are assessed using the random effects model (model level 3).

1.3.1 Assessment and management of the Gulf of Alaska Other Rockfish complex

The Other Rockfish complex consists of non-target species that are captured in more lucrative rockfish and other groundfish fisheries using trawl and longline gear types. Since the 1990's, there has been no directed fishery on the species in the complex with the exception of a silvergray (*S. brevispinis*) and yellowmouth (*S. reedi*) rockfish bottom trawl fishery in 1993 and a trial fishery for Pacific Ocean perch (*S. alutus*) and silvergray rockfish using trolling gear in 2004 and 2005 (Tribuzio and Echave, 2019). The Other Rockfish species have a low economic value (~ $1.19 per pound headed and gutted in 2018) compared to the targeted Thornyhead rockfish (*Sebastolobus spp.*) fishery that is valued around $3.04 per pound (pers. comm. Ben Fissel). The low economic value has resulted in a high discard rate, estimated at 46% (Tribuzio and Echave, 2019), and limited or no targeting of species in the Other rockfish complex.

The GOA management area is divided into five sub-management areas: 610, 620, 630, 640, and 650 (see Figure 1 in Chapter 2). The highest biomass for the complex is in the Eastern GOA (sub-area 640 and 650) based on fisheries catches and fishery-independent surveys. The biennial NOAA Alaska Fisheries Science Center bottom trawl survey has provided fishery-independent biomass estimates for the Other Rockfish complex since 1984. However, seven of the species in the complex live in high relief habitats that are only fishable using longline gear and are essentially inaccessible to bottom trawls. Currently, these seven rockfishes are managed as a part of the Other

Rockfish complex in four of the five GOA sub-areas. In the fifth sub-area, 650, where the majority of the catch for these species occurs, the seven rockfish species are assessed and managed in a separate complex known as the Demersal Shelf Rockfish complex. Additionally, northern rockfish (*S. polyspinis*) is assessed separately in the Central and Western GOA regions (sub-areas 610, 620, and 630) and included in the Other Rockfish complex in the Eastern GOA region due to low abundance. Harvest of the Other Rockfish species is below the aggregate complex catch limit; thus, overfishing is not occurring.

Management for the GOA Other Rockfish complex has evolved since the establishment of this general non-target rockfish complex as the "Other Slope Rockfish" in 1991, which began with a total of 16 Sebastes species. In 1993, the northern rockfish was removed from the complex, but was later reassigned to the complex in management sub-areas 640 and 650 in 1999. Yellowtail (*S. flavidus*) and widow rockfish (*S. entomelas*), originally belonging to their own Pelagic Shelf Rockfish complex, were moved to the 'Other Slope Rockfish' complex in 2012, and the complex was renamed the 'Other Rockfish' complex. In 2013, the seven Demersal Shelf Rockfish were included in the Other Rockfish complex in the management sub-areas 610 – 640. The most recent change was the inclusion of two new rockfish, aurora (*S. aurora*) and shortbelly (*S. jordani*), in the 2019 assessment (Tribuzio and Echave, 2019).

The Other Rockfish are divided into subunits based on data-level (i.e., tiers), where ACLs are calculated per tier and summed to produce a total ACL for the complex. The tiers include two data-limited tiers (Tier 4 and 5) and a data-poor tier (Tier 6). Species belonging to Tiers 4 and 5 are further subdivided into natural mortality groups, where a random effects model (model level 3; SAWG, 2013) is applied to each natural

mortality group to calculate biomass estimates, and the ACL is calculated for each Tier separately. The ACL for rockfish species in Tier 6 is based on a catch scalar method (i.e., maximum recorded catch from the previous four year).

1.4 Discussion

1.4.1 *Regional differences in the assessment and management of complexes*

Aggregating stocks into a single unit (i.e., a stock complex) can be an efficient, practical tactic to comply with federal mandates, but approaches to assessing and managing complexes are region-and case-specific. Data availability, resource accessibility (i.e., availability to fishery and survey gear), and economic importance influence the selection of assessment model and, often, dictate the management strategies applied to set ACLs for each complex. For example, regions that rely on fishery catch data, and often lack resources to conduct consistent fishery-independent surveys, tend to have more unassessed complexes and rely on catch scalars to set ACLs (e.g., the Caribbean, Gulf of Mexico, and Western Pacific regions) compared to regions with fishery independent surveys and more complete and detailed historical catch time series (i.e., the Pacific and North Pacific regions; Berkson and Thorson 2015). The PFMC and NPFMC tend to apply more data-rich and data-moderate methods due to their data and resource availability compared to other regions (Newman et al., 2015), which results in a larger variety of management strategies (e.g., complexes, individual assessments, indicator species, and a hybrid of management types).

When aptly selected, indicator species can be a useful tool to monitor the stock status of a complex. Indicator species should share similar productivity levels, be

consistently caught by the fishing gears, and demonstrate similar population trends as the remaining species in the complex. (Landres et al., 1988; Zacharias and Roff, 2001). While the indicator species have similar characteristics to other species in the complex, the indicator species should be among the more vulnerable species in the complex (i.e., 'weakest link' species; Shertzer and Williams, 2008). The single-species assessments for the indicator species can potentially provide more detailed, reliable results for the associated stock and infer stock status for the remaining species in the complex. However, selecting indicator species can be challenging; all the criteria for an indicator species are often not fulfilled and assumptions for when an indicator species is appropriate (e.g., having a stable community structure) are often violated (Niemi et al., Shertzer et al., 2009).

Each region tends to apply their own set of assessment approaches. Many models were developed specifically to aid in the assessments for a particular region (e.g., the random effects model in the North Pacific), while other regions use more generic platforms (e.g., stock synthesis 3, SS3, in the Pacific region). Regional disparities in assessment model selection, which go hand-in-hand with the applied management strategies, are due to data availability, management area, and other management resource factors (e.g., personnel; Berkson and Thorson, 2015). Most methods applied to assess stock complexes are not specifically designed for a group of aggregated species. Wide ranges in productivity and species resilience to environmental and anthropogenic pressures are common in stock complexes (DeMartini, 2019). To accommodate differences in productivity across species in a complex, it is common to partition the complex into smaller productivity sub-units and apply harvest control rules to those sub-

units (e.g., based on differential natural mortality groupings as is done with Other

Rockfish in the Gulf of Alaska; Tribuzio and Echave, 2019). However, there is a

necessary balance between defining biologically informative and realistic complexes (i.e.,

grouping as few species as is biologically appropriate) versus the practical aspects of

managing extremely data-limited species (i.e., reducing the number of assessed species to

reduce administrative and scientific burden).

1.4.2 Gulf of Alaska Other Rockfish complex research needs

The GOA Other Rockfish are not overfished and overfishing is not occurring

(Tribuzio and Echave, 2019). Most rockfish species in the complex are assessed using the

random effects model by natural mortality group, which serves as a way to capture some

of the species' productivity levels. However, the species that belong to the Other

Rockfish complex in the GOA management sub-areas 610-640, but are assessed

separately in the sub-area 650 as the Demersal Shelf Rockfish complex, rely on catch

scalars to set ACLs. In recent years, stock assessment scientists and management bodies

have questioned the decision to keep the seven species associated with the Demersal

Shelf Rockfish complex in the Other Rockfish complex in management sub-areas 610 –

640 (Tribuzio et al., 2017). More specifically, it has been suggested that verification is

needed to ensure "that these species [Demersal Shelf Rockfish] are more similar to each

other in their complex than to species in other complexes" using statistical approaches

(Tribuzio et al., 2017). The research in *Chapter 2* and *Chapter 3* address this question

using multivariate methods and species distribution modeling; here we provide further

review of the rationale for pursuing management by species complexes and information on how assessment and management of the GOA Other Rockfish complex is conducted.

1.4.3 The future of stock complexes

The management of complexes is not likely to be eliminated in the near future in the United States, because it provides a way to assess and set harvest recommendations for a large number of data-limited stocks. The success of managing a complex stems from the ability to assign stocks into appropriate groups. Most complexes are based on taxonomic groupings and distribution (Cope et al., 2011), but productivity-susceptibility analysis and other risk assessment methods that use expert judgement to rank species into vulnerability groups (e.g., Cope et al., 2011; Zhou et al., 2016) and multivariate analyses (e.g., Shertzer and Williams, 2008; Farmer et al., 2016) are also common. Ultimately, the management of complexes is only as good as the data and scientific information used to define the complexes (Fujita et al., 1998).

There were important advancements in data-limited methods when the MSRA required ACLs to be set for all federally exploited stocks (Newman et al., 2015), but there is now a clear need to improve the methods used for identifying and assessing stock complexes. Increased data collection and incorporating all available data are two ways to enhance the assessment of complexes. Improved cost-effective data collection methods, such as collecting length composition, can greatly benefit assessments for stock complexes (Dowling et al., 2016). Length data alone allows scientists to apply more data-limited methods to assess stock status, such as simple length-based indicators (e.g., Miethe et al., 2019) or length-based estimation of spawning potential ratio (Hordyk et al.,

2015). Other alternative data sources, such as local ecological knowledge (Beaudreau and Levin, 2014) and eDNA (Lacoursière-Roussel et al., 2016), can also be incorporated to group species and aid in assessment of stock complexes. Additionally, borrowing results from data-rich or data-moderate stocks to help inform the assessment of data-limited stocks (i.e., the 'Robin Hood' approach; Punt et al., 2011) or applying hierarchical Bayesian models (e.g., Jiao et al., 2009) can help advance data-limited methods for stock complexes. Life history characteristics within a family group have been shown to be similar and have been suggested as a potential alternative to infer missing productivity values (Thorson et al., 2017). However, all models assessing complexes should be investigated for sensitivity to the input data, which necessarily includes uncertainty in life history characteristics or the reliability of the catch and effort time series (e.g., Sagarese et al., 2019).

Models assessing complexes should be robust to differences in the species' productivity levels, susceptibility to different fishing gear types, and responses to external pressures that affect population levels. It is important to understand the similarity of aggregated species and how a complex might respond to changes in the environment from natural causes or human pressure. Each species in a complex has a niche in the ecosystem. Preserving species diversity within a complex will help maintain the stability of the system and prevent fisheries closures due to overharvest (i.e., the portfolio effect; Schindler et al., 2010). Moreover, diversity within a species complex can be difficult to conserve if researchers do not identify the effects of fishing pressures on species composition and size structure (Rochet et al., 2011).

Ultimately, there are no generic solutions for assessing data-limited species, particularly for stock complexes (Dowling et al., 2019). Likewise, applying an array of methods without considering the assumptions and sensitivities of the models can lead to inconsistencies and mis-representation of the stock complex status (Dowling et al., 2019). Each complex should be managed on a case-by-case basis even within the same region, because of differences in life history, fishing gear susceptibility, and habitat suitability (DeMartini, 2019). Additionally, individual stock populations will fluctuate with climate induced changes, anthropogenic impacts, and other environmental factors. However, developing a common suite of methods or generic practices that could be used to identify and assess stock complexes would be useful to better standardize assessment methodology for stock complexes worldwide. Stock complexes need to be carefully assessed and group membership periodically revised to ensure the species composition within the complex remains relatively stable, such that managing as a complex maintains the continuity and preserve species diversity.

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1.6 Tables

Table 1.1 A summary of the number of complexes, number of species (in parentheses), number of complexes per management type (i.e., unassessed, individual assessments, indicator species, as a complex, or both indicator species and complex), and model-level category for fish complexes (for the majority of stocks in complex [majority] and the most 'data-rich' assessment level for the complex [lowest]) for each Fishery Management Council (FMC) region. The model-level categories are; 1. data-rich with age- or length-structured model, 2. data-moderate model without age or lengths and estimated MSY values, 3. data-limited estimation model with MSY proxies, and 4. data-poor method that uses historical catches. The FMC include: Caribbean (CFMC), Gulf of Mexico (GMFMC), North Pacific (NPFMC), Pacific (PFMC), South Atlantic (SAFMC), Western Pacific (WPFMC), and Highly Migratory Species (in the Atlantic).

	CFMC	GMFMC	NPFMC	PFMC	SAFMC	WPFMC	HMS
No. complexes							
Fish complexes	35 (223)	5 (16)	17 (118)	13 (108)	6 (27)	10 (117)	2 (21)
Invertebrate complexes	1	5	3	-	5	15	-
Management type							
Unassessed	33	9	1	4	11	21	1
Individual	-	-	1	2	-	-	-
Indicator	-	1	6	4	-	-	-
Complex	-	-	8	3	-	3	1
Indicator & complex	3	-	4	-	-	1	-
Model level (majority) (only fish complexes)							
1	-	1	5	3	-	-	-
2	-	-	-	-	-	4	-
3	-	-	7	6	-	-	-
4	35	4	4	1	6	-	1
NA	-	-	1	3	-	6	1
Model level (lowest) (only fish complexes)							
1	-	1	7	3	-	-	-
2	-	-	1	-	-	4	-
3	-	-	7	6	-	-	-
4	35	4	1	1	6	-	-
NA	-	-	1	3	-	6	1

1.7 Figures
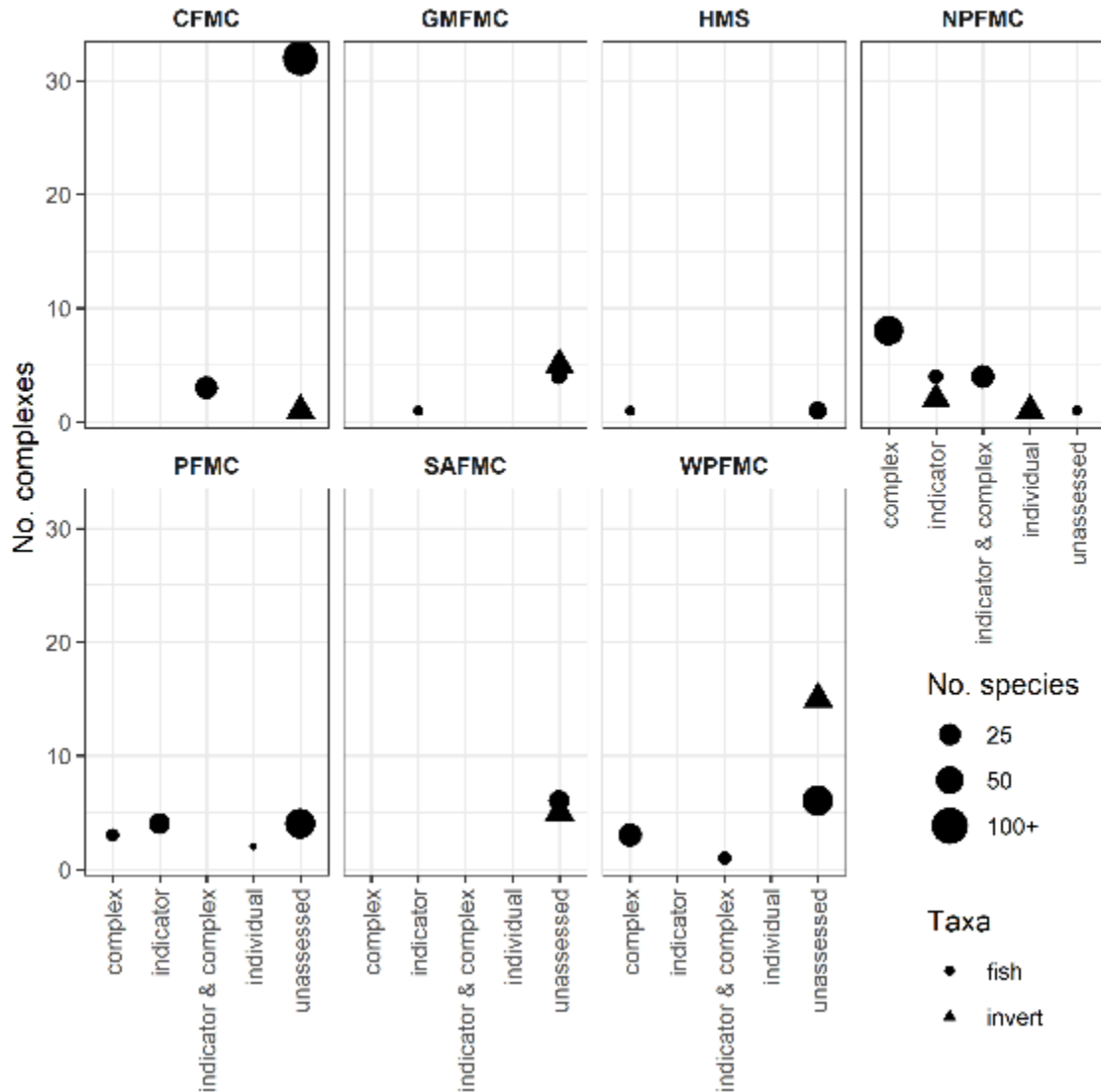
Fig. 1.1 Regional comparison of the number of complexes per each management type (unassessed, individual, complex, indicator, complex, and indicator & complex) for fish and invertebrate managed complexes with the shape size indicating the number of total species for the fish complexes. Number of species for invertebrate complexes are unknown for the majority of complexes. The regions for the Fishery Management Council include: Caribbean (CFMC), Gulf of Mexico (GMFMC), North Pacific (NPFMC), Pacific (PFMC), South Atlantic (SAFMC), Western Pacific (WPFMC), and Highly Migratory Species (in the Atlantic).

CHAPTER 2

Methods for Identifying Species Complexes Using a Novel Suite of Multivariate Approaches and Multiple Data Sources: a Case Study with Gulf of Alaska Rockfish

Abstract

International and national laws governing the management of living marine resources generally require specification of harvest limits. To assist with the management of data-limited species, stocks are often grouped into complexes and assessed and managed as a single unit. The species that comprise a complex should have similar life history, susceptibility to the fishing gear, and spatial distribution, such that common management measures will likely lead to sustainable harvest of all species in the complex. However, forming complexes to meet these standards is difficult due to the lack of basic biological or fisheries data to inform estimates of biological vulnerability and fishery susceptibility. A variety of cluster and ordination techniques are applied to bycatch rockfish species in the Gulf of Alaska (GOA) as a case study to demonstrate how groupings may differ based on the multivariate techniques used and the availability and reliability of life history, fishery independent survey, and fishery catch data. For GOA rockfish, our results demonstrate that fishing gear primarily defined differences in species composition, and we suggest that these species be grouped by susceptibility to the main fishing gears while monitoring those species with high vulnerabilities to overfishing. Current GOA rockfish complex delineations (i.e., Other Rockfish and Demersal Shelf Rockfish) are consistent with the results of this study, but should be expanded across the entire GOA. Differences observed across species groupings for the variety of data types and multivariate approaches utilized demonstrate the importance of exploring a diversity of methods. As best practice in identifying species complexes, we suggest using a productivity-susceptibility analysis or expert judgement to begin groupings. Then a variety of multivariate techniques and data sources should be used to identify complexes,

while balancing an appropriate number of manageable groups. Thus, optimal species complex groupings should be determined by commonality and consistency among a variety of multivariate methods and datasets.

2.1 Introduction

The requirement to implement catch limits for data-limited and previously unassessed stocks resulting from recent international policies, such as the Magnuson-Stevens Reauthorization Act of 2006 (MSRA, 2007) and Common Fisheries Policy (CFP, 2013), presents scientific and management challenges for regional fishery management entities. Managing an aggregation of fish stocks or species as a single unit is one approach utilized by fisheries managers in an attempt to comply with international and federal laws (Jiao et al., 2009), reduce the number of required stock assessments (Koutsidi et al., 2016), and create manageable harvest regulations. These aggregations, also known as stock or species complexes, are often determined by similarity in life history characteristics, vulnerability to the fishery, and geographic distributions (USOFR, 2009). Multiple stocks of a single species being managed together are likely to have strong similarities in life history and susceptibility, whereas complexes consisting of multiple species have more diverging characteristics in productivity (i.e., life history traits), behavior, and habitat preference. Species in a complex are typically caught in a multispecies fishery and often lack adequate data for a single species assessment (USOFR, 2009).

Assigning species to complexes can be a difficult, but critical task for implementing sustainable management of data-limited species. Complexes are often formed using a combination of life history traits, trophic roles, and fishing pressure (Shertzer and Williams, 2008). However, rarely is the full extent of this information available to adequately determine the appropriateness of a complex grouping, and there can be a mismatch in groupings when using life history traits compared to fishery

susceptibility (i.e., species caught together by the same gear types). Grouping species based on life history characteristics, which represent the population's productivity, is important because species with similar growth and maturity often demonstrate similar responses to fishing pressure (e.g., Farmer et al., 2016; DeMartini, 2019). From a management perspective, grouping by susceptibility to fishing gear (e.g., multispecies fisheries) is often simpler than grouping by life history traits, because management by gear type is less easily enforceable for complexes harvested by a variety of gears. Yet, the potential for disproportionate impacts on the species within the complex exists when complexes are formed using gear susceptibility and when selectivity or availability differs by species (DeMartini, 2019).

Aggregating species exclusively based on either life history or fishery traits can lead to unsuitable groupings. For example, a complex formed on fishing vulnerability may group species with divergent life history characteristics, and species that reproduce at earlier ages and are more fecund (i.e., have a higher productivity) are more resilient to fishing pressure compared to species that have lower fecundity and reproduce later in life (i.e., have a lower productivity). Alternatively, grouping species only on similarities in life history may be futile if the species are not vulnerable to the same fishing gear (e.g., Pikitch, 1991; Vinther et al., 2004).

Reconciling the need to balance fishery vulnerability and biological considerations for establishing species complexes remains a difficult scientific problem. No single method has proven robust for all species complex grouping approaches, and often development of species complexes relies on a combination of qualitative (i.e., expert judgement) and quantitative measures. Productivity-susceptibility analysis (PSA)

has been proposed as a tool for grouping data-limited species based primarily on expert judgement (Patrick et al., 2010; Cope et al., 2011). A PSA bins information (i.e., life history values and impact by fisheries indicators) in productivity or susceptibility categories based on expert judgement. The rankings within each category are calculated into an overall vulnerability score, which is thereby used to summarize species into groups. However, PSA may not be as useful when forming complexes with closely related species with poor quality data, because vulnerability rankings are likely to be too similar despite having the possibility of scoring differently in the susceptibility categories. For example, Cope et al. (2011) determined that vulnerability rankings from a PSA could not alone be used to establish complexes for rockfish species in the U.S. West Coast groundfish fishery. A hierarchical tiered approach was implemented by applying clustering analyses first using ecological distribution (i.e., depth and latitude), followed by using the vulnerability scores. Yet, the use of expert judgement for scoring vulnerability was considered problematic for species with such poor quality data.

Alternately, multivariate techniques (e.g., cluster analyses and ordination methods) are a quantitative tool used for identifying similarities among species when adequate species-specific data are available. Of the few quantitative studies that have developed species complexes, the combination of expert judgement and multiple data sources or multivariate approaches (or both) have typically been used to assign species to appropriate groups. For example, both ordination and clustering methods can be used to examine species assemblages using one data source (e.g., Lee and Sampson, 2000; Williams and Ralson, 2002), or multiple data sources with each dataset being analyzed separately, summarized and compared to determine species groupings (e.g., Shertzer and

Williams, 2008; Pennino et al., 2016). Other studies have developed methods to quantitatively synthesize findings of species co-occurrence when using multiple datasets. For example, Farmer et al. (2016) combined analysis of multiple catch data matrices along with a life history matrix to assign species to complexes by amalgamating the results from individual hierarchical cluster analyses into a weighted mean cluster association index. However, the weighted mean cluster association index depended on each cluster analyses from each data source to produce clear, sensible results (i.e., no chaining, which is when single units branch and form their own cluster). The array of quantitative studies used to identify species complexes have focused primarily on associations or similarities among species.

Conversely, other studies examining potential species complexes have grouped together similar catch units (i.e., within a specified area and temporal scale) based on similar species composition. Grouping species based on vulnerability to particular fishing gears allowed analysts to determine how different factors, such as depth (Rogers and Pikitch, 1992), influenced the species composition, while providing potential species assemblages based on fishery susceptibility that many east management and enforcement. Koutsidi et al. (2016) developed a unique method that combined biological traits with fishing operation data to examine how the different fishing sectors tended to catch species with similar biological traits. This study concluded that it could be advantageous to consider functional biological traits in management decisions for data-limited species that lack traditional assessments. The method that Koutsidi et al. (2016) applied required knowledge of a variety of life history, behavior, distribution, ecology and habitat

attributes in addition to species-specific catch data from the fisheries, which may not be available for data-limited species.

Management of several of the Gulf of Alaska (GOA) rockfish species (Figure 1) is an example where managers have identified species complexes, but further quantitative analysis would be desirable to validate these assignments. GOA rockfish (genus *Sebastes*) are caught as bycatch (i.e., unintended catch that is either discarded or retained) in a variety of fisheries. Rockfish in the GOA pose a unique challenge due to their range in life history values, habitat preferences, and behavior. Optimally, the rockfish in each complex should withstand similar fishing pressures, have comparable distributions, and common productivity levels. Currently, most of the non-targeted rockfish in the GOA are assessed in two complexes: the Other Rockfish complex, which consists of species that are classified as the "slope", "pelagic shelf" and "demersal shelf" rockfish assemblages; and the Demersal Shelf Rockfish complex, which separates the group of seven "demersal shelf" species from the remaining rockfish species in one management area (NPFMC, 2019). These complex delineations often combine species with different habitat preferences, which ultimately affects their spatial distributions (i.e., based on gear selectivity and availability). Additionally, the species compositions of the GOA rockfish complexes have undergone multiple changes throughout their management history. In 2011, a PSA indicated that select GOA rockfish had high vulnerability scores due to their low productivity and medium susceptibility level in the fisheries (Ormseth and Spencer, 2011), which implies that the rockfish assemblages should be carefully monitored and managed judiciously. However, further quantitative analysis is warranted to identify whether current GOA complexes should be restructured.

In this study, the goal is to explore the consistency of various quantitative methods for identifying species complexes, while also providing an approach to aggregate data across different spatial areas and gear types. The GOA Other Rockfish and Demersal Shelf Rockfish species are used as a case study, because identifying consistent species groupings has proven difficult for these species. Most of the GOA rockfish species are generally not targeted and have high discard rates due to little economic value. A combination of life history traits, fishery dependent, and fishery independent data sources are used to assemble species complexes with hierarchical and non-hierarchical clustering methods and ordination techniques. Two modes of analyses were implemented to the catch data for the clustering methods: 1) aggregate similar species together based on catch presence and abundance; 2) group similar sampling units based on common catch composition. The species assemblages are compared across multivariate techniques and data types to explore patterns of consistency and identify species complexes for management. These results provide new insight into how the data quality and quantitative methodology utilized may influence groupings for implementing species complexes. Additionally, this is the first quantitative analysis to identify species complexes in the GOA.

2.2 Materials and Methods

2.2.1 Management Units and Species

The GOA is partitioned into the National Marine Fisheries Service (NMFS) subareas: 610, 620, 630, 640 and 650 (Figure 1). These subareas are used in the analyses to examine differences in the species composition by area. The GOA Other Rockfish

35

complex comprises 25 *Sebastes* species in the GOA management area. Seven of the 25

species are managed in a separate complex (Table 1), Demersal Shelf Rockfish, in

subarea 650, but are included in the Other Rockfish complex in all other subareas in the

GOA. The State of Alaska assesses the Demersal Shelf Rockfish in subarea 650, and

manages their catch in parallel with state waters fisheries for these species. Additionally,

northern rockfish (*S. polyspinis*) are only included in the Other Rockfish complex in

subareas 640 and 650 for management, but they are assessed as part of a single species

stock assessment for the entire GOA. Northern rockfish catch data from all subareas are

included in our analyses for comparison, but are not a candidate for reassignment.

Other Rockfish species vary widely in their distribution, habitat selection, and life

history traits. With an exception of harlequin (*S. variegatus*), these rockfish in the GOA

are at the northern limits of their distribution, which span the U.S. West Coast from

Southern California to Alaska (Love et al., 2002). Harlequin are found primarily in

northern waters from British Columbia to Alaska (Tribuzio et al., 2019). Species in the

Other Rockfish complex occur in depths up to 800 m, but typical are found in depths

ranging from 100 to 275 m (Love et al., 2002). Adult habitats include high relief rocks,

reefs or crevices, low relief rocky bottoms, mudflats, vegetative areas, and mixed habitat

(Johnson et al., 2003; Conrath et al., 2019). Some individuals are more solitary, whereas

others tend to aggregate in mixed-species assemblages (Johnson et al., 2003). In general,

rockfish species are characterized by their late maturity, longevity, and their ability to

bear live young (Love et al., 2002; Beyer et al., 2015). However, there is a wide range of

life history values within the Other Rockfish complex (Table 1; see Section 2.2.1).

The Other Rockfish complex consist of bycatch species captured in more lucrative rockfish and other groundfish fisheries using trawl and longline gear. More than half of the species belonging to the Other Rockfish complex are rarely caught (< 1% of the total catch of the Other Rockfish complex). These rockfish have a low economic value (B. Fissel, AFSC, pers. comm.) resulting in a high discard rate estimated at 56% over the entire time series (Tribuzio et al., 2019). Based on biomass, most of the Other Rockfish are caught in the trawl fisheries. Within the complex, some species tend to be caught more on longline gear (e.g., yelloweye rockfish in in subarea 630), and others across gear types (e.g., redbanded rockfish), highlighting the variability within the complex. Species in the Demersal Shelf Rockfish complex managed in subarea 650 are commonly found in rocky, high relief habitats (Tribuzio et al., 2019), where trawling fishing gear is prohibited. Demersal Shelf Rockfish species are primarily caught by longline gear fisheries (i.e., hook-and-line and jig) targeting sablefish (*Anoplopoma fimbria*) and Pacific halibut (*Hippoglossus stenolepis*; Table 1).

2.2.2 Data Sources

Life History Data

The life history parameters were assembled from peer-reviewed articles, grey literature, assessment data from NMFS, and global predictions using *FishLife* (Thorson et al., 2017). Although species data from the GOA or northern ranges were used when available, most life history studies examining maximum age or age/length at maturity were completed in lower latitudes. When no data were available from the GOA, life history information from southern areas were utilized, despite the potential for

differential growth rates by latitude (e.g., splitnose rockfish [*S. diploproa*]; Gertseva et al., 2010). Depending on data availability, the included life history data for the analyses were: age and length at maturity (A_{mat} and L_{mat}, respectively), maximum age recorded (as a proxy for longevity, A_{max}), mean maximum length from the von Bertalanffy growth curve (L_∞), and von Bertalanffy growth parameter (*k;* Table 1). Natural mortality, *M*, was not included in the life history analysis, because *M* is frequently derived from other life history traits, such as maximum age, for these species, and is thus directly correlated.

Fishery Catch Data

Fishery catch information from 2010 to 2018 was used to estimate presence/absence and catch-per-unit-effort (CPUE) for each of the species. Other Rockfish species are incidentally caught in other groundfish fisheries by five gear types including non-pelagic trawl (NPT), pelagic trawl (PTR), longline hook and line (LL), pot (POT), and jig (JIG). The majority of the rockfish bycatch species by biomass are caught in the trawling gear (NPT and PTR), which primarily targets pollock, Pacific cod, flounders, and target rockfish species, in all subarea except 650. They are also caught in fishery longline gear types (LL and JIG) in all subareas that target sablefish and Pacific halibut. Fisheries species-specific catch information is gathered from the Alaska Regional Office Catch Accounting System (CAS) using data from 2010 (when quality data were first available for these rockfish species) to 2018. The sampling unit for the catch data is determined by each unique vessel trip identifier each week for each subarea as reported by fishermen, ranging from <10 to over 8,000 vessel trips for each gear type and subarea

over the entire time period. The CPUE input data used for the analyses are defined as biomass (mt) caught per vessel trip for each species based on available fisheries data.

Survey Data

The NMFS Alaska Fisheries Science Center (AFSC) bottom trawl survey (von Szalay and Raring, 2018) and annual longline survey (Malecha et al., 2019) were used as fishery independent data sources. Other Rockfish species information has been collected on the Alaska bottom trawl survey in the GOA since 1980. The bottom trawl survey used a triennial time scale from 1984 - 1996, followed by a biannual basis (1999 - current). Years included in this dataset range from 1984 to 2017. The trawl survey covers depths up to 1000 m, sampling around 320,000 km^2 from late May - early August using a stratified-random design including an average of 235 hauls that catch at least one species in the Other Rockfish complex. The sampling unit for the trawl survey is biomass (kg) per km^2 calculated by the biomass caught per area swept by the trawl net. General habitat types (i.e., gully, shelf, and slope), depth and latitude and longitude are recorded.

The NMFS annual longline survey targets sablefish (*Anoplopoma fimbria*), but also catches Other Rockfish species. The longline survey can sample areas that are deemed untrawlable (e.g., areas with high relief and rocky habitat), providing catch information for species that might not be susceptible to the trawl gear. Data on rockfish from the longline survey used in this study range from 1995 to 2017. The sampling unit for the longline survey is number of individuals caught per set of hooks. Other factors that influence survey catch, such as depth bins, latitude and longitude, are available.

2.2.3   Multivariate Analyses Background

A variety of quantitative multivariate clustering and ordination methods were implemented to explore potential alternative species groupings. We considered a species complex 'appropriate' for management advice if there was high consistency in clustering among different multivariate methods and types of data. Two clustering methods and one ordination technique were applied to each data type as suggested by Lee and Sampson (2000) and Shertzer and Williams (2008). The two clustering methods conducted in this study are Ward's minimum variance and *k*-mediods; the ordination technique that is implemented is either canonical correspondence analysis (CCA) or non-metric multidimensional scaling (NMDS). These methods are described in Manly (2005), Zurr et al. (2007) and Legendre and Legendre (2012). All analyses were conducted in the R software language (R Core Team, 2020).

Both hierarchical (Ward's minimum variance) and non-hierarchical (*k*-mediods) cluster analysis are implemented to identify and compare consistency in species groupings. Ward's minimum variance analysis is a hierarchical, agglomerative clustering technique, which uses the centroid method to iteratively group closest objects together (Ward, 1963). Ward's analyses were conducted in R package "stats" (R Core Team, 2020), and a bootstrap resampling method was applied to determine the stability of each grouping with 1000 bootstrap samples in R package "fpc" (Hennig, 2007; Hennig, 2020). For each bootstrap sample, the new dataset was formed by drawing samples from the original dataset with replacement and applying the Ward's clustering analysis. The Jaccard coefficient, *J*, was calculated to examine the similarity in the cluster membership between the original cluster with each bootstrap cluster. The mean Jaccard coefficient

values, $\bar{J}$, were computed for each cluster, where a higher value indicated more stability in the cluster. A value of 0.75 or greater implies that the original cluster is stable; values ranging from 0.6 to 0.75 suggest there are patterns in the data, but uncertainty in the cluster (Hennig, 2007). Dendrograms were used to aid in the interpretation of the results. The non-hierarchical cluster method, *k*-mediods, is a more robust variant of the traditional *k*-means (Kaufman and Rousseeuw, 1990). This *k*-mediods method finds optimal groupings by minimizing the distance between all objects and their nearest cluster center (mediod). The k-mediods analyses were conducted using R package "stats" (R Core Team, 2020). The optimal number of desired groupings for *k*-mediods was determined *a priori* using the average silhouette width (Rousseeuw, 1987) in R package "factoextra" (Kassambara and Mundt, 2020). The silhouette width is the measure of quality of the clustering by examining the (dis)similarities of an object to the other objects within the same cluster compared to objects belonging to other clusters (Rousseeuw, 1987), where the number of *k* clusters selected is based on the highest average silhouette width. An average silhouette width less than 0.25 signifies that there is not enough structure in the data to support natural clusters (Kaufman and Rousseeuw, 1990).

Additionally, for either method it is possible to use either of two different clustering techniques: R-mode (comparing variables or descriptors) or Q-mode (comparing objects; see Figure 2; described in Legendre and Legendre, 2012). R-mode directly identifies relationships among species (variables) by examining species similarities based on the catch in each sampling unit, whereas Q-mode identifies clusters by grouping units based on commonality in species composition. Q-mode is particularly

useful for identifying groupings of sampling units (e.g., year and gear combinations) in multispecies catch data, but requires further analysis to examine species composition groupings within sampling units (e.g., Rogers and Pikitch, 1992).

The ordination techniques that were utilized to identify relationships among species are CCA and NMDS. The CCA technique is commonly used to examine species relationships and environmental variables that influence community composition. This analysis uses a set of weighted linear regressions to describe the relationship among species catch and explanatory variables (e.g., gear, depth, or location). It assumes that the species data are unimodal and vary along the gradients of the explanatory variables. Here, depth or depth bins, general substrate type, gear, and NMFS subarea were included as factors in CCA when applicable. In contrast to CCA, NMDS accommodates different magnitudes in the data, because it preserves the order of the distances rather than the magnitude of the distances. The NMDS technique also does not assume an underlying response model (Legendre and Legendre, 2012). Both ordination methods were conducted using R package "vegan" (Oksanen et al., 2019) and the first two dimensions of ordination space were used for visual representation.

2.2.4   Application of Multivariate Analyses

Analyses of Life History Characteristics

Both Ward's and *k*-mediods analyses were applied to identify species groupings based on life history characteristics using R-mode. The input life history table used in the analysis had species as the rows and life history characteristics as the columns with entries being the associated life history values. Three versions of the life history table

were used for the analyses: species-specific values for each characteristic when data were available (species with no information were removed from this table, n = 21), species-specific values with missing values estimated from *FishLife* (Thorson et al., 2017, Table 1), and binned data based on four percentile bins (0-25%, 26-50%, 51-75%, and 75-100%). Binned data allowed for data gaps and data uncertainty. The data in the species-specific life history tables were standardized by dividing each characteristic value by the mean for each life history characteristic. The standardization process ensures the magnitude of the data are similar so that the life history values are weighted the same in the analyses. The Euclidean distances were then calculated to develop the final dissimilarity matrix before Ward's and *k*-mediods analyses were implemented. Lastly, NMDS was applied to the dissimilarity matrix to assist in visualizing the species groupings and show any relationships among species and life history characteristics.

Sub-unit Matrices of Catch and Survey Data

There are two scales of aggregation of the data, sub-unit and a more aggregated 'unit' scale (Figure 2). At the 'sub-unit' scale, input data matrices had entries of presence/absence or CPUE of a species (represented in the rows) for a given sampling unit (i.e., the smallest sampling unit of either haul, tow, or set in the columns). A matrix was created for every area and gear combination for all years combined. The application of the multivariate methods for each individual data sub-unit matrix ensured that each gear in the fisheries and surveys and each area are treated independently.

Ward's analysis, k-mediods and CCA were applied to the commercial catch and survey matrices. The R-mode for the cluster analyses was implemented for the sub-unit

data matrices. The multivariate analyses using R-mode allowed direct identification of species groupings for each gear type and NMFS subarea in the GOA when using the sub-unit matrix. Once the data matrices were created, the CPUE sub-unit matrices were standardized using a root-root transformation to down-weight highly abundant and prevalent species. Subsequently, the dissimilarity matrices were computed using Sorensen distance for presence/absence data matrix and chi-square measure of distance for the standardized CPUE sub-unit matrix prior to the application of cluster analyses. Other data standardizations and distance measures were implemented, but did not change the results. The sub-unit CPUE input data matrices were assembled with the sub-units as rows and species as columns for the CCA. A chi-square transformation was applied on the data matrices before implementing a CCA. External factors, such as depth, latitude, longitude and substrate type, were included in the survey catch analyses for each sub-unit.

Proportion Matrix of Catch and Survey Data

The second scale of aggregation was the aggregated 'unit' scale, which developed an input 'proportions' matrix. This proportions matrix consolidated the individual sub-unit matrices into a combined matrix. While in the 'sub-unit' matrices the columns represented the smallest sampling unit (i.e., haul, tow, or set), the columns of the proportions matrix were defined as a 'unit', which encompassed a temporal, spatial, and gear component. Here, each column was a unique combination of year, month, subarea, and gear while rows were species. The gear indicates the gear types used in the commercial catch and fishery-independent surveys, such that the gear categories are:

NPT, PTR, LL, POT, and JIG for the fisheries gear and "trawl survey" and "longline survey" for the NMFS surveys. The entries were the proportion of tows that a species was present within that unit (i.e., the sum of tows with a species present divided by the total number of tows within the unit). The proportions matrix combined data for all gear categories (i.e., commercial and survey gears) into a single matrix, which allowed the exploration of similarity in the species catch composition among different gears and areas. The proportions matrix can also be useful to limit the impact of abundant and frequently caught species by reducing the difference between the number of null or zero catches for less common species and high valued positive catches for prevalent species.

Ward's analysis and k-mediods were applied to the proportions matrix using both R-mode and Q-mode. Similar to the R-mode application of the cluster analyses on the sub-unit matrices, the R-mode allows direct comparison of species relationships. The Q-mode, which used the transpose of the proportions matrix as the input data, required more detailed investigation to identify species groupings because clustering was by unit, not species. The species groupings that comprised each cluster were visually examined to determine which characteristics (i.e., gear, subarea, month, season and year) influenced the clustering. The proportions matrix (or transpose thereof) already reduced the catch of species to comparable scales, thus, no standardization was necessary. Chord distances were calculated to obtain the dissimilarity matrices for the proportions matrix prior to applying the cluster analyses. The Chord distance is a type of Euclidean distance measure that can accommodate non-normalized data and is not sensitive to outliers (Shirkhorshidi et al., 2015). For the CCA, the proportions input matrix was assembled with the units as rows and species in the columns. A chi-square transformation was applied before

implementing a CCA. Gear and subarea for each unit in the proportions matrix was

included as external factors.

2.3 Results

2.3.1 Analyses of Life History Characteristics

The rockfish in the GOA have a wide range of life history values (Table 1).

Results for Ward's analysis and k-mediods on the life history tables differed slightly, but

provided the same general conclusion. The multivariate analyses on the life history table

supplemented with *FishLife* values are reported here; results based on the life history

table with missing values and binned data are similar and reported in the Supplementary

Material (Supplementary Figure 1 and 2).

Results from Ward's analysis had weakly supported groupings based on the

bootstrap resampling for species with mid to lower values of length and ages associated

with maturity, growth, and longevity ($\bar{J}$ values ranging from 0.63 to 0.69). The bootstrap

resampling suggested patterns in the data for the grouping of three or four clusters with

similar $\bar{J}$ values ranging from 0.63 to 0.83, but the clusters lack stability. Only the low

productive species (i.e., tiger, blackgill, and yelloweye) remained in their own grouping

in both k= 3 or 4 clusters in Ward's analysis with $\bar{J}$ values of 0.73 and 0.83, respectively.

The NMDS plot with results from Ward's analysis represents three clusters, one with the

low productivity group (i.e., high length and age values), one with relatively higher

productivity (i.e., lower length and age values), and the third group with varying levels of

productivity (Figure 3A). When k= 4 clusters, two species, redbanded and bocaccio,

separate into their own group; these two species have low A_{max} and high L_{mat} and L_∞ compared to the other species in their cluster when k=3.

Results from k-mediods split the rockfish into two clusters based on the highest silhouette width of 0.30. The first cluster contained rockfish with life history values with high length and age values (i.e., low productivity). The second cluster consisted of rockfish with medium to high productivity (Figure 3B).

Comparing the results from the different clustering methods, the methods tended to group species by large or small lengths (L_∞ and L_{mat}) and younger or older maximum age (A_{max}) and age at maturity (A_{mat}), but most clusters were weakly supported. There were a few species that were placed in the same group regularly. These species tend to fall on the ends of the rockfish productivity spectrum (i.e., all high or low values for age and length associated with maturity, growth, and longevity). For example, tiger, blackgill, and yelloweye rockfishes all have high L_{mat}, A_{mat}, L_∞, and A_{max} values (i.e., low productivity) and were consistently clustered together for k-mediods and Ward's analysis. There are other rockfish species that have opposing life history characteristics. For example, splitnose has a high A_{max}, but low L_∞, while bocaccio has low A_{max} and A_{mat} and high L_∞ and L_{mat}. These species tended to waver between clusters depending on the method and suggested number of clusters. Overall, larger, older rockfish tended to cluster together, but there is a wide variation and spread of life history values among and within the clusters resulting in no distinct support for clusters.

2.3.2 Sub-unit Matrices of Catch and Survey Data

Exploratory runs were performed with all methods applied to the catch and survey data to determine whether results were robust to the inclusion of rare species (i.e., species comprising less than 1% of total catch). Due to poor performance (i.e., lack of clustering and chaining in Ward's analyses) in exploratory runs when rare species were included, it was determined that these species should be removed from further analyses of the catch and survey data. Species removal varied considerably for sub-unit analyses (see Supplementary Material 1 and Supplementary Figure 3 for species composition and sparseness across gears and subareas).

When each gear and area were analyzed separately using the sub-unit matrix, some analyses demonstrated poor performance (e.g., high prevalence of chaining or lack of clustering). Generally, results demonstrated that the more abundant and more frequently caught species tended to group together, while the less abundant species also commonly clustered together (Supplementary Figure 4). This pattern is demonstrated in both types of cluster analyses for all subareas of the GOA and all gear types for both presence/absence and CPUE data matrices. However, these results should be interpreted with care, given the performance issues encountered. The ordination analyses (CCA) did not yield discernable groupings nor strong associations with the additional explanatory information (e.g., depth, longitude, latitude, and substrate type; Supplementary Figure 5). Thus, the analyses using the sub-unit matrix were of limited insight for grouping of species complexes.

2.3.3 Proportions Matrix of Catch and Survey Data

The exploratory runs with the proportions matrix indicated that rare species should be excluded to provide better clustering performance. A total of 14 species remained in the unit proportions matrix after rare species were excluded. The total number of species remained the same across analyses and modes.

Aggregating the data into units (i.e., by year, month, subarea, and gear) in the proportions matrix enabled the cluster analyses to find stronger relationships among the species using R-mode. Although the groupings from the k-mediods analysis using the unit aggregation led to similar results as using the sub-unit matrix, Ward's analyses tended to aggregate species by co-occurrence. The bootstrap resampling method indicated that $k= 2$ or 3 clusters were supported with $\bar{J}$ values ranging from 0.69 to 0.84. For the two-cluster output, one stable cluster ($\bar{J} = 0.84$) contained species that are only within the Other Rockfish complex with the exception of rosethorn (Figure 4). The other cluster aggregated species predominately found in the Demersal Shelf Rockfish group ($\bar{J} = 0.82$). For the three-cluster output, the clustering data suggested that two species (i.e., canary and yellowtail could be weakly separated into their own group ($\bar{J} = 0.69$), whereas these species are aggregated with the Demersal Shelf Rockfish cluster when $k=2$ (Figure 4).

The clustering and ordination analyses indicated that gear and occasionally subarea influenced the groupings using Q-mode. There did not appear to be any seasonal or temporal trends. Ward's analysis performed poorly due to the common chaining issue and there was no appropriate number of groupings found based on the bootstrapping. Conversely, the k-mediods method provided discernable groupings. The optimal number of clusters (k) for k-mediods was 5 based on the average silhouette width of 0.32.

However, the optimal number of clusters based on where the average silhouette width first reaches its asymptote was $k = 2$ at a silhouette width value of 0.29 (Figure 5). Thus, results from the $k = 2$ and $k = 5$ clusters are presented.

Results from k-mediods with $k = 2$ clusters yielded clearly defined groups differentiated primarily by gear type (Figure 6A). The first cluster contained trawling gears (i.e., NPT, PTR, and the trawl survey), as well as the pot gear (POT). The second cluster consisted of longline gear types (i.e., LL, JIG, and the longline survey). Differences in subareas could also be discerned (Figure 6B); the first cluster mostly contained subareas 610, 620, and 630, whereas cluster 2 comprised all subareas. The division of subareas can be attributed to specific fishing gear in certain subareas (Supplementary Figure 3). For example, NPT and PTR gear types do not fish in subarea 650, whereas JIG gear is primarily used in subareas 630 and 650.

The majority of the species belonging to the Demersal Shelf Rockfish complex (i.e., china, yelloweye, tiger, rosethorn, quillback and canary) had a higher proportion of presence in the cluster associated with the longline gear (cluster 2; Figure 6C). In comparison, most of the species that only belong to the Other Rockfish complex (i.e., widow, sharpchin, redstripe and harlequin) were present in higher proportion in the cluster that contained mostly all trawl gear and subareas 610, 620 and 630 (cluster 1; Figure 6C). For comparison, northern rockfish are caught in almost 100% of the units in cluster 1 (Figure 6C), which is as expected because the northern rockfish is a target species, assessed separately, and caught solely by trawl gears in subareas 610, 620, and 630. The northern rockfish results suggest that the clustering is accurately reflecting the data. There were some species that did not follow this pattern. Two species (i.e.,

silvergray and redbanded) that were commonly found in all gear types (Supplementary

Figure 3), but belong only to the Other Rockfish complex, were found in 41% and 46%,

respectively, of the total units in cluster 1 (affiliated with trawl gear; Figure 6C), whereas

these two species were in 56% and 68% of the units in cluster 2 (affiliated with longline

gear; Figure 6C). Additionally, yellowtail was present more frequently in the units in the

cluster associated with longline gear (cluster 2; Figure 6C) than the cluster associated

with trawl gear (cluster 1; Figure 6C), despite the species only being assigned to the

Other Rockfish complex.

Although the results when k=5 clusters generated more mixed groupings

compared to $k = 2$, there was some separation among gear types (Figure 7A). The major

fishery gears (i.e., NPT, JIG, and LL) each separated into their own clusters with some

overlap between LL and JIG gear (i.e., clusters 3, 4, and 5, respectively, in Figure 7A).

Cluster 1 consisted of a mix of all trawl gear (fishery and survey), while cluster 2

included mostly all longline survey and LL units (Figure 7A). The separation of subareas

in the clusters followed a similar pattern to the k=2 cluster results. Most clusters

contained a mix of subareas (Figure 7B); however, some gear types do not fish in specific

subareas.

There were several species that were abundant in most clusters and some species

that were specific to a few clusters when $k = 5$ (Figure 7C). For example, yelloweye was

present in 75% or more of the units in all but cluster 1 (Figure 7C). In contrast, harlequin

was generally associated only with trawling gear types and subareas 610, 620 and 630

(i.e., clusters 1 and 3; Figure 7C). Similar to the species composition when $k = 2$ clusters,

many of the Demersal Shelf Rockfish species were found in higher proportion in clusters

associated with longline gear (LL, JIG, and longline survey in clusters 2, 4, and 5 covering all subareas; e.g., quillback). Yellowtail was found in higher proportion in clusters with JIG and LL (i.e., clusters 4; Figure 7C) and in low presence (i.e., < 10%) in clusters linked with longline survey and all trawl gear (Figure 7C).

Although CCA results from the proportions matrix did not reveal any species aggregations in ordination space, the results did reveal general groupings primarily by gear (Figure 8) and secondarily by subarea (Supplementary Figure 6). The groupings indicated that there were underlying differences in the species composition by gear and subarea. The other variables (i.e., year, month, and temporal factors) did not influence the groupings and were excluded from further CCA analyses. About a third (36%) of the variation could be explained by the gear and subarea variables, which suggested that these variables were correlated with the species composition. The first axis, CCA1, represented a strong gradient and explained ~40 % of the CCA variation. The second axis, CCA2, explained ~25% of the CCA variation (Supplementary Table 1). Based on CCA1 and CCA2, the longline survey, LL and JIG all separated (Figure 8). The various trawl gear units (NPT, PTR and trawl survey) appeared to be mixed in ordination space along the CCA axes. The POT fisheries gear overlapped with both the trawl gears and LL (Figure 8). A few species are moderately associated to specific gears according to the CCA results, such as yellowtail, canary and China rockfish to JIG, longline survey, and LL. Axis CCA1 separated subarea 650 from the other subareas (Figure 8). However, all the other subareas were not affiliated with the CCA axes, indicating that gear types contributed to most of the variation.

2.4 Discussion

Our analyses demonstrate the importance of exploring a variety of quantitative methods for determining species complexes based on both life history and catch or survey data. Although each multivariate approach has associated pros and cons, utilizing multiple methods can help identify consistent trends across data and statistical approaches. The use of multiple data types and methods for identifying species complexes should be considered best practice for the management of data-limited fisheries. Our results demonstrate that reliance on single methods or a single type of data may provide limited interpretations that may lead to suboptimal species groupings and, ultimately, poor management performance.

Specific to our case study, our analyses indicate that an alteration in the complexes for management of these species may be warranted. We suggest that the Demersal Shelf Rockfish species should be separated from the remainder of the Other Rockfish complex in all subareas in the GOA for assessment purposes. The remaining bycatch rockfish from this study can be grouped together as one complex. There were no clear divisions of species based on the life history characteristics due to the uncertainty and diversity in values, and unstable clustering among methods. The application of multiple methods (clustering and ordination techniques, R- and Q-mode, and data structure) and examination of the catch and survey data provided a basis to develop possible complexes. Some methods were unsuccessful (e.g., sub-unit analyses), while others delivered sensible groupings (*k*-mediods in Q-mode for proportions matrix). The rockfish groupings separated mainly by gear in our analyses, which suggested that the

assessment models providing management advice for these complexes should incorporate the associated survey gear.

2.4.1 GOA Bycatch Rockfish Results and Study Limitations

Wide ranges in productivity and resilience of species' populations are not uncommon when applying methods to identify species complexes (DeMartini, 2019). The life history cluster analysis results indicated that rockfish in the GOA tended to group by higher (i.e., earlier age and smaller size at maturation) and lower (i.e., older age and larger size at maturation) productivity levels, but generally demonstrated a wide range in life history values. A few rockfish species had conflicting levels of productivity with different life history characteristics (e.g., long-lived with early age-at-maturity), which made it challenging to define a species with high or low productivity compared to other rockfish. The uncertainty in the life history values limits interpretation of the results. One source of uncertainty is that life history values were borrowed from outside of the GOA when data were not available and research suggests that there can be regional differences in values (Boehlert and Kappenman, 1980; Gertseva et al., 2010; Keller et al., 2012). Additionally, studies for a given species often showed variability, making it difficult to place a species into high or low productivity groupings. Given the uncertainties in the data, the results did not yield definitive groups and were deemed less reliable than the outputs of the cluster analysis using catch and survey data. Yet, based on PSA results, GOA rockfish, as a genus, fall in the lower productivity spectrum (Ormseth and Spencer, 2011). Rockfish results from Ormseth and Spencer (2011) concur with the U.S. West Coast groundfish PSA results (Cope et al., 2011) that included more rockfish species.

Given that rockfish are generally less productive compared to the other species in the GOA, they tend to be more vulnerable to fishing pressure.

Each rockfish species faces different susceptibility to the widely varying fisheries that operate in the GOA, but one particular challenge is the placement of rare or ubiquitous species into a species group using cluster analyses. We had a range of 3 to 13 species included in the sub-unit cluster analyses depending on the gear type and subarea due to the exclusion of rare species (species with < 1% of total catch). There were 11 of the 25 species that made up < 1% of the units (year-month-subarea-gear) with positive catch for the proportions matrix. The multivariate methods in this study were unable to provide species association or coexistence relationships for these rare species. Likewise, species that are captured across many gear types and areas are difficult to assign to groups. The clustering results did not indicate specific species associations for these abundant rockfish.

Most of the clustering analyses also failed to provide consistent or reliable results when applied to each gear and subarea dataset separately through application to the sub-unit matrix. When the various methods were applied to the sub-unit matrices there were no clearly delineated relationships of commonly caught species or rarer species. We had anticipated that the finer-scale approach might provide insight into the co-occurrence among species. However, the lack of identified co-occurrence relationships (i.e., similarities among species) with the sub-unit matrices was likely because the R-mode groups by similar catch in each unit or sub-unit. As a result, the more abundant and more frequently caught species are commonly grouped. Thus, the differences in magnitude and frequency of the catch mask the less obvious relationships among species.

Aggregating all the datasets into a single data matrix enabled gears, subareas, and temporal components to be compared, while major categories that influenced the groupings could be identified. The challenge is determining logical and biologically informed clusters (e.g., balancing too few or too many clusters that may result in a narrow or wide range of species productivity), while balancing the practical management of species that are exploited across varying gear types and subarea. Using the k-mediods analysis, either two or five clusters were recommended. The suggested $k = 5$ clusters identified specific relationships among different gear types and occasionally subareas. Some species appeared to be associated with only a specific cluster (or clusters), whereas other species were commonly found in all clusters. The rockfish that occur in medium to high frequency in all or most of the clusters are species that are found ubiquitously in the GOA and are caught by most gear types. The results with $k = 2$ clusters indicated that the species composition caught by longline gear types clearly separated from trawling gear types. Overall, the analysis of the catch and survey data indicated that gear was the biggest contributing factor in grouping similar units of rockfish species composition. NMFS management subarea could have influenced the cluster results, as there was a strong interaction between fishery gear and subarea (i.e., certain gears only operate in specific subarea). These analyses suggest that rockfish species that are only predominately caught by a specific gear could be assigned to a rockfish complex that commonly associates with that gear for assessment and management purposes.

These analyses, particularly the proportions matrix analyses, provided a way to examine the species composition from the fishery catch with the survey data. Our results indicated that the trawl survey and trawl fisheries gear tended to be grouped together

more frequently than the longline gear types (i.e., the longline survey, LL, and JIG). Williams and Ralston (2002) found that the bottom trawl survey reflects the trawl fishery sector well off the coast of California and Oregon, USA, which includes non-pelagic and pelagic trawl, because it catches species that are typically found at the bottom (e.g., Keller et al., 2008) or distributed in the water column (e.g., widow rockfish, Wilkins, 1986). In contrast, the longline survey is a fixed station survey that targets primarily commercially important sablefish (Malecha et al., 2019). The longline survey did not always catch species typically caught in the longline fishery gear types (Supplementary Figure 3). Of the top five Other Rockfish species caught in the longline survey by numbers, only three are designated in the Demersal Shelf Rockfish complex. This result suggests that the longline survey alone is not representative of the populations within the complex or caught by the longline gear fisheries. If the Demersal Shelf Rockfish complex is extended to all subareas of the GOA, other data resources will be needed to assess this assemblage. For example, the Demersal Shelf Rockfish assessment utilizes submersibles to estimate abundance trends to set quotas in NMFS subarea 650 (Olson et al., 2018). Studies have identified that commercial catch data do not necessarily reflect the species composition in the survey data (i.e., species composition in the ecosystem; Lee and Sampson, 2000; Pennino et al., 2016), but surveys should include a broader diversity of species than that found in the commercial catch. Given the diversity of gear types utilized in the GOA, as well as specific gears fishing in habitat-specific areas (e.g., Rooper et al., 2012) and habitat-specific preferences of some rockfish (Laidig et al., 2009; Conrath et al., 2019), it is not surprising that the longline survey does not perfectly reflect the species composition of the various longline gear fisheries. Yet, the paucity of data

available for the bycatch rockfish species in the GOA requires that any data on catch rates and composition should be utilized. We suggest the incorporation of the longline survey data in the analysis of species complexes in the GOA, despite some limitations in the overlap of the survey catch composition compared to the longline gear species composition. In the future, other survey types, such as submersibles, which are used in the current Demersal Shelf Rockfish assessment (Olson et al., 2018), should be investigated when survey data underrepresent the species composition of the fishery.

2.4.2 GOA Bycatch Rockfish Management Recommendations

The management of the bycatch of GOA rockfish poses a challenge because these species have a diverse range in life history values, habitat preferences, spatial distribution, and fishing vulnerability. Based on the summary of our analyses, as well as consideration of previous work with GOA rockfish complexes (e.g., the PSA of Ormseth and Spencer, 2011), we propose an alteration for management of the rockfish complexes in the GOA (Table 2). The current GOA Other Rockfish complex consists of species that are classified as the "slope", "pelagic shelf", and "demersal shelf" rockfish assemblages and the group of seven "demersal shelf" species are separated into the Demersal Shelf Rockfish complex in subarea 650. Our results indicated that the current delineation that split the GOA Other Rockfish and Demersal Shelf Rockfish complexes is appropriate. The analysis of catch and survey data indicated that these two complexes tended to separate by the main fishing gear types, trawl and longline, gulf-wide with the Demersal Shelf Rockfish more closely associated with the latter gear. We suggest that the Demersal Shelf Rockfish species be placed into their own complex for all subareas in the GOA.

Some alterations and considerations may be warranted, particularly for highly prevalent or rare species. For instance, silvergray and redbanded rockfish were commonly found in all gear types and were equally common in both the longline and trawl groupings. We suggest that the few species that are caught in high prevalence by all gear types should be placed in the group of species that associates with the gear that catches the species in the highest abundance (see Table 2 for these assignments). Although these bycatch rockfish are frequently caught, they do not have enough data to warrant a single-species assessment. Similar approaches will likely be appropriate for rare species, which were excluded from this analysis (but included in Table 2 based on gear association). We suggest placing rare species in the species group associated with the gear in which they are most commonly caught. By doing so will help ensure that the rare species are managed consistent with the fishing pressure that they encounter. However, rare species may be more prone to localized depletion or other conservation concerns and should be carefully monitored.

Further specific alterations to the current complexes also should be investigated. One species, yellowtail rockfish, which is assigned to the "pelagic shelf" assemblage by the North Pacific Fishery Management Council (NPFMC, 2019) and assessed in the Other Rockfish complex, was associated more closely with the longline gear grouping. However, this species was caught in both main fishery gear types, trawl and longline, but only caught in the trawl survey. We suggest that yellowtail rockfish remain in the Other Rockfish complex, but should be monitored due to its association with species from the Demersal Shelf rockfish complex (Table 2). Careful consideration should be applied to all species belonging to the "pelagic shelf" assemblage classified by the North Pacific

Fishery Management Council (NPFMC, 2019), because results from this analysis split the "pelagic shelf" rockfish into opposing groups based on species association, but have different gear associations.

One method to help provide guidance for the management and sustainability of species in complexes is to identify indicator species. An indicator species should be commonly observed in the gear types associated with the clusters, demonstrate similar population trends, and share similar life history traits (e.g., reproductive success) as other species, and not have a noticeable competitive relationship with the rest of the species in the group (Landres et al., 1988; Simberloff, 1998; Zacharias and Roff, 2001). Additionally, they should exhibit the highest vulnerability or be near the lower end of the productivity spectrum for the complex (i.e., be a "weakest link" species; Shertzer and Williams, 2008). The community structure must also be relatively stable to manage a complex based on an indicator species; yet, studies often show large marine ecosystem shifts (Shertzer et al., 2009). Thus, these assumptions are often violated or no species is able to fulfill all the requirements for an appropriate indicator species (Niemi et al., 1997). However, an indicator species can still be useful by providing supplementary precautions and buffers for the complex by demonstrating potential instability within the group if the variation in the population of the indicator species increases or there are drastic changes to the population.

To help ensure sustainability for all rockfish in the complexes, it may be useful to select one or two precautionary indicator species that are on the lower end of the productivity spectrum for the complex, but are commonly observed by the predominant gear type (i.e., they are not rare species). Based on the PSA results from Ormseth and

Spencer (2011), Cope et al. (2011), and our analyses on the life history characteristics, we suggest that redbanded and silvergray in the Other Rockfish complex and yelloweye in the Demersal Shelf rockfish complex may be appropriate indicator species given their low productivity and relatively high frequency of observation (Table 2). We believe that these general groupings are both practical for management advice (i.e., bycatch quotas can be enforced because groupings align by common gear types) and biologically relevant (i.e., all rockfish genus fall on the lower end of the productivity spectrum). We suggest that future research explore the possibility of identifying indicator species for the GOA Other Rockfish complex and whether redbanded and silvergray might be appropriate representatives.

Given the data limitations for the GOA Other Rockfish species (e.g., lack of consistent life history data, a number of diverse gear types, and the high occurrence of rare species that are seldom observed), the groupings for the complexes should be re-evaluated when new or updated data are available. In particular, the uncertainty in life history values used in these analyses hindered the ability to develop clusters based on productivity. For example, length data are not collected for many species in this study, but length data collection could inform key life history values. To be able to adequately represent these data-limited species, particularly rare species, improved data collection will be the only reliable solution to implement the type of species clustering approaches used in this study. Future focus on the collection of biological data from discards of rare species would be a helpful for better managing bycatch rockfish species.

In the current study, we were unable to include environmental or habitat features to the proportions matrix analyses due to the lack of data from the various fishery sectors,

as well as, the problematic issue of identifying broad-scale features for entire management subareas. However, many studies examining species association or identifying species complexes have determined depth (Rogers and Pikitch, 1992; Lee and Sampson, 2000; Gomes et al., 2001; Williams and Ralston, 2002; Rooper, 2008), broad substrate or habitat structure (Ann et al., 2009) or a combination of factors (Tolimieri and Levin et al., 2006) affect the species composition. Additionally, when multiple fishing gears are included in analyses to examine species composition in a given area, it is often found that different combinations of gear type, environmental, and spatial features influence the species catch (e.g., Vinther et al., 2004; Pennino et al., 2016; Tuda et al., 2016). Nonetheless, most of these studies focus on only one gear type or utilize survey data collected by submersibles, which enables researchers to determine main environmental or habitat features influencing the grouping. Further work is warranted to collect data and determine if habitat or environmental variables might help to better identify rockfish species complexes.

2.4.3 General Species Complex Recommendations

Appropriate methods for identifying species complexes are likely to vary on a case-by-case basis because each region and fishery has different attributes that need to be evaluated. Oftentimes, life history characteristics are unknown or complexes formed based on productivity do not necessarily align with vulnerability to the fishery or spatial distribution of the species. When there are conflicting results on groupings, managers must consider alternative options. A PSA or other risk assessment methods (e.g., Sustainability Assessment for Fishing Effects, Zhou et al., 2016) can help guide

groupings for management as a preliminary tool (Cope et al., 2011), but this method may not accurately depict fishing dynamics in the susceptibility scores for all species (Hordyk and Carruthers, 2018). As previously discussed, Cope et al. (2011) recommend a step-wise method for assigning species to complexes using commonalities among species in depth preferences, spatial distribution, and vulnerability scores (i.e., based on levels of productivity and susceptibility to exploitation). Based on our analyses, we recommend that gear type needs to be considered in this step-wise grouping method, because certain species are more susceptible to specific gears than others. Incorporating gear types enables the comparison of species' vulnerability to different fishing pressures due to differences in spatial distribution (McCully Phillips et al., 2015), patchy distributions (Silva et al., 2012), and habitat preferences (e.g., Jagielo et al., 2003; Conrath et al., 2019).

The use of a variety of multivariate methods helps validate the appropriateness of the suggested groupings. We recommend using a combination of multiple data types, data aggregation scales, and the application of several multivariate analyses to develop species complexes. Each data-limited situation requires context-specific methods tailored to intricacies of the species and fishery being managed. For example, the inadequacies of our analyses using the sub-unit matrices to identify species co-occurrence demonstrates the importance of applying multiple analyses at multiple data aggregation scales to develop robust groupings. Likewise, we suggest that exploring both R-mode and Q-mode multivariate methods is warranted, especially when fishery and survey catch are the primary sources of data. Although not as widely used for analysis of species complexes, Q-mode can be valuable to identify commonalities in species groupings across gear types

and management subareas. R-mode analysis provides a more direct clustering approach by species, which is useful when reliable life history data are available or a limited number of gear types (or a single multispecies fleet) harvest the primary species of concern (e.g., reef fishes that are fished using longline gear types along the southeastern coast of the U.S. [Shertzer and Williams, 2008] and Gulf of Mexico [Farmer et al., 2016]). However, it can be difficult to get reliable outputs from R-mode when a variety of gears differentially exploit the diversity of species under consideration across a broad spatial range (i.e., management subareas). In our study, Q-mode analysis proved to be useful when determining manageable species complexes. Ultimately, there is not a single universal approach to determining species complexes that is robust to all species traits and data availability situations. Our study demonstrates that a diversity of quantitative multivariate approaches is warranted when exploring potential species complexes, while Q-mode analysis should be more widely explored, especially for situations where there are multiple gear types. Thus, the optimal groupings should be determined by commonality and consistency among a variety of different multivariate methods and datasets.

2.4.4 Conclusions

Managing data-limited species as a complex can be a practical approach for reducing the number of required stock assessments when insufficient data and ecological knowledge exists to perform individual stock assessments (Koutsidi et al., 2016), but the management of the complex is only as good as the information used to define the groupings (Fujita et al., 1998). We provide one of the first explorations of species

complex groupings based on the combination of clustering from multiple data types (e.g., life history, catch, and survey data), multiple data aggregation scales (e.g., by sub-unit and at an aggregated "unit" scale), and a wide variety of multivariate methods (e.g., Ward's analysis, k-mediods, CCA, and NMDS), as well as, different modes (e.g., R-mode and Q-mode). Exploration of each of these approaches was important for making management recommendations for the GOA Other Rockfish complex, because certain approaches (i.e., analyzing sub-unit matrices for the catch and survey data) failed their diagnostics of model adequacy, and data (i.e., life history characteristics) had varying levels of quality. By analyzing all of these approaches, we were able to address consistency and reliability across methods, thereby developing species complex advice that is likely more robust compared to using any single approach.

We found that the species designations for the Other Rockfish and Demersal Shelf Rockfish complexes appear to be appropriate, but these complexes should be extended across all management subareas in the GOA (i.e., the Demersal Shelf Rockfish complex is currently only delineated in subarea 650). Despite our methodology being more resource intensive and providing the same complex assignment as existing, less analytically thorough, approaches, these results are likely specific to this case study. We would expect that in other situations, using our suite of quantitative methods would result in different species assignment compared to more commonly used qualitative approaches. However, our approach does require increased resources, including both funding and personnel, which needs to be weighed against the desire to improve species assignment, assessment, and management of species complexes.

Although these results are based on the best data currently available, there is a clear need for improved data collection on bycatch species in the GOA. Collection and incorporation of other data could improve clustering analysis in the future by providing improved data on species distributions, habitat associations, and co-occurrence. As fish move poleward and into deeper depth subareas due to changing climactic conditions (e.g., Perry et al., 2005; Pinsky et al., 2013; Kleisner et al., 2017), there is likely to be a northward shift in the center of gravity for many of the GOA rockfish species examined here, which are at the northern extent of their range in the GOA. Improved data collection will be paramount for identifying changing distributions, which are likely to alter the frequency and abundance of rockfish catch by fisheries and surveys. Thus, the combination of new data collection approaches and further refinement of methods for identifying species complex groupings will be crucial to detect changes in species composition and abundance and implementing sustainable fisheries management.

2.5 References

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2.6 Tables

Table 1. Life history characteristics for each Gulf of Alaska Other Rockfish (GOA OR) and Demersal Shelf Rockfish (DSR) species. Assessment Group indicates the current species complex assignment. Life history values included are: maximum age (A_{max}), age-at-maturity (A_{mat}), length-at-maturity (L_{mat}), average maximum length (L_∞) and von Bertalanffy growth parameter, k. Regions or states (i.e., California= CA, Oregon= OR, Washington= WA, British Columbia= BC, Alaska= AK) and citation (in Appendix 1) are listed in parentheses.

Common name	*Sebastes* sp.	Assessment Group	A_{max}	A_{mat}	L_{mat} (mm)	L_∞ (mm)	k
blackgill	*S. melanostomus*	GOA OR	90 (OR/CA; 1)	21 (OR/CA; 1)	350 (OR/CA; 1)	548 (OR/CA; 1)	0.04 (OR/CA; 1)
bocaccio	*S. paucispinis*	GOA OR	45 (WA; 2)	4 (CA; 12)	450 (CA; 12)	909 (BC; 22)	0.088 (BC; 22)
canary	*S. pinniger*	DSR	71 (CA; 3)	9 (CA; 12)	480 (BC; 20)	580 (BC/WA/OR/CA; 23)	0.16 (BC/WA/OR/CA; 23)
Chilipepper	*S. goodie*	GOA OR	35 (OR/CA; 4)	2.5 (OR/CA; 4)	260 (OR/CA; 4)	575 (OR/CA; 4)	0.252 (OR/CA; 4)
China	*S. nebulosus*	DSR	78 (AK; 5)	4 (CA; 12)	270 (CA; 12)	450 (AK; 28)	0.19 (WA/OR/CA; 31)
copper	*S. caurinus*	DSR	50 (AK; 5)	6 (CA; 12)	340 (CA; 12)	400 (AK; 28)	0.13 (WA/OR/CA; 31)
darkblotched	*S. crameri*	GOA OR	105 (6)	8.4 (OR; 13)	365 (OR; 13)	455 (OR; 24)	0.185 (6)
greenstriped	*S. elongates*	GOA OR	54 (AK; 5)	8.5 (WA/OR/CA; 14)	230 (CA; 12)	355 (BC; 25)	0.115 (BC; 25)
harlequin	*S. variegatus*	GOA OR	34 (AK; 7)	9.0*	230 (AK; 20)	323 (AK; 7)	0.110 (AK; 7)
northern	*S. polyspinis*	Subareas: 640,650	72 (AK; 7)	13 (AK; 15)	360 (AK; 15)	404 (AK; 7)	0.155 (AK; 7)
pygmy	*S. wilsoni*	GOA OR	26 (BC; 5)	6.0*	183.9*	230 (AK; 28)	0.180*
quillback	*S. maliger*	DSR	90 (AK; 8)	5 (AK; 16)	260 (CA; 12)	610 (AK; 28)	0.113*
redbanded	*S. babcocki*	GOA OR	106 (AK; 5)	4 (CA; 12)	420 (BC; 20)	698 (BC; 22)	0.042 (BC; 22)
redstripe	*S. proriger*	GOA OR	55 (BC; 5)	8 (16)	290 (BC; 20)	420 (BC; 22)	0.15 (BC; 22)
rosethorn	*S. helvomaculatus*	DSR	87 (AK; 5)	8 (CA; 12)	210 (AK; 20)	319 (BC; 22)	0.079 (BC; 22)

sharpchin	*S. zacentrus*	GOA OR	58 (AK; 7)	10 (16)	270 (AK; 16)	350 (AK; 7)	0.122 (AK; 7)
silvergray	*S. brevispinis*	GOA OR	75 (AK; 7)	10 (BC; 17)	460 (BC; 16)	623 (AK; 7)	0.093 (AK; 7)
splitnose	*S. diploproa*	GOA OR	103 (BC; 9)	7 (CA; 12)	218 (WA/OR/CA; 21)	314 (BC; 9)	0.155 (BC; 9)
stripetail	*S. saxicola*	GOA OR	38 (30)	4 (CA; 18)	200 (BC; 20)	327 (CA; 18)	0.147 (CA; 18)
tiger	*S. nigrocinctus*	DSR	116 (AK; 5)	15.0*	391.1*	610 (AK; 28)	0.083*
vermilion	*S. miniatus*	GOA OR	60 (AK; 5)	6 (CA; 18)	330 (CA; 18)	688 (CA; 18)	0.164 (CA; 27)
widow	*S. entomelas*	GOA OR	60 (BC; 5)	5 (CA; 12)	370 (CA; 12)	516 (OR; 26)	0.15 (OR; 26)
yelloweye	*S. ruberrimus*	DSR	117 (AK; 10)	22 (AK; 16)	475 (AK; 16)	644 (AK; 10)	0.046 (AK; 10)
yellowmouth	*S. reedi*	GOA OR	99 (BC; 5)	11 (BC; 32)	380 (BC; 20)	469 (BC; 32)	0.12 (BC; 32)
yellowtail	*S. flavidus*	GOA OR	64 (BC; 11)	9 (WA/OR/CA; 19)	410 (WA/OR/CA; 19)	530 (BC; 22)	0.20 (BC; 22)

Table 2. Suggested assemblages for species complexes based on the analysis of all available data and clustering techniques. These complexes should be assessed and managed as such throughout the entire GOA. Species in bold italics are assigned based on occurrence in gear types, but should be carefully monitored. Species in bold are commonly caught in all gears and have been assigned to the complex that is associated with the gear in which they are most commonly caught. Rare species (species that comprise <1% of total catch) are provided in italics and are similarly assigned to the complex related to the gear in which they are most frequently caught. Other management considerations (e.g., enforcement issues) might be warranted to reassign common and rare species to different complexes. An "*" is used to identify suggested precautionary indicator species for each complex based on the low productivity from the life history cluster analyses.

GOA Other Rockfish	GOA Shelf Rockfish
blackgill	canary
bocaccio	china
chili*pepper*	*copper*
darkblotched	quillback
greenstriped	rosethorn
harlequin	tiger
northern	**yelloweye***
pygmy	
redbanded*	
redstripe	
sharpchin	
silvergray*	
splitnose	
stripetail	
vermilion	
widow	
yellowmouth	
yellowtail	

2.7 Figures
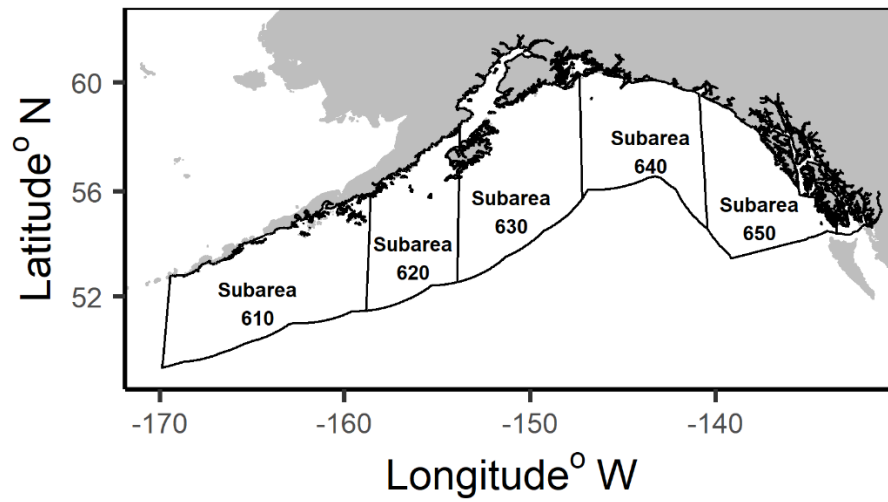
Figure 2.1. Map of the National Marine Fisheries Service (NMFS) management subareas in the Gulf of Alaska

Data	Life History		Catch/Survey					
Clustering Technique	Ward's	k-mediods	Ward's			k-mediods		
Mode	R		R		Q	R		Q
Matrix Structure	Life History Characteristic by Species		Subunit (e.g., tows)	Proportion (i.e., unit)	Proportion (transpose R-mode)	Subunit (e.g., tows)	Proportion (i.e., unit)	Proportion (transpose R-mode)
Example Matrix	**Life History** — Species (Sp1, Sp2, Sp3) × (L_∞, A_{max}, F_{mat}): Species-specific values		**Sub-units** — Species (Sp1, Sp2, Sp3) × (Tow1, Tow2, Tow3): CPUE or Presence/Absence	**Units (year-month-stratum-gear)** — Species (Sp1, Sp2, Sp3) × (Unit1, Unit2, Unit3): Proportion #tows sp. present / total tows in unit	**Species** — Units (year-month-stratum-gear) (Unit1, Unit2, Unit3) × (Sp1, Sp2, Sp3): Proportion #tows sp. present / total tows in unit	**Sub-units** — Species (Sp1, Sp2, Sp3) × (Tow1, Tow2, Tow3): CPUE or Presence/Absence	**Units (year-month-stratum-gear)** — Species (Sp1, Sp2, Sp3) × (Unit1, Unit2, Unit3): Proportion #tows sp. present / total tows in unit	**Species** — Units (year-month-stratum-gear) (Unit1, Unit2, Unit3) × (Sp1, Sp2, Sp3): Proportion #tows sp. present / total tows in unit

Figure 2.2. Design of the model analyses identifying data, clustering technique and input matrix structure for each aspect of the cluster analyses.
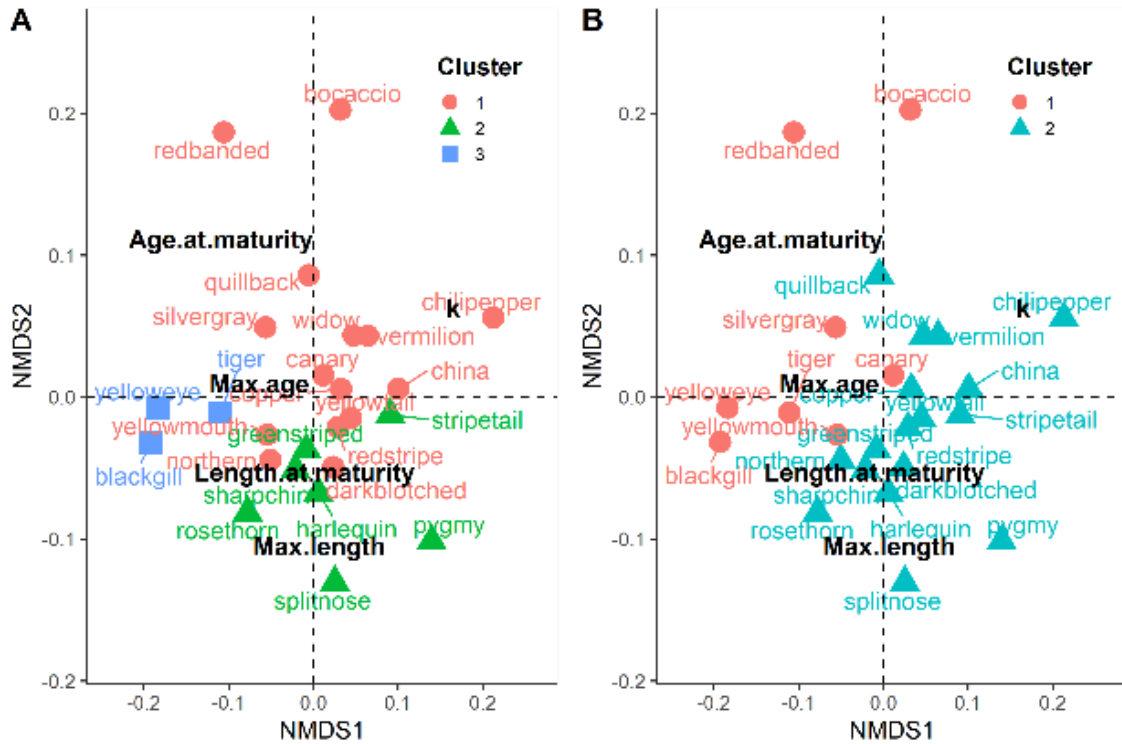
Figure 2.3. NMDS plot of species' clusters identified from life history values estimated from *FishLife* for missing values from (A) Ward's hierarchical cluster analysis and (B) *k*-mediods. In Ward's analysis three or four clusters were supported by the bootstrapping resampling method; results with four clusters separated redbanded and bocaccio into their own cluster.
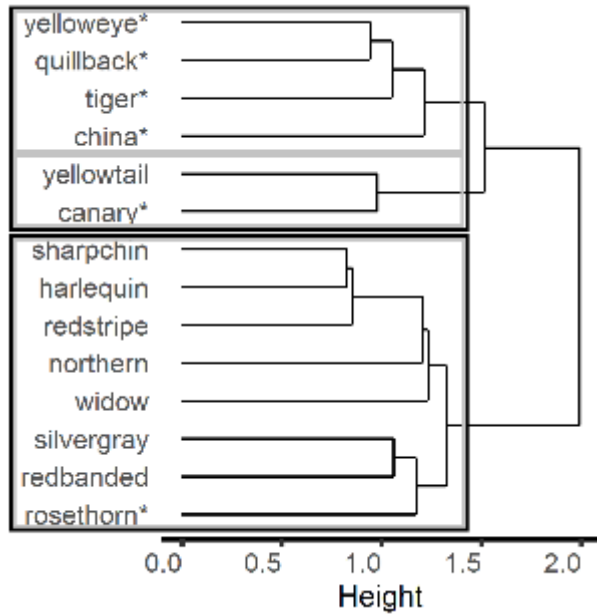
Figure 2.4. Results from Ward's hierarchical cluster analysis using the proportions matrix with "units" (year-month-subarea-gear) in R-mode where 2 (black lines) or 3 (grey lines) clusters are supported by the bootstrap resampling method. The "*" indicates species that currently belong to the Demersal Shelf Rockfish complex.
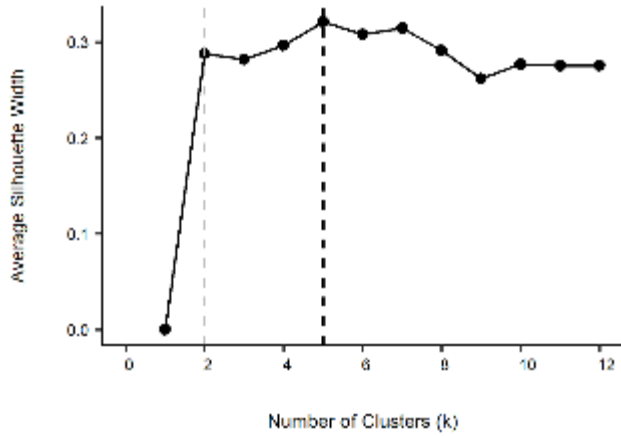
Figure 2.5. Average silhouette width from Q-mode k-mediods cluster analysis using the proportions matrix with "units" (year-month-subarea-gear). The suggested optimal number of clusters is $k=5$ (black dashed line), but the average silhouette width plateaus at $k=2$ (grey dashed line).
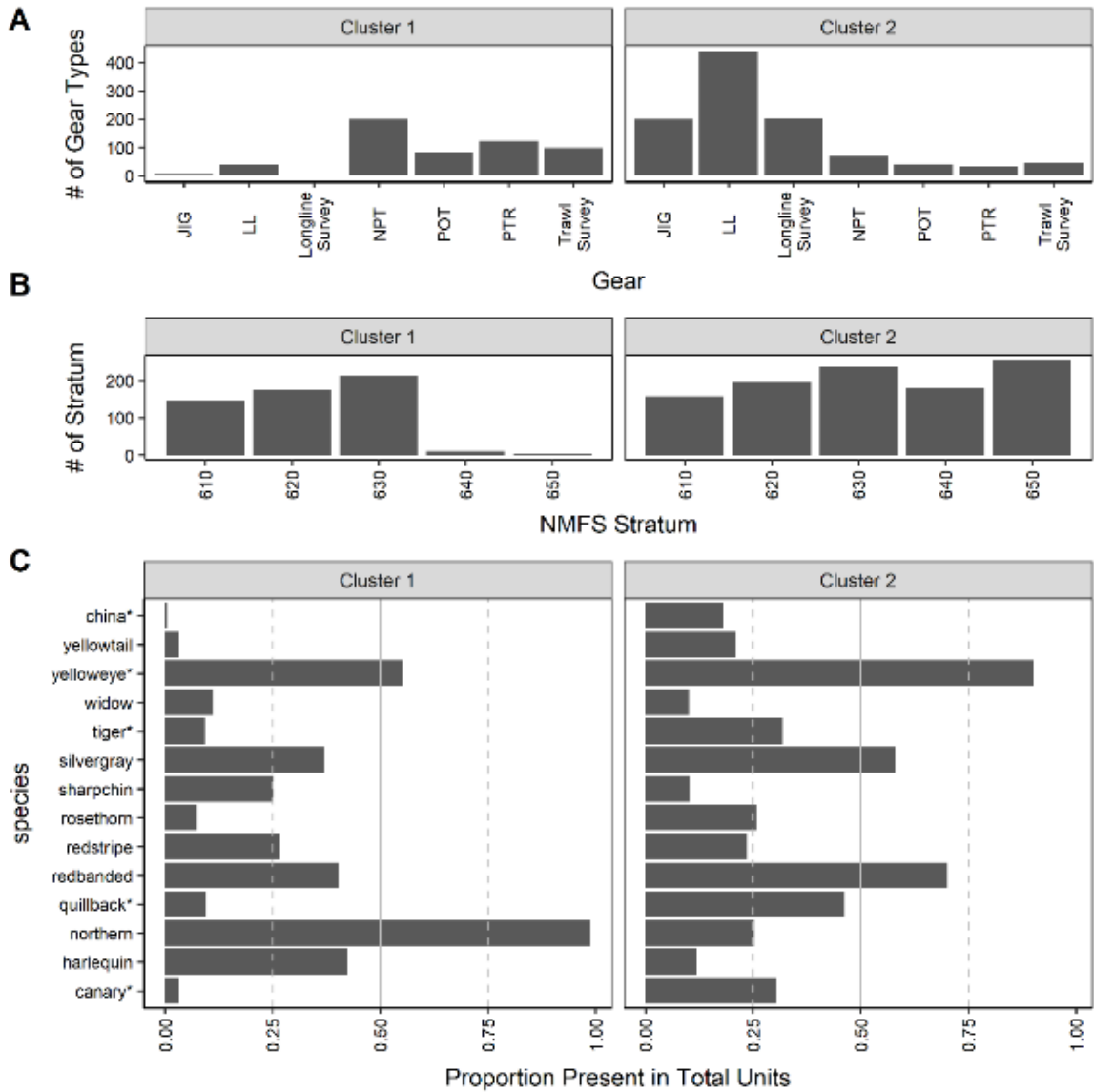
Figure 2.6. Results from Q-mode *k*-mediods using the proportions matrix with "units" (year-month-subarea-gear) to synthesize all gear types (fishing gear: jig [JIG], longline hook and line [LL], non-pelagic trawl [NPT], pot [POT], and pelagic trawl [PTR]; and surveys: longline and trawl) and subareas into one dataset when *k*= 2 clusters. In (A) the number of units where each gear type was present in each cluster is shown. In (B) the number of units where each subarea were present in each cluster is illustrated. In (C) the proportion of units (year-month-subarea-gear) that a species is present out of the total number of units assigned to each cluster is provided to represent the species composition in each suggested cluster when *k*= 2. Species that currently belong to the Demersal Shelf Rockfish complex are indicated by "*".
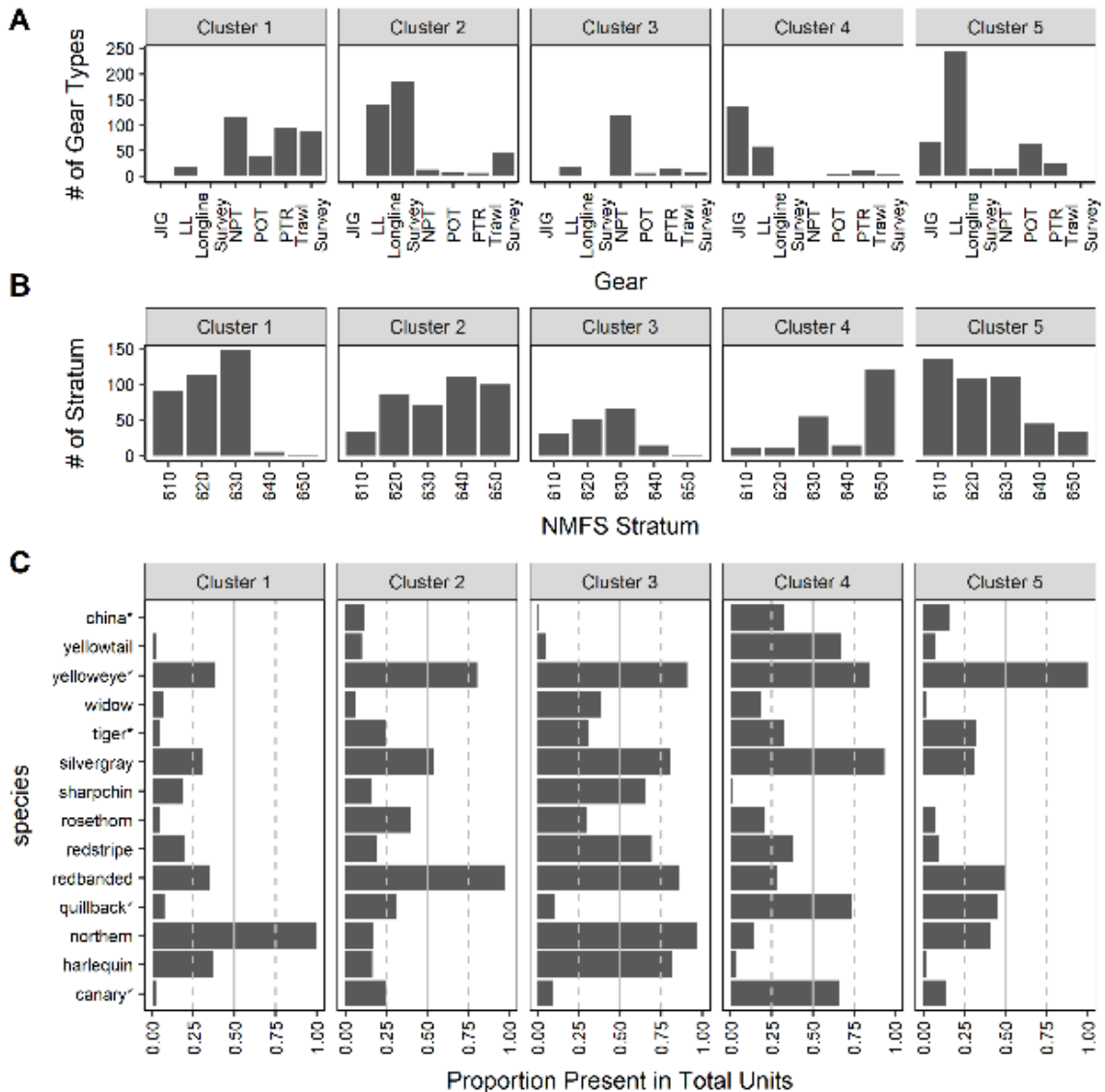
Figure 2.7. Results from Q-mode *k*-mediods using the proportions matrix with "units" (year-month-subarea-gear) to synthesize all gear types (fishing gear: jig [JIG], longline hook and line [LL], non-pelagic trawl [NPT], pot [POT], and pelagic trawl [PTR]; and surveys: longline and trawl) and subareas into one dataset when *k*= 5 clusters. In (A) the number of units where each gear type was present in each cluster is shown. In (B) the number of units where each subarea were present in each cluster is illustrated. In (C) the proportion of units (year-month-subarea-gear) that a species is present out of the total number of units assigned to each cluster is provided to represent the species composition in each suggested cluster when *k*= 5. Species that currently belong to the Demersal Shelf Rockfish complex are indicated by "*".
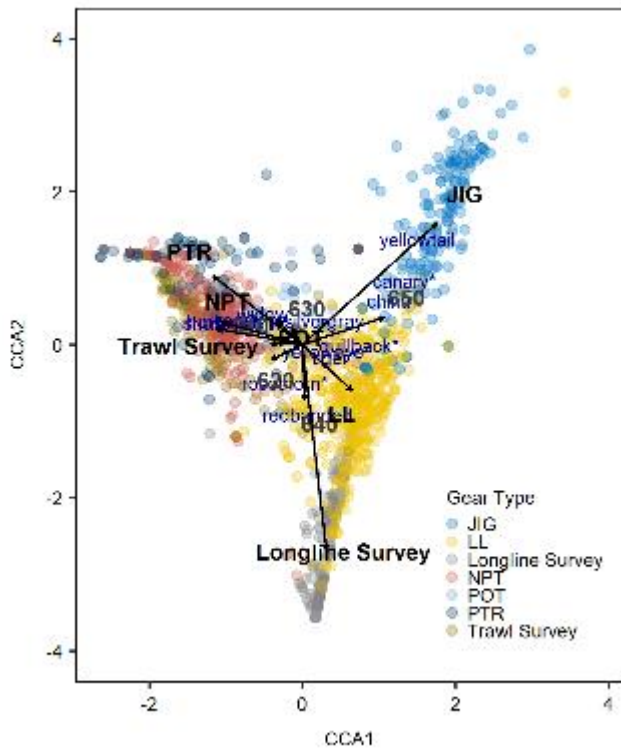
Figure 2.8. CCA results using the proportions matrix with units (year-month-subarea-gear) plotted on the first two CCA axes. Gear type is color coded, species are marked in blue text (with species currently assigned to the Demersal Shelf Rockfish marked with "*") and factors (i.e., gear and subarea) provided in black bold text. Gear types include fishing gear (jig [JIG], longline hook and line [LL], non-pelagic trawl [NPT], pot [POT], and pelagic trawl [PTR]) and surveys (longline and trawl surveys).

2.8 Appendix Life History Parameter Value Sources

Table A.1. Reference number with associated source from the life history parameters of rockfish from Table 1.

Reference number	Source
1	Stevens, M.M., Andrews, A.H., Cailliet, G.M., Coale, K.H., Lundstrom, C.C., 2004. Radiometric validation of age, growth, and longevity for the blackgill rockfish (*Sebastes melanostomus*). Fish. Bull., U.S. 102, 711–722.
2	Piner, K.R., Wallace, J.R., Hamel, O.S., Mikus, R., 2006. Evaluation of ageing accuracy of bocaccio (*Sebastes paucispinis*) rockfish using bomb radiocarbon. Fish. Res. 77, 200–206.
3	Andrews, A.H., Kerr, L.A., Cailliet, G.M., Brown, T.A., Lundstrom, C.C., Stanley, R.D., 2007. Age validation of canary rockfish (*Sebastes pinniger*) using two independent otolith techniques: Lead-radium and bomb radiocarbon dating. Mar. Freshwater Res. 58, 531–541.
4	Field, J.C., 2007. Status of the chilipepper rockfish, *Sebastes goodei*, in 2007. Santa Cruz, CA.
5	Munk, K.M., 2001. Maximum ages of groundfishes in waters off Alaska and British Columbia and considerations of age determination. AK Fish. Bull. 8, 12–21.
6	Gunderson, D.R., Zimmermann, M., Nichol, D.G., Pearson, K., 2003. Indirect estimates of natural mortality rate for arrowtooth flounder (Atheresthes stomias) and darkblotched rockfish (*Sebastes crameri*). Fish. Bull., U.S. 101, 175–182.
7	Malecha, P.W., Hanselman, D.H., Heifetz, J., 2007. Growth and mortality of rockfishes (Scorpaenidae) from Alaska Waters. U.S. Dep. Commer., NOAA Tech. Memo. NMFS-AFSC-172, 61 pp.
8	Kerr, L.A., Andrews, A.H., Munk, K., Coale, K.H., Frantz, B.R., Cailliet, G.M., Brown, T.A., 2005. Age validation of quillback rockfish (*Sebastes maliger*) using bomb radiocarbon. Fish. Bull., U.S. 103, 97–107.
9	Gertseva, V.V., Cope, J.M., Matson, S.E., 2010. Growth variability in the splitnose rockfish *Sebastes diploproa* of the northeast Pacific Ocean: Pattern revisited. Mar. Ecol. Prog. Ser. 413, 125–136.
10	Andrews, A.H., Cailliet, G.M., Coale, K.H., Munk, K.M., Mahoney, M.M., O'Connell, V.M., 2002. Radiometric age validation of the yelloweye rockfish (*Sebastes ruberrimus*) from southeastern Alaska. Mar. Freshwater Res. 53, 139–146.

11   Chilton, D.E., Beamish, R.J., 1982. Age Determination Methods for Fishes
        Studied by the Groundfish Program at the Pacific Biological Station. 102
        pp.

12   Echeverria, T.W., 1987. Thirty-four species of California rockfishes:
        maturity and seasonality of reproduction. Fish. Bull., U.S. 85, 229–250.

13   Nichol, D.G., Pikitch, E.K., 1994. Reproduction of darkblotched rockfish
        off the Oregon Coast. Trans. Am. Fish. Soc.,123, 469–481.

14   Hicks, A.C., Haltuch, M.A., Wetzel, C., 2009. Status of greenstriped
        rockfish (*Sebastes elongatus*) along the outer coast of California, Oregon,
        and Washington. Northwest Fishery Science Center, 2725 Montlake, Blvd.
        E., Seattle, WA.

15   Heifetz, J., J.N. Ianelli, Clausen., D.M., 1997. Slope rockfish. Stock
        assessment and fishery evaluation (SAFE) report for the groundfish
        resources of the Gulf of Alaska, pp. 247-288. North Pacific Fisheries
        Management Council, Anchorage.

16   Bechtol, W.R., 1998. A synopsis of life history and assessment of Cook
        Inlet rockfish. Regional Information Report No. 2A98-40. Alaska Dept. of
        Fish and Game, 333 Raspberry Road, Anchorage, AK. Available at:
        http://www.adfg.alaska.gov/FedAidPDFs/RIR.2A.1998.40.pdf.

17   Stanley, R.D., Kronlund, A.R., 2005. Life history characteristics for
        silvergray rockfish (*Sebastes brevispinis*) in British Columbia waters and
        the implications for stock assessment and management. Fish. Bull., U.S.
        103, 670–684.

18   Phillips, J.B., 1964. Life history studies on ten species of rockfish (genus
        Sebastodes). Cal. Dep. Fish Game Fish Bull. 126.

19   Tagart, J., Wallace, F., Ianelli, J.N., 2000. Status of the yellowtail rockfish
        resource in 2000. Pacific Fishery Management Council, 7700 NE
        Ambassador Pl #101, Portland, OR.

20   Westrheim, S.J., 1975. Reproduction, maturation, and identification of
        larvae of some *Sebastes* (Scorpaenidae) species in the northwest Pacific
        Ocean. J. Fish. Res. Bd Can. 32, 2399–2411.

21   Gertseva, V.V., Cope, J. M., 2011. Population dynamics of splitnose
        rockfish (*Sebastes diploproa*) in the Northeast Pacific Ocean. Ecol. Model.
        222, 973–981.

22   Westrheim, S.J., Harling, W.R., 1975. Age-length relationships for 26
        Scorpaenids in the Northeast Pacific Ocean. Fisheries and Marine Service
        Research and Development Technical Report 565.

23   Wilson, C.D., Boehlert, G.W., 1990. The effects of different otolith ageing
        techniques on estimates of growth and mortality for the splitnose rockfish,

Sebastes diploproa, and canary rockfish, *S. pinniger*. Cal. Fish Game 76, 146–160.

24   Nichol, D.G., 1990. Life History Examination of Darkblotched Rockfish (*Sebastes crameri*) off the Oregon Coast. [Master's thesis, Oregon State University, Corvallis] Available at: http://ir.library.oregonstate.edu/xmlui/handle/1957/11341.

25   Keller, A.A., Molton, K.J., Hicks, A.C., Haltuch, M., Wetzel, C., 2012. Variation in age and growth of greenstriped rockfish (*Sebastes elongatus*) along the U.S. west coast (Washington to California). Fish. Res. 119–120, 80-88.

26   Lenarz, W., 1987. Ageing and growth of widow rockfish, pp. 31-35. In Widow rockfish, proceedings of a workshop, Tiburon, California, December 11-12, 1980. U.S. Dep. Commer., NOAA Tech. Rep. NMFS-48.

27   MacCall, A.D., 2005. Assessment of Vermilion Rockfish in Southern and Northern California. Pacific Fishery Management Council, 2130 SW Fifth Ave, Suite 224, Portland, OR 97220. 128 pp.

28   Kramer, D.E., O'Connell, V.M., 1988. Guide to northeast Pacific rockfishes: genera *Sebastes* and *Sebastolobus*, Marine Advisory Bulletin 25. Alaska Sea Grant College Program, University of Alaska, Fairbanks, AK.

29   Froese, R., Pauly, D., 2010. FishBase. *Assessed*: 5/25/2020. https://fishbase.org

30   Love, M.S., Yoklavich, M., Thorsteinson, L., 2002. The rockfishes of the northeast Pacific. Univ. Calif. Press, Berkeley, CA.

31   Cope, J., Dick, E.J., MacCall, A., Monk, M., Soper, B., Wetzel, C. 2015. Data-moderate stock assessments for brown, china, copper, sharpchin, stripetail, and yellowtail rockfishes and English and rex soles in 2013. Pacific Fishery Management Council, 7700 Ambassador Place NE, Suite 200, Portland, OR 97220. 298 pp.

32   Edwards, A.M., Haigh, R., Starr, P.J., 2012. Stock assessment and recovery potential assessment for yellowmouth rockfish (*Sebastes reedi*) along the Pacific coast of Canada. DFO Can. Sci. Advis. Sec. Res. Doc. 2012/095. iv + 188 p.

2.9 Supplementary Material

Supplementary Material 1

General Catch and Survey Data Summaries

In general, the rockfish species diversity and quantity decreased in the catch data from east to west in the GOA (Supplementary Figure 2) with NPT and LL as the dominant gear types. Subareas 640 and 650 (Eastern GOA) and subarea 630 (eastern part of Central GOA) had the highest diversity and catch compared to other regions, while the highest diversity was observed in the lower southeast GOA. Some species were caught in most gears and subareas, such as yelloweye (*S. ruberrimus*), silvergray (*S. brevispinis*), redbanded (*S. babcocki*) and rosethorn (*S. helvomaculatus*; Supplementary Figure 2). In comparison, other species were only caught by specific gear, such as china rockfish (*S. nebulosus*) by LL and JIG (Supplementary Figure 2).

The two dominant gear types, NPT and LL, each had their highest catch in subarea 630 (Supplementary Figure 2). The NPT and PTR had higher catch of Other Rockfish species compared to the other commercial gear types (Supplementary Figure 2). The average annual catch across all subareas, excluding commercially targeted northern rockfish, for NPT was 805 mt compared to 324 mt for LL. However, LL caught more rockfish species in more subareas in the GOA. The JIG gear fishery mainly occurred in two subareas, 630 and 650, but had a similar catch composition as LL.

The two surveys, trawl and longline, tended to catch a different species composition from one another (Supplementary Figure 2). An average of 17 Other Rockfish species were caught by the trawl survey per year. However, there were eight species that constituted 90% of the total catch for the Other Rockfish complex, which

were redbanded, silvergray, sharpchin (*S. zacentrus*), harlequin, yelloweye, redstripe (*S. proriger*), rosethorn and greenstriped (*S. elongates*). The longline survey caught an average of 1,340 individuals from the Other Rockfish complex per year with about 515 set-depth combinations. The longline survey typically caught 7 rockfish species in the Other Rockfish complex. Of the top five most caught Other Rockfish species in the longline survey by numbers, only three (yelloweye, canary and rosethorn) have been designated to the Demersal Shelf Rockfish complex in subarea 650.

Supplementary Tables

Supplementary Table 1. Variance associated with each CCA axis from the CCA
proportions matrix with units (year-month-subarea-gear).

CCA Axis	Variance
1	0.3895
2	0.2542
3	0.1603
4	0.0434
5	0.0244
6	0.0176
7	0.0108
8	0.0081
9	0.0007
10	0.0001

Supplementary Figures
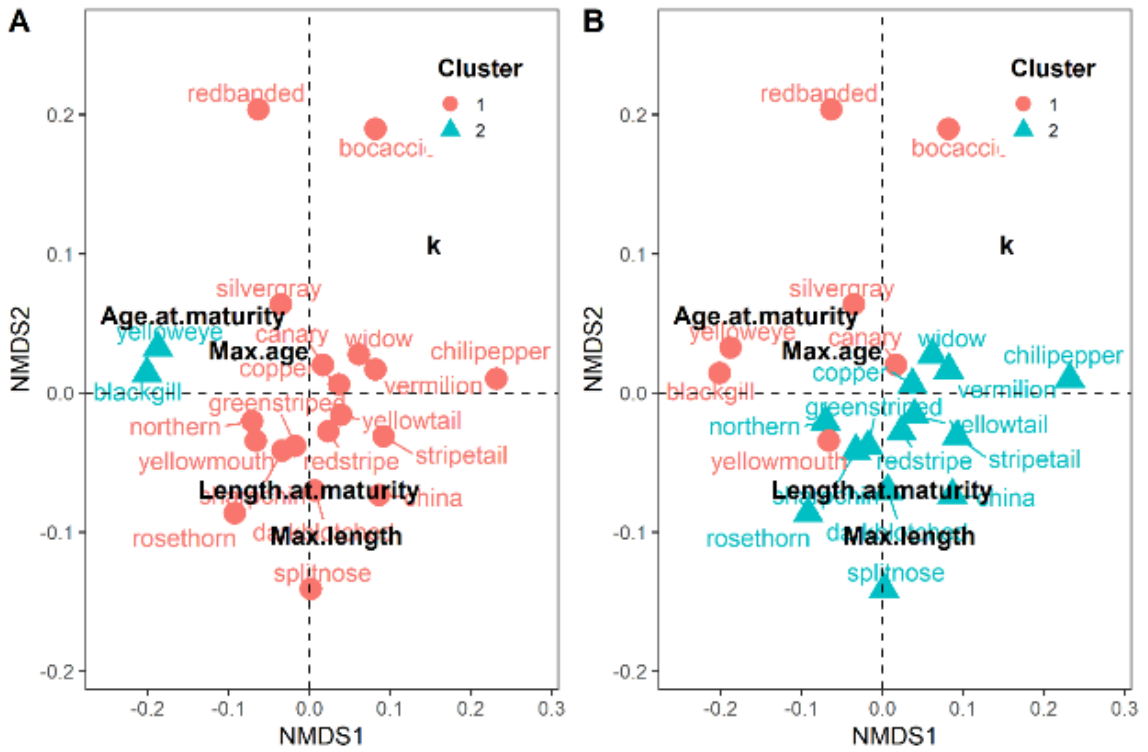
Supplementary Figure 1. NMDS plot of species' clusters identified from the life history table using species with all values (complete cases) from (A) Ward's hierarchical cluster analysis and (B) *k*-mediods.
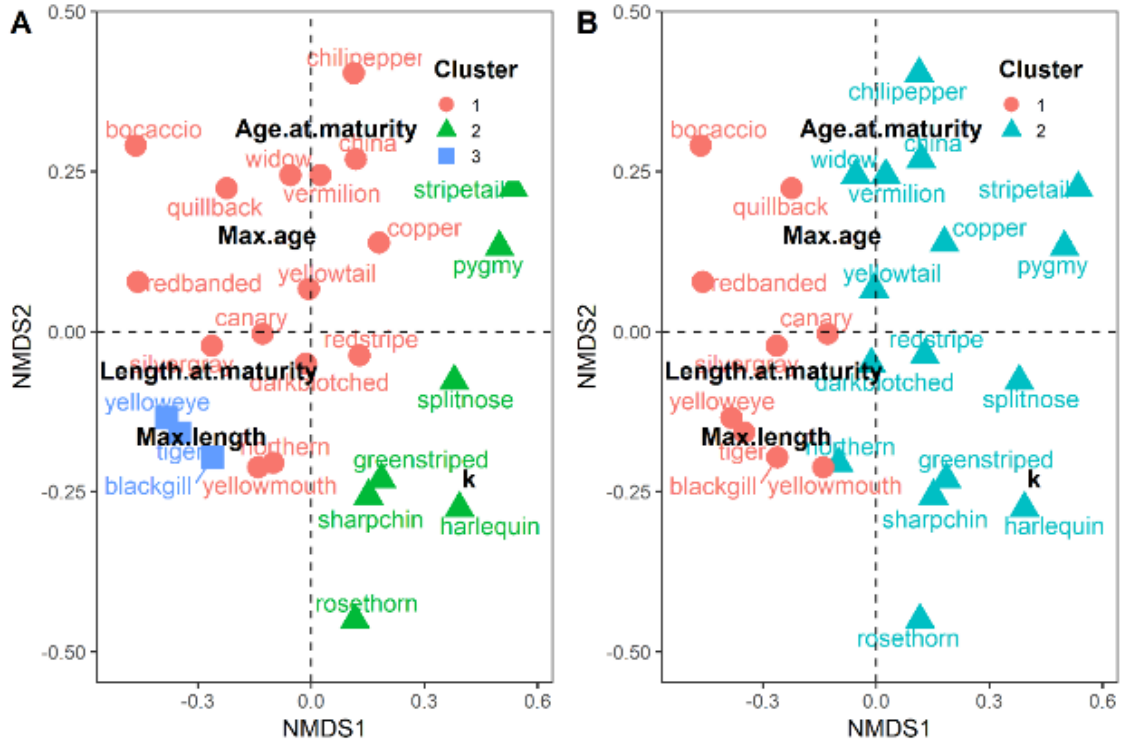
Supplementary Figure 2. NMDS plot of species' clusters identified from the life history table with binned values (0-25%, 26- 50%, 51-75%, and 76-100% percentile bins) from (A) Ward's hierarchical cluster analysis and (B) *k*-mediods.
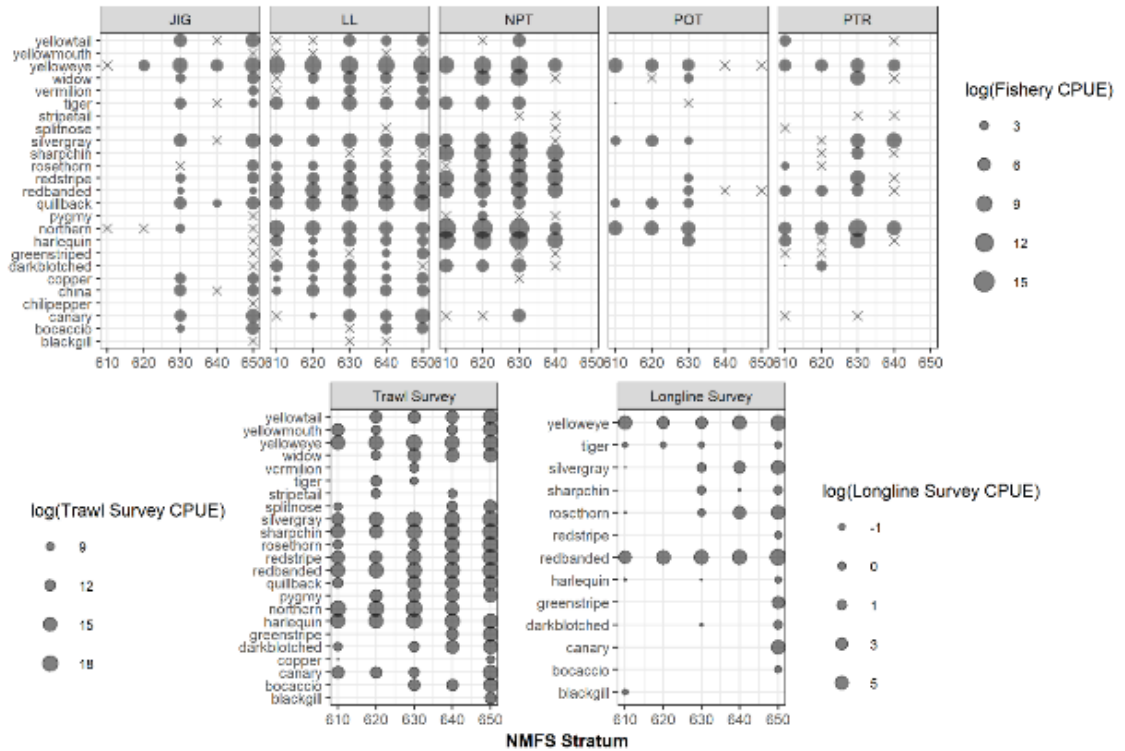
Supplementary Figure 3. Total log(CPUE) for each fisheries gear type (top panel; jig [JIG], longline hook and line [LL], non-pelagic trawl [NPT], pot [POT], and pelagic trawl [PTR]) in each NMFS subarea and survey gear (bottom panel; longline and trawl). CPUE is measured in metric tons caught per vessel trip for all fishery gear types, kilograms per km^2 swept for the trawl survey and number of individuals caught per hook set for the longline survey. NMFS subarea are arranged from 610 (western GOA) to 650 (southeastern GOA). Confidential data are indicated by an "x".
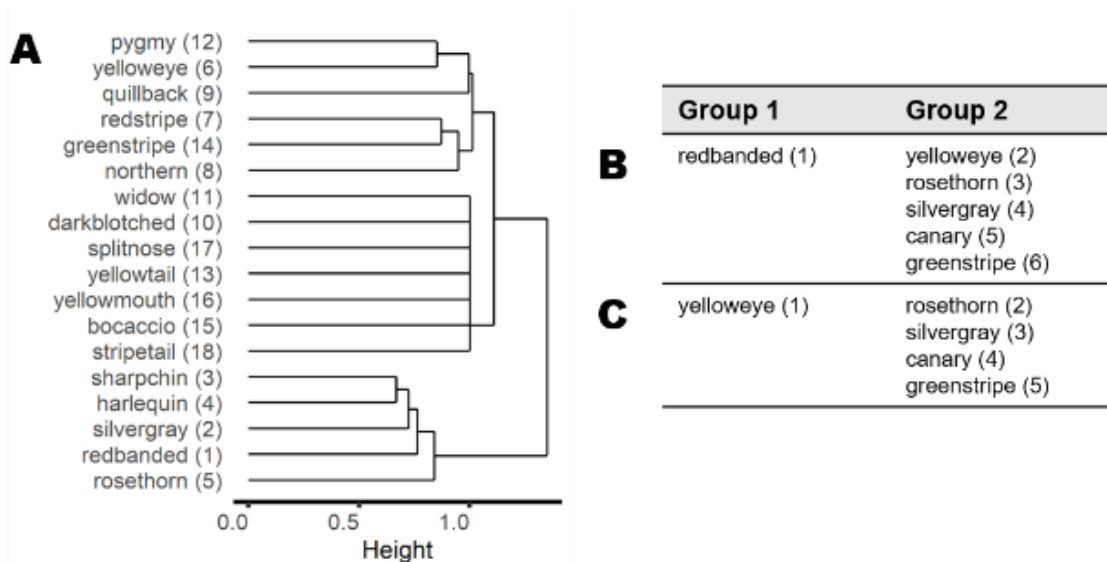
Supplementary Figure 4. Typical examples of results from cluster analyses using R-mode with individual sub-unit matrices. (A) A dendrogram of Ward's hierarchical cluster analysis using transformed presence-absence data from the NMFS bottom trawl survey in NMFS subarea 640. Suggested groupings from k-mediods based on the highest average silhouette width using transformed presence-absence data from the NMFS longline survey in NMFS subarea 650 with the rank of presence of rockfish from highest to lowest indicated by parentheses with (B) and without (C) redbanded rockfish, which is the most highly abundant species in subarea 650.
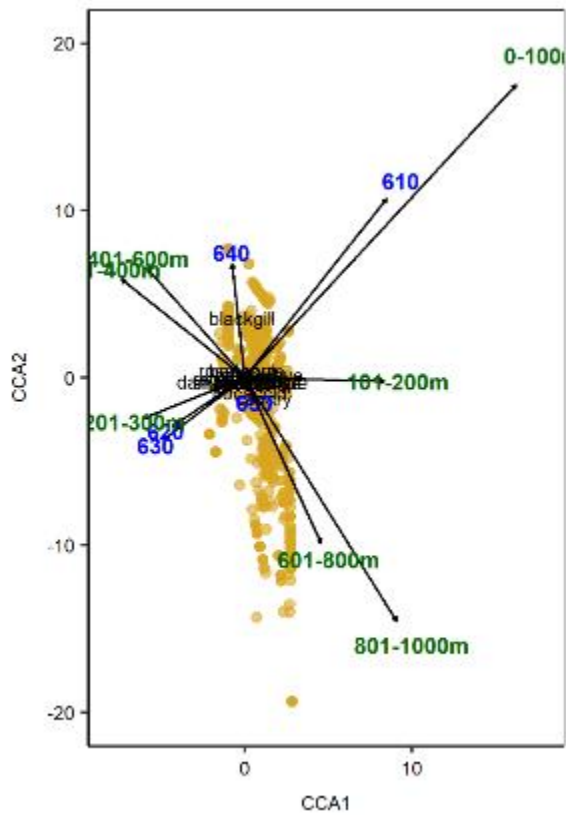
Supplementary Figure 5. Example of a CCA ordination using individual sub-unit matrix from the NMFS longline survey with individual haul units (points), species (black text) and additional environmental factors, including depth bins (green text) and NMFS subarea (blue text). Arrows indicate the strength and direction of the environmental factor.
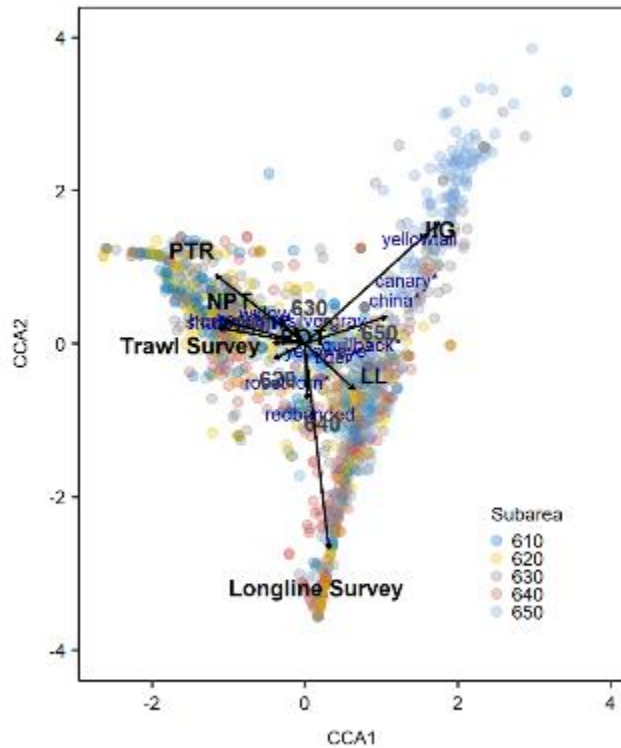
Supplementary Figure 6. CCA results using the proportions matrix with units (year-month-subarea-gear) plotted on the first two CCA axes with each unit color coded by NMFS subarea designation, species marked in blue text (with species currently assigned to the Demersal Shelf Rockfish marked with "*") and factors, gear and subarea, in black bold text.

CHAPTER 3

Identifying species complexes based on spatial and temporal clustering from joint, dynamic species distribution models

Abstract

Data-limited species are often grouped into a species complex to simplify management. Commonalities between species that may indicate if species can be adequately managed as a complex include: shared habitat utilization (e.g., overlapping fine-scale spatial distribution), synchrony in abundance trends, consistent fishing pressure or gear susceptibility, or life history parameters resulting in similar productivity. In this study, we present the first attempt to determine spatial and temporal similarities among species for the purpose of developing species complexes using the vector autoregressive spatio-temporal (VAST) model, which is a joint, dynamic species distribution model. Using fishery-independent trawl survey data, we compare: 1) the spatial and 2) temporal model covariance among species using Ward's hierarchical cluster analysis of harvest fractions and life history characteristics to examine similarity in species clustering using species belonging to the Gulf of Alaska Other Rockfish complex as a case study. Results indicate that all species demonstrated a positive spatial correlation and a positive or neutral correlation in temporal changes. We conclude that there are some Gulf of Alaska Other Rockfish species that consistently group together (Group 1: canary and yellowtail; and Group 2: silvergray and yellowmouth), but the arrangement and number of clusters differ slightly depending on the data used. Developing species complexes for fisheries management requires a variety of analytical approaches, of which both species distribution models and cluster analyses should be included, applied across the full extent of available data sources.

3.1 Introduction

The management of non-target species, those being caught incidentally to the primary species, can be a challenge, particularly when the fisheries span a wide, heterogeneous geographic area. Non-target species typically have limited economic value, have low population densities, are previously allocated towards a different target fishery, or are preserved as forage for other ecosystem components (e.g., Davies et al., 2009). Despite potential limited economic importance, adequate management of non-target catch is necessary to maintain individual populations and ensure overall ecosystem health, particularly when the accumulated biomass of non-target species exceeds the targeted species biomass or for species with high vulnerability to overfishing (e.g., Lewison et al., 2004; Piet et al., 2009; Cope et al., 2011; Rezende et al., 2019). Many non-target species have sparse life history data, undocumented species-specific catch histories, or unknown spatial distributions. Additionally, fishery-independent surveys, if available, do not typically optimize sampling for non-target species. Yet, international fishery policies, particularly in the United States and the European Union, mandate catch limits on all exploited species, including data-limited species (e.g., Magnuson-Stevens Reauthorization Act of 2006, MSRA, 2007; Common Fisheries Policy, CFP, 2013).

One approach to comply with management requirements is to assess an assemblage of non-target species as a unit, known as a species complex (Jiao et al., 2009). Complexes are typically designated for species caught in a multispecies fishery where adequate data or technical support are often lacking to perform single species stock assessments, or where gear interactions make single species management difficult to implement (USOFR, 2009; Reuter et al., 2010). While species complexes are

characterized as a group of species having similar life history characteristics, susceptibility to the fishing gear, and geographic distributions (MSRA, 2007), information is typically missing to satisfy all requirements. For example, estimates of life history values (e.g., maximum age, age-at-maturity) can be sparse for data-limited species. Although recent efforts have predicted these for all fish species using taxonomic and life-history correlations (Thorson et al., 2017; Thorson, 2020), these predictions are correlated within taxa. As a result, species are often partitioned into family or similar aggregations (DeMartini, 2019). Moreover, the fishery vulnerability and geographic overlap conditions for a complex can be difficult to address when the area of management spans a wide diversity of habitat and fishing gears. Ideally, species within a complex would demonstrate high spatial overlap and would sustain similar environmental and fishing pressures reflected by synchrony in temporal trends of abundance (Cope and Punt, 2009).

Understanding of spatio-temporal distributions of non-target species can help to better identify appropriate stock complex groupings. Overlapping fine-scale distributions for species in a complex indicates co-existence, which can occur when it is mutually beneficial for both (or all) individuals (e.g., schooling for increased predator protection; Morse, 1977; Parrish, 1991), species' fitness levels are comparable to one another (i.e., have similar abilities for reproductive success; Chesson and Kuang, 2008), resources are not limiting (Neves et al., 2018), or habitat complexity enables a diversity of species to cohabitate (Almany, 2004). However, understanding all the drivers that promote co-existence is a challenge (Neves et al., 2018). Species belonging to a complex should fulfill similar niches in the ecosystem (i.e., niche overlap; Hutchinson, 1957), such that

external forces would similarly influence the productivity and status of all species in the complex. Additionally, identifying commonality in spatial distributions can help determine the degree of similarity in harvest pressure across species. Species that demonstrate spatial synchrony are more likely to be harvested at similar rates (if they have similar susceptibility to the gear), thereby reducing the possibility of localized depletion if the complex is managed for sustainability (Jarillo et al., 2018).

A common ecological tool for identifying spatial synchrony and structure of biological populations are species distribution models (SDMs), which are becoming increasingly prevalent for fisheries applications (Planque et al., 2011; Berger et al., 2017). A critical advancement in SDMs, which has allowed a more thorough understanding of species distributions given limited observed data, has been the incorporation of spatial autocorrelation (Legendre, 1993; Dormann et al., 2007). The assumptions of spatial autocorrelation (i.e., spatial covariation among locations) imply that neighboring locations are more similar than locations further away, which enables an SDM to interpolate across space and estimate abundance for model grid cells that may not have data (Dormann et al., 2007; O'Leary et al., 2020). A wide variety of potential explanatory covariates can be incorporated into SDMs to establish correlations to observed features and aid in extrapolation when data on abundance are sparse. For instance, many SDMs incorporate abiotic factors as covariates in the model, including temperature, depth, sediment or bottom type, salinity, and spatially varying responses to regional oceanographic conditions (e.g., Nishida and Chen, 2004; Perry et al., 2005; Godefroid et al., 2019; Thorson, 2019). While abiotic factors can increase the predictive performance of presence or density estimates, there are many unknown factors that

similarly influence a species' distribution. More recently, SDMs have been extended to incorporate random effects to account for unobserved or unexplained processes affecting the spatial distribution of species (Thorson et al., 2015).

Identifying co-existence or asynchrony among species can help inform spatial distributions in the same way as abiotic factors, particularly when spatial abiotic factors are unknown. Joint, dynamic SDMs (JDSDM) allow for the simultaneous estimation of spatio-temporal densities for multiple species. Incorporating species associations can be particularly useful for data-poor species due to sparse observation data. Thus, identifying and incorporating species' relationships can improve spatio-temporal extrapolations and aid in estimating species distribution (Ovaskainen and Soininen, 2011; Thorson et al., 2015; Thorson and Barnett, 2017). Modeling both spatial and temporal correlations for multiple species simultaneously can better delineate direct relationships among species' distributions and detect spatio-temporal changes in respect to biotic, abiotic, and anthropogenic factors (Godefroid et al., 2019). JDSDMs can generate community dynamic spatio-temporal trends in addition to individual abundance indices (Thorson et al., 2016). Therefore, a single model to identify fine-scale spatial correlation along with similarities in temporal trends among multiple data-limited species can help validate species complexes.

The goal of this research is to explore a new application of JDSDMs as a tool for identifying species complexes for data-limited species. We demonstrate the approach through exploration of the spatial and temporal patterns of non-target rockfish belonging to two management complexes in the Gulf of Alaska (GOA): Other Rockfish and Demersal Shelf Rockfish. The model accounts for unobserved spatial and temporal

variation in a delta-model that estimates the unknown variables in both the encounter and positive catch given presence model components. The JDSDM model is applied to examine the spatial and temporal correlations along with overlap in distributions of the species in the non-target GOA rockfish complexes by modeling the species simultaneously. Then we apply a clustering method to the results of the JDSDM to group species based on spatial and temporal synchrony in abundance and distribution. Finally, we compare resultant species complexes suggested by the JDSDM to species complex delineations based on harvest rates and on life history characteristics, along with recent assignments to complexes suggested by Omori et al. (2021; Chapter 2). We show that identifying spatio-temporal correlations using JDSDMs can be a useful tool for identifying species complexes, which is a useful addition to the suite of analytical clustering approaches currently considered for identifying species complexes in data limited situations.

3.2 Methods

3.2.1   Case Study: GOA Non-target Rockfish

The GOA Other Rockfish complex consists of over 20 non-target *Sebastes* species within the GOA management area with more than half that are rarely caught (<1% of the total GOA Other Rockfish catch). The nine Demersal Shelf Rockfish species are a subset of species within the GOA Other Rockfish, but are separately managed in one of the five areas (650; Supplementary Material Fig. SM1). For the purposes of this document, "Other Rockfish" will refer to species within both complexes in the GOA. Members of the Other Rockfish complexes vary widely in their distributions and habitat

preferences, with many being at the northern limits of their distributions in the GOA, which typically span the U.S. West Coast from Southern California to Alaska (Love et al., 2002). Rockfish tend to be found near the benthic substrate in a variety of habitats including high relief rocks, reefs, and boulders, to low relief rocky substrate and mudflats (Johnson et al., 2003; Conrath et al. 2019). The Other Rockfish species are typically found in depths ranging from 100 to 275 m, but can be found at depths up to 800 m (Love et al., 2002). Rockfish species generally have late maturity, are long-lived, and bear live young (Love et al. 2002; Beyer et al. 2015). These low productivity characteristics tend to place rockfish into a high vulnerability category, requiring careful management (Cope et al., 2011; Ormseth and Spencer, 2011).

The Other Rockfish species are incidentally caught in trawl and longline groundfish fisheries. Around 46% of these non-targeted species are discarded (Tribuzio and Echave, 2019) due to their low economic value (pers. Comm. Ben Fissel), relatively small body size compared to other rockfish species, and low catch rates. Most of the species in the Other Rockfish complex are caught in the GOA trawl fisheries, while a subgroup of rockfish are primarily caught by longline gear fisheries in rocky, high relief habitats (Tribuzio and Echave, 2019).

3.2.2 GOA Fishery Independent Trawl Survey Dataset

For our analyses, we use the National Marine Fisheries Service (NMFS) bottom trawl survey because this fishery-independent survey represents the most cohesive and spatially extensive source of data on all Other Rockfish species. The NMFS trawl survey is also currently used as the basis of the GOA Other Rockfish complex stock assessment

and management advice (Tribuzio and Echave, 2019). The NMFS bottom trawl survey, further referred to as the 'trawl survey', has collected species-specific data for the Other Rockfish species, including weights of each species caught per tow, since 1984; the GOA was surveyed on a triennial rotation from 1984 – 1996, followed by a biennual time scale from 1999 – present (von Szalay and Raring, 2018). We include years from 1984 – 2019, which totals 16 surveyed years. The survey is conducted from May through August and follows a stratified random sampling design with, on average, 725 tows per year (Supplementary Material Fig. SM1). The bottom trawl survey reaches depths up to 900 m depending on the year. Each tow covers on average 0.032 km^2 swept per tow. Species-specific data are entered as biomass caught per tow with area swept as an offset. Due to the extreme rarity of some bycatch species in the Other Rockfish complex, we demonstrate our modeling approach using a subset of nine rockfish with the requirements that each chosen species make up more than 1% of the total catch biomass in the survey over the entire time series (Table 1). These nine species have been consistently identified throughout the timeseries.

3.2.3 Model Structure

We implement a JDSDM that applies spatial dynamic factor analysis to identify spatial and temporal commonality among the Other Rockfish species. More specifically, we applied the Vector Autoregressive Spatio-Temporal (VAST) model version 3.4.0 (downloaded from https://github.com/James-Thorson-NOAA/VAST) developed by Thorson et al. (2015 and 2016) to account for latent spatial and temporal variation. VAST estimates the latent (i.e., unknown) variables as "factors", and allows locations to be

spatially autocorrelated and years to be independent, random, or correlated with previous time steps. This JDSDM framework allows flexibility of delta-model variants, which separates the catch into two parts: encounter probability and catch probability given presence.

We apply a Poisson-link delta-gamma model (Thorson, 2018; Thorson et al., 2021) to estimate the density of each species at every location in each year. The symbols used below to describe the model are defined in the Supplementary Material Table SM1 and the notation follows Thorson (2019). The delta model estimates the encounter and positive catch separately. The encounter probability, approximated by the first linear predictor, p_1, and positive catch probability, approximated by the second linear predictor, p_2, for each observation i, which represents each location s, species c, and year t, are modeled as:

$$p_*(s_i, c_i, t_i) = \underbrace{\mu_{\beta*}(c_i) + \sum_{f=1}^{n_{\beta*}} L_{\beta*}(c_i, f)\beta_*(t_i, f)}_{temporal\ variation} + \underbrace{\sum_{f=1}^{n_{\omega*}} L_{\omega*}(c_i, f)\omega_*(s_i, f)}_{spatial\ variation}\ , \qquad (1)$$

where "*" replaces the "1" or "2" subscripts corresponding to the first (p_1; encounter) and second (p_2; positive catch) linear predictor equations, respectively. There is a $\mu_{\beta*}$ intercept for each observation that represents the time-average for each species. The temporal variation is represented by $\beta_*(t_i, f)$ for each year and factor, f (latent variable), with the associated loadings matrices denoted as $L_{\beta*}(c_i, f)$. Here, the temporal variation follows a random walk:

$$\beta_*(t_i, f) = \begin{cases} \delta_*(t_i, f) & \text{if } t = t_{min} \\ \beta_*(t_i - 1, f) + \delta_*(t_i, f) & \text{if } t > t_{min} \end{cases} \qquad (2)$$

where $\delta_*(t_i, f)$ follows a standard normal distribution. The $\omega_*(s_i, f)$ is the spatial variation for each location and factor, and $L_{\omega_*}(c_i, f)$ components are the loadings matrices. We use a full rank model by defining the number of factors in the model as the total number of species, such that

$n_{\beta*} = n_{\omega*} = n_c = 9$, for both the temporal and spatial variation in each linear predictor.

The spatial variation (ω_*) is estimated as a Gaussian Markov Random Field to account for spatial autocorrelation:

$$\boldsymbol{\omega}_*(s_i, f) \sim MVN(0, \mathbf{R}_*) \tag{3}$$

The spatial correlation matrix, $\mathbf{R}_*$, is modeled using a Matérn correlation function, which assumes that nearby locations are more correlated and the correlation decreases by distance (Thorson, 2019).

The predicted density, $d(s_i, c_i, t_i)$, is estimated using a Poisson-link that assumes that areas with a higher expected encounter rate also have a higher expected biomass for each encounter. By "linking" the two model components (encounter and positive catch probabilities) in a Poisson-link model, the number of parameters that are estimated can be reduced compared to a typical delta-model. The predicted density from the Poisson-link model for each observation using the first and second linear predictors (Eq. 1) is:

$$d(s_i, c_i, t_i) = r_1(s_i, c_i, t_i) \times r_2(s_i, c_i, t_i) \tag{4}$$

$$\text{where } r_1(s_i, c_i, t_i) = 1 - \exp(-a_i \times \exp(p_1(s_i, c_i, t_i))) \tag{5}$$

$$\text{and } r_2(s_i, c_i, t_i) = \frac{a_i \times \exp(p_1)}{r_1(s_i, c_i, t_i)} \times \exp(p_2(s_i, c_i, t_i)). \tag{6}$$

The density is based on the predicted biomass (metric tons, mt) per area-swept, a_i

(km^2), where the area-swept is included as an offset in the model in Eqs. 5 and 6. The

link function for the probability of a non-zero catch (encounter probability) is r_1 and the

link function for positive catch is r_2. The encounter and positive catch probabilities are

modeled in the delta-gamma model to obtain the probability distribution of biomass catch

as:

$$\Pr(b(s_i, c_i, t_i) = B) = \begin{cases} 1 - r_1(s_i, c_i, t_i) & if\ B = 0 \\ r_1(s_i, c_i, t_i) \times Gamma\{B\ |k = \frac{1}{\sigma_c^2}, \lambda = r_2(s_i, c_i, t_i) * \sigma_c^2\} & if\ B > 0 \end{cases}, \quad (7)$$

where the observed biomass catch data ($b(s_i, c_i, t_i)$) is for each location s, species c, and

year t. The positive catch is modeled using a reparameterized gamma distribution for

the probability density function, where the shape, k, and scale, λ, are functions of the

expected catch given a presence, $r_2(s_i, c_i, t_i)$ (Eq. 6), and residual biomass sampling

variation, σ_c^2, for species c (i.e., measurement error).

Model diagnostics that are used to determine model fit include the comparison of

empirical distributions to simulated distribution using Q-Q plots and density histograms

(Supplementary Material Fig. SM2 and Fig. SM3).

The flexible model structure includes fixed effects (σ_c^2, $\mu_{\beta*}$intercepts, $L_{\beta**}(c_i, f)$,

$L_{\omega**}(c_i, f)$) and random effects ($\beta_*(t_i, f)$ and $\omega_*(s_i, f)$). Fixed effects are estimated by

maximizing the marginal likelihood while integrating across the random effects. A

Laplace approximation is used to approximate the marginal likelihoods (Skaug and

Fournier, 2006). To improve efficiency of estimation, VAST creates a mesh of discrete

locations (i.e., knots) to represent a reduced set of locations to approximate the sampling

area (Thorson et al., 2015). The knots are determined internally in VAST by a k-means

cluster algorithm, which distributes the knots based on the proportionality of sampling intensity (Shelton et al., 2014; Thorson et al., 2015). We use 500 knots (estimated locations, *s*) in our model with a 10 x 10 km grid size. VAST is executed in Template Model Builder (TMB; Kristensen et al., 2016) and uses R statistical program (R Core Team, 2021) as a platform to identify the maximum likelihood estimates of fixed effects. Lastly, we use Microsoft R Open 3.5.3 (https://mran.microsoft.com/) to improve computational efficiency. The VAST model structure is described in further detail in Thorson (2019) and the VAST code is available online (www.github.com/james-thorson-NOAA/VAST).

3.2.4 Estimated and Derived Quantities

The individual covariance matrices for each linear predictor are calculated using the estimated loadings matrices where the temporal loading matrices, $\hat{L}_{\beta *_*}(c_i, f)$, and spatial loading matrices, $\hat{L}_{\omega *_*}(c_i, f)$, are denoted as $\hat{\mathbf{L}}_1$ and $\hat{\mathbf{L}}_2$ for the first and second linear predictor. We compute a single, joint covariance matrix, $\hat{\mathbf{V}}_{\mathbf{total}}$, for each model component, temporal (β) and spatial (ω), by summing the individual covariance matrices from the first and second linear predictors as follows:

$$\hat{\mathbf{V}}_{\mathbf{total}} = \hat{\mathbf{L}}_1^{\mathrm{T}}\hat{\mathbf{L}}_1 + \hat{\mathbf{L}}_2^{\mathrm{T}}\hat{\mathbf{L}}_2. \tag{8}$$

The $\hat{\mathbf{V}}_{\mathbf{total}}$ are examined to determine temporal and spatial similarities among species by examining the positive, negative, or neutral individual variance between two species c_1 and c_2, $\hat{v}_{total}(c_1, c_2)$ in the $\hat{\mathbf{V}}_{\mathbf{total}}$. We calculate the combined loading matrices for the temporal and spatial model components using a Cholesky decomposition on each $\hat{\mathbf{V}}_{\mathbf{total}}$ in

order to examine the association of species with latent factors. Then we apply a principal

component analysis (PCA) approach on the combined loading matrices to rotate the

species' loadings to visualize the temporal and spatial factors (Thorson et al., 2016). The

proportion of variation explained by each linear predictor for spatial and temporal model

components is calculated by dividing the sum of the eigenvalues from $\hat{\mathbf{L}}_1$ and $\hat{\mathbf{L}}_2$ by the

sum of eigenvalues from both $\hat{\mathbf{L}}_1$ and $\hat{\mathbf{L}}_2$. The proportion of variation explained by each

factor for each model component is calculated by dividing the eigenvalues associated

with each factor by the sum of all eigenvalues in each model component.

To examine the similarities in temporal trends among species, we use the indices of

abundance, $\hat{I}(c,t)$, for each species and each year derived from estimates in the model for

the GOA management area by summing all the locations, n_s, in the spatial grid:

$$\hat{I}(c,t) = \sum_{s=1}^{n_s} \left(a(s) \times \hat{d}(s,c,t) \right), \tag{9}$$

where $\hat{d}(s,c,t)$ is the predicted density in kg/km^2 at each location and is expanded by the

area at each location, $a(s)$, in km^2.

3.2.5 Cluster Analyses and Comparison

We apply Ward's hierarchical clustering (Ward, 1963) on the $\hat{\mathbf{V}}_{\textbf{total}}$ to investigate

species groupings based on the temporal and spatial relationships to compare with the

PCA results. The distances $\gamma(c_1, c_2)$ between each set of species, c_1 and c_2, used in the

clustering method on the covariance matrices, $\hat{\mathbf{V}}_{\textbf{total}}$, are calculated by:

$$\hat{\gamma}(c_1, c_2) = \sqrt{\hat{v}_{total}(c_1, c_1) + \hat{v}_{total}(c_2, c_2) - 2\hat{v}_{total}(c_1, c_2)}, \quad (10)$$

using the variance of each species, $\hat{v}_{total}(c_1, c_1)$ and $\hat{v}_{total}(c_2, c_2)$, and covariance between

the two species, $\hat{v}_{total}(c_1, c_2)$. A distance matrix composed of elements $\hat{\gamma}(c_1, c_2)$ is

calculated for each of the temporal and spatial component using the temporal, $\mathbf{\hat{V}_{\beta total}}$, and

spatial, $\mathbf{\hat{V}_{\omega total}}$, covariance matrices. We calculate the average silhouette width to

determine the optimal number of clusters, where the highest value indicates the preferred

number of clusters (Rousseeuw, 1987). The average silhouette width measures the

similarity of objects within the same cluster compared to other clusters and is calculated

using R package "factoextra" (Kassambara and Mundt, 2020).

We calculate the spatial and temporal centroids for each cluster from the Ward's

analysis to compare spatial and temporal trends between clusters. The individual species

and location specific spatial estimates from the first, $\hat{\omega}_1(c, s)$, and second, $\hat{\omega}_2(c, s)$,

linear predictors that are derived from the spatial variation component in Eq. 1 are

summed to obtain a total spatial estimate for each species at each location ($\hat{\omega}_{total}(c, s) =$

$\hat{\omega}_1(c, s) + \hat{\omega}_2(c, s)$). We average the total spatial estimates of each species belonging to

the cluster to obtain the average spatial value for each cluster g, $\hat{\omega}_{total}(g, s)$. Then we

map the average spatial value, $\hat{\omega}_{total}(g, s)$, for each cluster to visualize the spatial

pattern associated with each cluster. The temporal centroids from the Ward's clusters are

calculated differently from the spatial centroids because the temporal variation follows a

random walk. First, we sum the individual temporal estimates for each species and each

year from the two linear predictors ($\hat{\beta}_1(c, t)$ and $\hat{\beta}_2(c, t)$) derived from the temporal

variation component in Eq. 5 to obtain the total temporal estimates, $\hat{\beta}_{total}(c, t)$. Then the

difference between the total temporal estimates for each species for each year

$(\Delta\hat{\beta}_{total}(c, t) = \hat{\beta}_{total}(c, t) - \hat{\beta}_{total}(c, t - 1))$ for $t > t_{min}$ are calculated. Next, we

average the $\Delta\hat{\beta}_{total}(c, t)$ for all the species belonging to the cluster, g, each year to

obtain a $\Delta\hat{\beta}_{total}(g, t)$ as the average temporal value for each year after t_{min}. Finally, the

cumulative sum of the $\Delta\hat{\beta}_{total}(g, t)$ for each cluster are calculated to transform back into

the original random walk scale.

We compare the clustering results based on the spatial and temporal components of

the JDSDM (i.e., VAST model) with species clusters based on life history characteristics

and fisheries data (Supplementary Material Table SM2 and SM3). The comparison of life

history attributes is based on values determined from a literature review of GOA Other

Rockfish species (Omori et al., 2021). The values utilized in this study are: age- and

length-at-maturity (A_{mat} and L_{mat}, respectively), maximum age observed (as a proxy for

longevity, A_{max}), and mean maximum length from the von Bertalanffy growth curve

(L_∞). The resultant life history table is standardized (i.e., divided by its mean) to give

equal weight to each life history characteristic before calculating the Euclidean distances

(i.e., similarity among species). To compare similarities in harvest impacts, we calculate

the annual harvest fraction for each species by dividing the total species-specific fisheries

catch in the GOA by the estimated abundance (Eq. 9) for each year modeled in the

JDSDM. The species-specific fisheries catch data is gathered from the NMFS Alaska

Regional Office Catch Accounting System (Cahalan et al. 2014) using data from 2010 to

2019, representing years when robust species-specific fisheries data have been reported.

Each harvest fraction is normalized by dividing by the largest harvest fraction in the

dataset, followed by calculating the Euclidean distance to determine similarity among

fisheries harvest fractions across species (Supplementary Material Table SM3). Finally,

we apply Ward's clustering analyses to the life history and harvest fraction distance

datasets to identify species clusters, using the R package "stats" (R Core Team, 2021).

Dendrograms are used to compare the relationships among rockfish included in the

JDSDM from the temporal and spatial covariance matrices and the life history and

harvest fraction data sources. We use the average silhouette width to determine optimal

number of clusters for each data source.

3.3 Results

3.3.1 Spatial Overlap, Correlation, and Clusters

GOA Other Rockfish have varying levels of spatial overlap. Density estimates

suggest that some species are found in deep waters throughout the GOA (i.e., harlequin

and yelloweye), while others have a GOA-wide distribution, but have densities that are

more concentrated in the southeastern GOA (i.e., canary, yellowtail, and yellowmouth;

Fig. 1). The remaining species also tend to have higher densities in the southeastern

GOA, but have a more gradual decreasing density gradient moving westward (e.g.,

redbanded, redstripe, sharpchin, and silvergray; Fig. 1).

The majority of the spatial variation is explained in the first linear predictor,

encounter probability (81%). For the combined spatial component, the first three rotated

factors out of nine comprise 72%, 9%, and 7% of the total spatial variation, respectively

(Supplementary Material Table SM4). Factor 1 from the combined spatial component

appears to be associated with both differences between the southeastern GOA and other

areas along with distance from land. Factor 2 demonstrates a more centralized association

with the southeastern GOA, but no distinguishable association with distance from land

throughout the remaining GOA (Fig. 2). Based on the PCA rotation of the spatial factors,

the rockfish separate into three groups (Fig. 2, see Supplementary Material Table SM5

and Fig. SM4 for Factor 3 factor loadings). Two species, canary and yellowtail, which

have high concentrations in the southeastern GOA, clustered together and separate on the

Factor 2 axis. Another group consisting of harlequin, redstripe, sharpchin, and yelloweye

has small, negative Factor 2 rotated loadings and larger Factor 1 rotated loadings (Fig. 2).

The four species belonging to this group tend to have higher densities throughout more

areas in the GOA (e.g., higher densities between Prince William Sound and Cook Inlet;

Fig. 1) compared to the other two groupings. The third group with redbanded, silvergray,

and yellowmouth has small, positive Factor 2 rotated loadings (Fig. 2). The species in

this third group have higher density concentrations in the southeastern GOA, but most are

also found in other areas in the GOA in lower densities (Fig. 1). While all rockfish

demonstrate positive spatial correlation with one another, there are varying strengths of

correlation (Supplementary Material Fig. SM5). For example, canary and yellowtail

demonstrate strong positive spatial correlation, but have weaker correlation with the other

rockfish (Supplementary Material Fig. SM5). Overall, the strength of the correlations

among species varied, but were all positive.

Ward's clustering using the spatial covariance matrix results in similar groupings

as those found in the PCA rotation from the spatial component, with three suggested

groupings: 1. canary and yellowtail, 2. harlequin, yelloweye, redstripe, and sharpchin, 3.

redbanded, silvergray, and yellowmouth (Fig. 3a). The centroid of cluster 1 (containing

canary and yellowtail) has high values in southeastern GOA (Fig. 4). The centroid of

cluster 2 (harlequin, yelloweye, redstripe, and sharpchin) is elevated further from the land, as well as waters between Prince William Sound and Cook Inlet, and Cluster 3 (redbanded, silvergray, and yellowmouth) have a higher concentration in southeastern GOA with more extended densities into the eastern area (Fig. 4).

3.3.2 Temporal Overlap, Correlation, and Clusters

The calculated indices of abundance do not appear to track one another over time, which is supported by the weak and wide range of positive temporal correlations among species (Supplementary Material Fig. SM6). However, the abundance indices for many GOA Other Rockfish at the end of the time series are at or above their median yearly biomass indicating a relatively stable or an increase in abundance in the more recent years (Fig. 5). Redbanded, silvergray, and yelloweye abundance increases throughout the survey time series, while others show higher variability (i.e., canary and sharpchin). A few species, such as redstripe, sharpchin, and silvergray, have an estimated biomass almost tenfold higher than the other species included in the model (Fig. 5).

The second linear predictor explains 81% of the total temporal variation, which is the variance of a random walk process, while the first linear predictor explains only 19% of the total temporal variation. The first three rotated factor loadings out of nine of the combined temporal component account for 67%, 16%, and 12% of the total temporal variation, respectively (Supplementary Material Table SM4). Yellowtail and canary appear to separate from the other rockfish along with from one another based on Factor 1 and 2 after the PCA rotation (Fig. 6; see Supplementary Material Table SM6 and Fig. SM6 for Factor 3 factor loadings).

Results from Ward's clustering suggests two temporal groupings for this set of rockfish (Fig. 3b). Canary and yellowtail separate into their own cluster (Cluster 1), and appear to have a decrease in temporal estimate values in the early 1990's compared to the remaining species in the other cluster (Fig. 7). The average temporal values (i.e., the average yearly temporal values for the cluster on the random walk scale) of the two species cluster (Cluster 1) fluctuate more than the other cluster with seven species (Cluster 2), but both clusters appear to demonstrate a slight increase in the end of the time series where the majority of the average temporal values in the latter years are above their median value (Fig. 7).

3.3.3 Cluster Analyses Comparison

The clustering on the annual harvest fractions separated the species based on levels of exploitation, with three clusters defined by high, intermediate, and low harvest fractions (Fig. 3c; Supplementary Material Table SM3). Similarly, the three clusters using the life history data are divided into low, medium, and high productivity levels (Fig. 3d; Supplementary Material Table SM2), where low levels of productivity correspond to large sizes at 50% maturity and maximum length, and older ages for 50% maturity and maximum age.

There are two pairs of species that are clustered together consistently for all data types (i.e., spatial overlap, temporal synchrony, harvest fractions, and life history characteristics): 1) canary and yellowtail, and 2) silvergray and yellowmouth (Fig. 3). However, these pairs of species are differentially clustered with other rockfish in two or three clusters depending on the data source.

3.4 Discussion

Our results using a set of non-target rockfish species indicate that fine-scale SDMs can be a useful tool to identify species complexes. In particular, JDSDMs (i.e., VAST, in this example) can help determine co-existence and correlation among data-limited species, because shared information, particularly for infrequently caught species, improves the predictive powers of the model (e.g., Ovaskainen and Soininen, 2011; Pacifici et al., 2014; Thorson et al., 2015). The JDSDM applied here helps improve the understanding of fine-scale spatial distributions as well as the detection of spatial overlap across species, especially compared to using broad-scale distributions of species.

Because fine-scale JDSDMs can detect both spatial and temporal correlations among species, they can be used by managers to group species with overlapping distributions to help better understand spatial community structure. By clustering non-target species in multispecies fisheries, the application of a joint, dynamic SDM can aid managers in determining incentives or appropriate regulations to decrease the fishing pressure on areas with high densities of non-target species (e.g., Dolder et al., 2018; Stock et al., 2020). Moreover, major changes in fishing practices or large environmental perturbations can potentially be detected across the community of a species complex or may be detected early if population trajectories of particularly susceptible species rapidly alter (Pollock et al., 2014). For example, the model can help identify population shifts in the center-of-gravity (Thorson and Barnett, 2017), which will become increasingly important as more species continue to move northward (Pinsky et al., 2013). However, large differences in the individual species' biomass in a complex can lead to one species component becoming overfished when large discrepancies in population sizes exist

(PFMC, 2013). Careful consideration and evaluation when developing complexes is warranted, particularly for species, such as rockfish, that are vulnerable to overfishing (Cope et al., 2011; Ormseth and Spencer, 2011).

The results of a joint, dynamic SDM applied to fishery-independent trawl data for GOA rockfish species indicate that spatial factors are a key element linking these species together. The model gave evidence that the density estimates for most species is highest in the southeastern area of the GOA. The non-target rockfish species analyzed in this study cluster by spatial density, with three main spatial patterns: high density concentration in only the southeastern GOA; high density in the eastern GOA, but found throughout the GOA; and ubiquitously distributed throughout the GOA. We did not see strong temporal correlations among species, suggesting that these rockfish demonstrate differential responses to environmental and fishing pressures. We note that no single species demonstrated a severe decrease in abundance during the time series, although harlequin decreased initially then demonstrated constant biomass throughout the rest of the time series. Excluding the first few years of the survey data when there were small changes in the survey design (von Szalay and Raring, 2018) can alter the inference of the time series. If we excluded the first few years of the survey in this study, the estimated biomass for some rockfish species would be increasing, while others would appear to be stabilized. As noted, differential responses to perturbation can help stabilize a complex as a whole, which might be ideal for a group of species known for their longevity and late maturation (Love et al., 2002; Ormseth and Spencer, 2011). Managing species in a complex with differential responses to perturbation aligns with the holistic approach of

ecosystem-based fishery management, such that the complex as a whole can help maintain its role and the biodiversity within the ecosystem (Link, 2002).

There are a few species that consistently clustered together based on the spatial and temporal correlation, harvest fractions, and life history characteristics: 1) canary and yellowtail; and 2) silvergray and yellowmouth. However, all the rockfish did not group into the same distinct clusters for all data sources. In particular, most of the rockfish grouped in similar clusters except in either the harvest fractions or life history clusters. For instance, sharpchin, harlequin, and redstripe grouped together in all, but the harvest fraction clusters, whereas redbanded moved between groupings. As suggested in Cope et al. (2011), a hierarchical, step-wise grouping method can provide a way to assign rockfish to complexes by identifying important attributes (e.g., spatio-temporal overlap) that can be first used to separate the species. Subsequently, the groups can be sub-divided utilizing other factors (e.g., fishing susceptibility or productivity) rather than comparing all variables concurrently.

Omori et al. (2021; Chapter 2) performed a more broad-scale (i.e., based on management area reporting) clustering analysis to identify GOA rockfish groupings, which combined several surveys and fishery catch datasets, and included a different subset of rockfish due to the additional datasets. Despite differences in methodology and included species, a handful of the spatial groupings from the current fine-scale SDM are also identified in the broad-scale analysis. The most interesting results from the current study and those by Omori et al. (2021; Chapter 2) regard the treatment of the Demersal Rockfish Complex managed exclusively in GOA management area 650. In this current study, we only included two species that belong to the Demersal Shelf Rockfish complex,

canary and yelloweye, because the remaining species in the complex are not caught in high enough numbers in the trawl survey to be modeled with a fine-scale SDM. Yet, both studies suggested that the Demersal Shelf Rockfish species should be separated from the Other Rockfish for the entirety of the GOA instead of only in management area 650. Yelloweye grouped with the other non-target rockfish commonly caught in the trawl survey gear. However, yelloweye is assigned with the Demersal Shelf Rockfish because it constitutes the majority of the catch for the Demersal Shelf Rockfish group, despite being caught and distributed Gulf-wide (Tribuzio and Echave, 2019). We suggest that yelloweye continue to be managed with the Demersal Shelf Rockfish complex, but note that the other species in the complex have a smaller habitat range. The JDSDM results suggest both fine-scale spatial and temporal differences for canary and yellowtail compared to the other species in the model. Mainly, canary and yellowtail rockfish are concentrated primarily in the southeastern GOA with a few other patches of higher density, whereas yelloweye was spread evenly throughout the GOA. While yellowtail consistently grouped with canary in the broad-scale clustering as well as the fine-scale model, yellowtail should be carefully examined for placement into a complex because it is not considered a Demersal Shelf Rockfish.

Future spatial and temporal relationships could likely be better detected with improvements to the fine-scale SDM by incorporating other surveys that cover a wider breadth of habitat, including untrawlable areas. The trawl survey catches select species associated with the trawlable areas, which excludes habitat with high complexity. As a result, the trawl survey does not adequately sample many of the Demersal Shelf Rockfish species and other rockfish species that are associated with complex habitat (e.g.,

harlequin; Rooper and Martin 2012). Further, the trawl survey depths can be restricted such that depths greater than 500 m are not surveyed in all years. Including the NMFS fishery-independent longline survey (Siwicke et al., 2021) and the International Pacific Halibut Commission longline survey (Erikson and Ualesi, 2020), for instance, could extend the surveyed habitat to cover areas with increased sloping gradient and rocky habitats. The longline surveys sample a different community of rockfish species, including more Demersal Shelf Rockfish species. More surveyed habitat and different gear selectivity may help confirm the strength of the spatial correlations among non-target rockfish and increase the spatial estimation extent. Additionally, VAST can include habitat covariates in the model to help improve the density estimates as well as determine the amount of variation associated with the covariates. Rockfish are often associated with a mix of habitat types including high relief rocks, reefs, and crevices, to mudflats and vegetative areas (Johnson et al., 2003; Conrath et al., 2019). Theoretically, because most of the variation in our model is associated with the spatial component, adding habitat covariates, such as rocky habitat, substrate type, or depth, would help identify key attributes that influence spatial overlap of rockfish species.

Our results highlight that, when survey data are available, fine-scale SDMs can be applied to validate or construct species complexes. We demonstrate how SDMs can be used to examine both spatial and temporal similarities among species to detect fine-scale species distribution overlap and asynchronous or synchronous changes in abundance. Modeling multiple data-limited or rare species simultaneously can detect fine-scale, species-specific relationships. In comparison, typically applied broad-scale multivariate approaches, which utilize a wider variety of data but often at a broader spatio-temporal

scale, provide a more general overview of potential species complexes. JDSDMs can also help detect individual and community responses to environmental or anthropogenic perturbations, and can be used to predict how the complex may be impacted by future shifts in the ecosystem (Ovaskainen and Soininen, 2011). As species distributions continue to expand, contract, or shift, fine-scale SDMs can aid in detecting changes in correlations among species and major shifts in their distributions. Modeling species in a complex simultaneously when species-specific data are available can help scientists provide improved management advice with limited data. In the development and management of species complexes, we advise simultaneously applying both fine-scale SDMs and broad-scale multivariate modeling techniques (e.g., Omori et al., 2021; Chapter 2), applied across the full extent of available data, to validate and/or create species complexes. Additionally, a hierarchical, step-wise structure can be used to assign species to complexes by identifying regional influential factors to separate species (Cope et al., 2011). By applying the full complement of methods, including the JDSDM approach suggested here, there is greater likelihood to detect a variety of species relationships. Similarly, strong species correlations are likely to persistently appear across multiple methods and data sources, allowing the identification and validation of more robust species complexes.

3.5 References

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3.6 Tables

Table 3.1. List of non-target rockfish species (*Sebastes sp.*) included in the multispecies VAST model, including the associated total number of trawl survey tows with a non-zero catch (i.e., encounters) and the total biomass from the bottom trawl survey catch for all years combined for each species.

Common Name	Scientific name (Sebastes)	Encounters	Total Biomass (kg)
canary	*S. pinniger*	72	3,399
harlequin	*S. variegatus*	886	22,135
redbanded	*S. babcocki*	1,256	6,270
redstripe	*S. proriger*	369	19,913
sharpchin	*S. zacentrus*	881	36,719
silvergray	*S. brevispinis*	815	34,266
yelloweye	*S. ruberrimus*	304	2,034
yellowmouth	*S. reedi*	54	1,331
yellowtail	*S. flavidus*	74	1,651

3.7 Figures
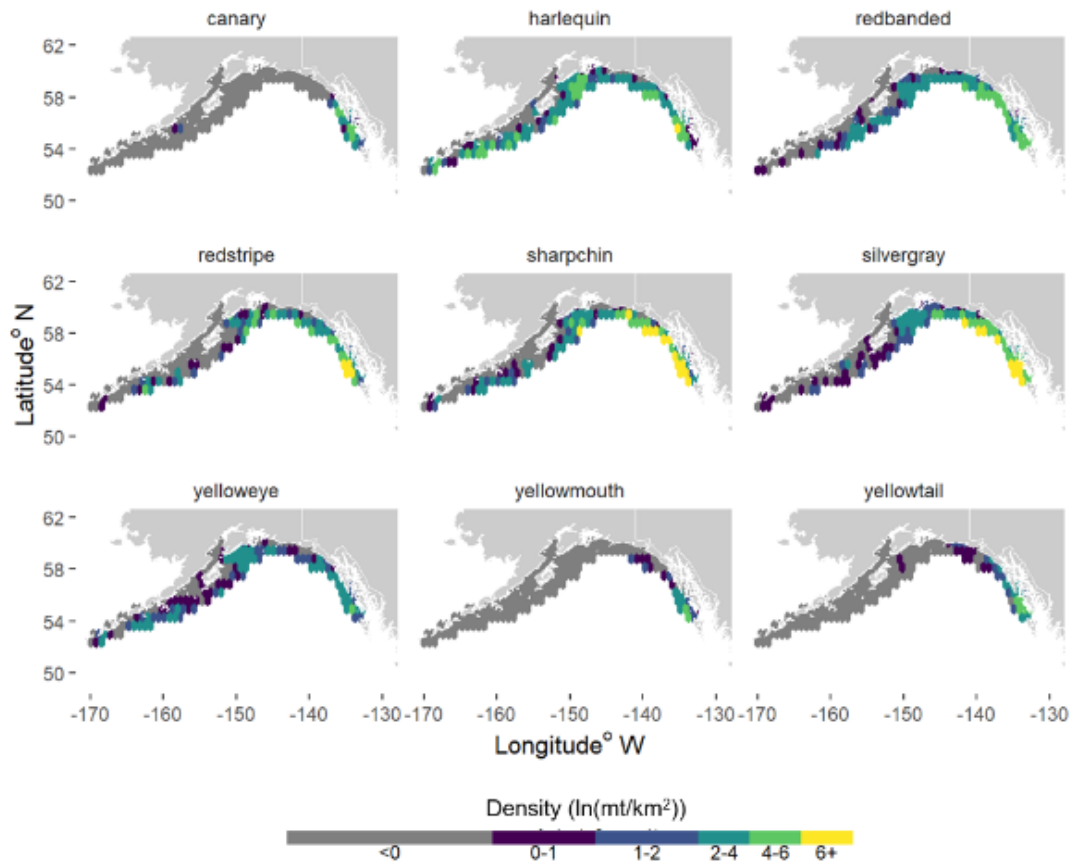
Fig. 3.1 VAST estimated average density (ln(mt/km^2)) of each rockfish species across all GOA trawl survey years.
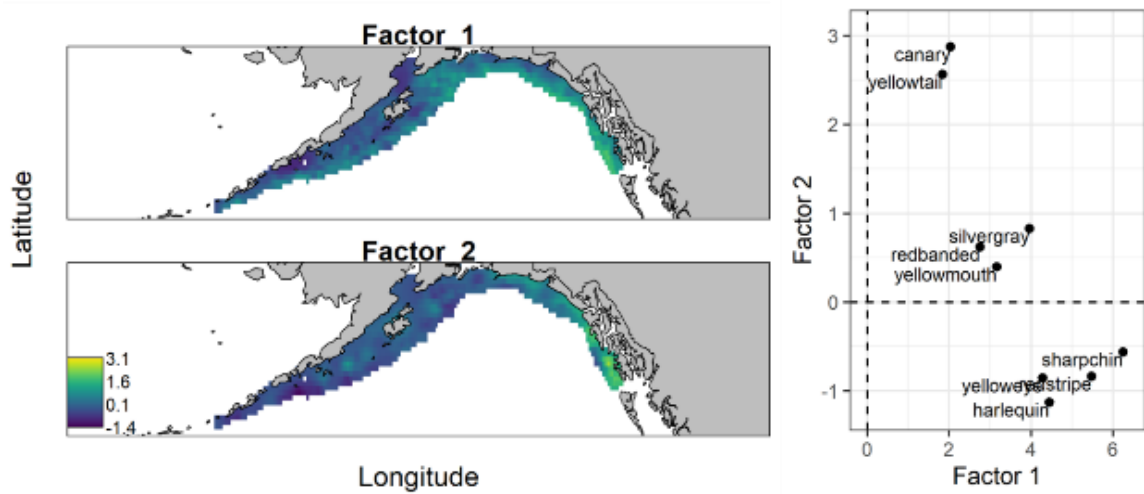
Fig. 3.2. Combined results of the two linear predictors from the spatial component $(\omega(c, s))$ of the model. The left two panels represent maps of the first two factors after the PCA rotation. The right panel provides the first two factor loadings after a PCA rotation on the combined spatial covariance matrix for all species.
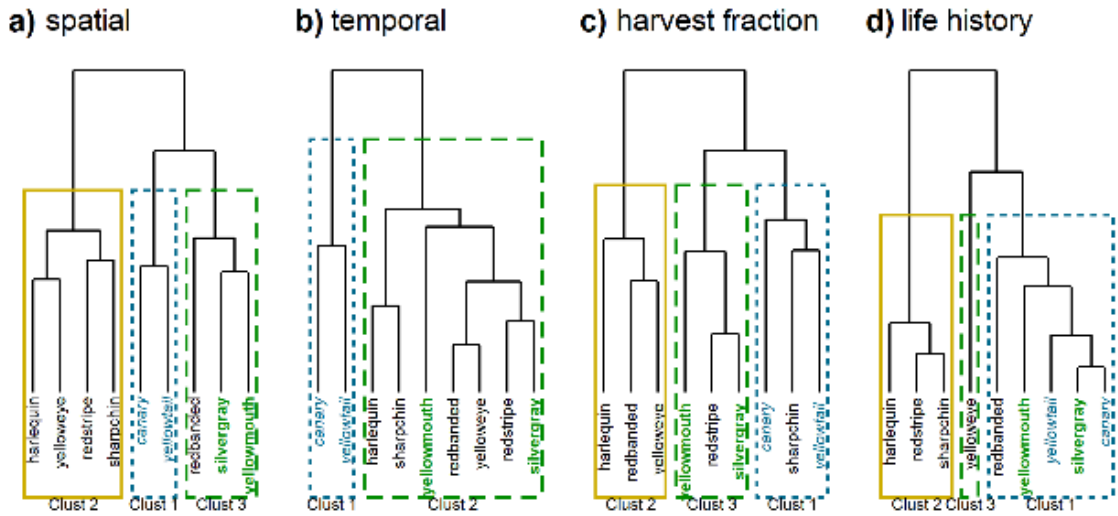
Fig. 3.3. Ward's hierarchical clustering dendrograms from the spatial component (a), temporal component (b), harvest fraction (c), and life history (d). Box colors and line type indicate different cluster groupings with labeled cluster below, where each data type is independent from one another. Italicized species in blue and bold species in green indicate two sets of rockfish that consistently group together.
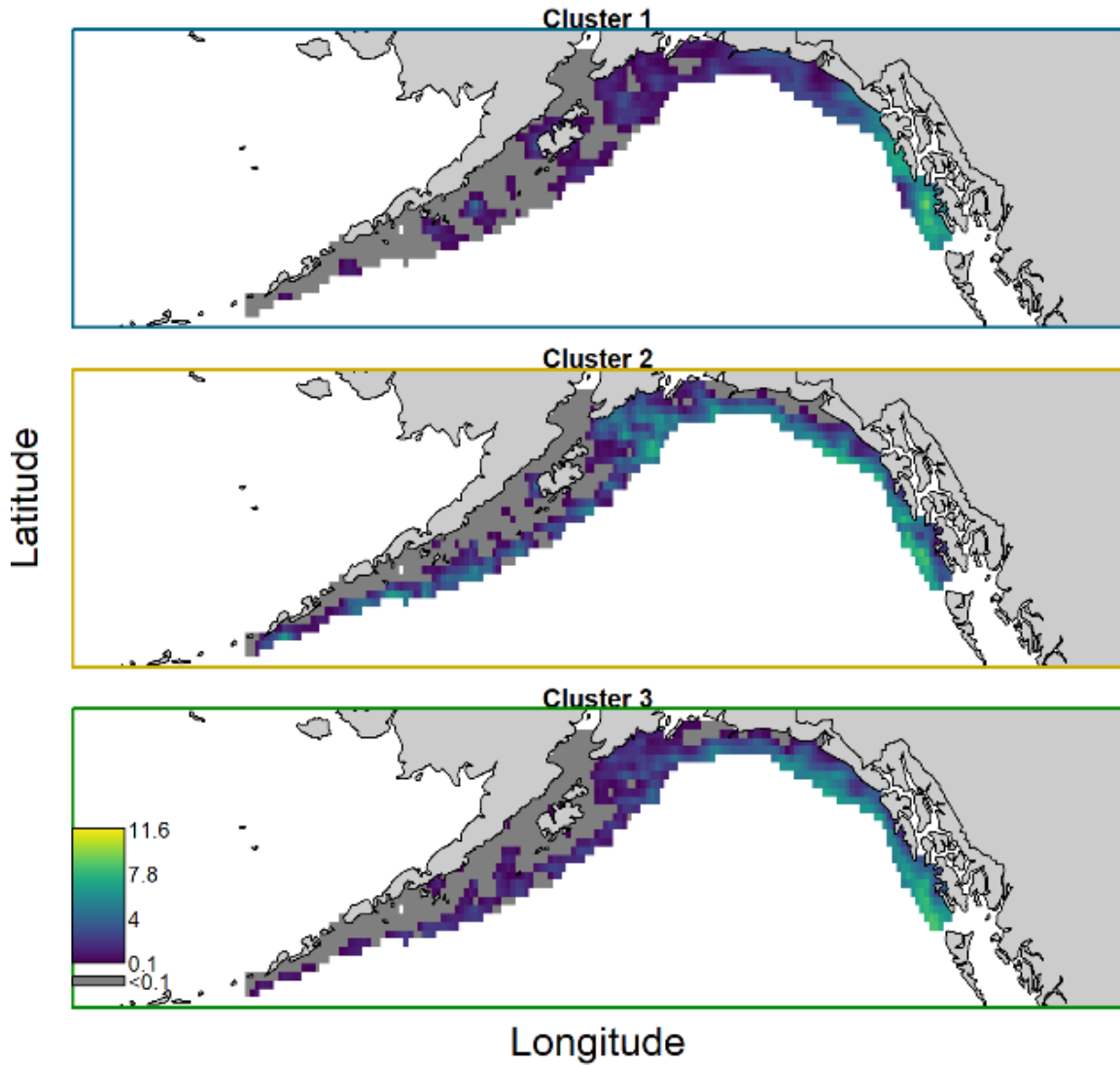
Fig. 3.4. Average distribution of the spatial component clusters identified by the Ward's clustering results (Fig 3.3a, $\hat{\omega}_{total}(g,s)$). Values that are less than 1% of the maximum value are represented by dark gray and box colors correspond with spatial clusters from Fig. 3.3a.
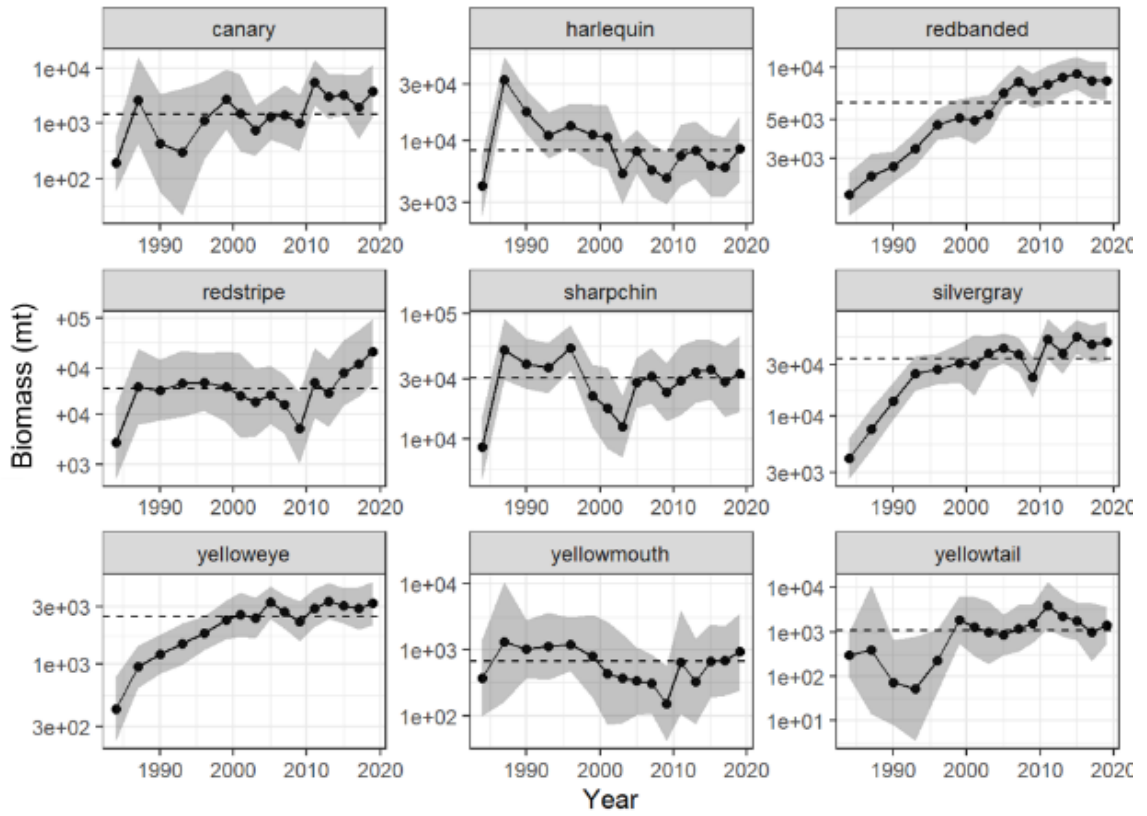
Fig. 3.5. VAST estimated indices of abundance (black line and points) with 95% confidence interval (gray shading) and median estimate (dashed horizontal line for non-target rockfish species.
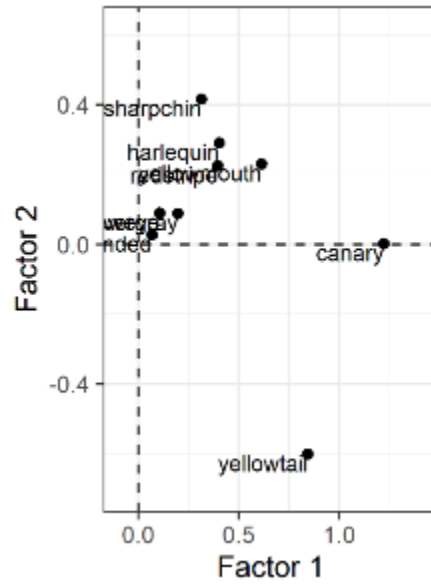
Fig. 3.6. The first two factor loadings of the temporal variation component, $\beta(c, t)$, after a PCA rotation on the combined covariance from the first and second linear predictors, where the temporal variation follows a random walk.
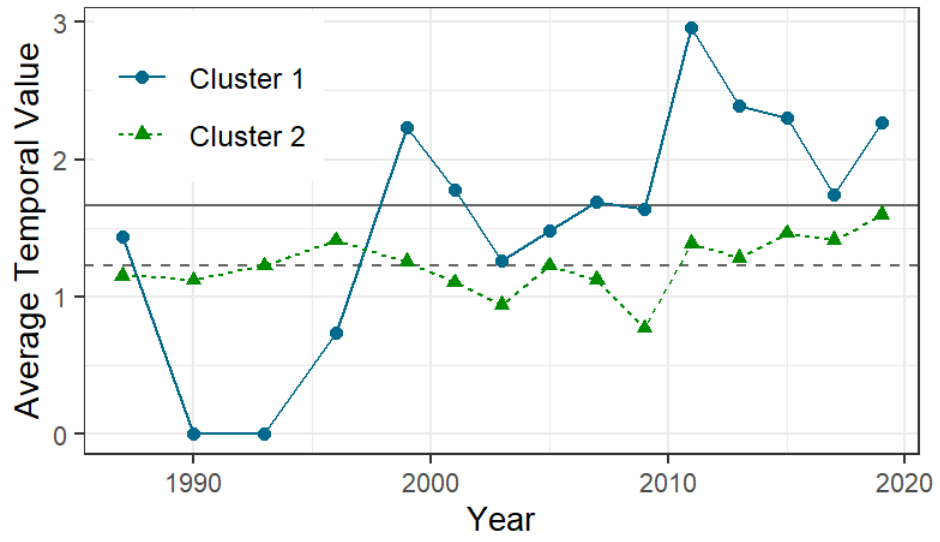
Fig. 3.7. Average temporal values ($\hat{\beta}_{total}(g, t)$) for each cluster based on the Ward's clustering results.

3.8 Supplementary Material

Supplementary Tables

Table SM1. List of symbols used in the joint, dynamic species distribution model following notation from Thorson (2019).

Symbol	Description	Dimensions (n = number)	Type
i	Observation	−	Index
c	Category (i.e., species)	−	Index
s	Spatial location	−	Index
t	Time interval (i.e., year)	−	Index
f	Factor	−	Index
g	Cluster	−	Index
n_i	Number of observations	$n_i = 11601$	−
n_s	Number of locations	$n_s = 500$	−
n_c	Number of species	$n_c = 9$	−
n_t	Number of years	$n_t = 16$	−
$n_{\beta 1}$	Number of temporal factors in linear predictor 1	$n_{\beta 1} = 9$	−
$n_{\beta 2}$	Number of temporal factors in linear predictor 2	$n_{\beta 2} = 9$	−
$n_{\omega 1}$	Number of spatial factors in linear predictor 1	$n_{\omega 1} = 9$	−
$n_{\omega 2}$	Number of spatial factors in linear predictor 2	$n_{\omega 2} = 9$	−
b_i	Biomass (i.e., survey catch) data	n_i	Data
a_i	Area-swept for each observation	n_i	Data
$a(s)$	Area associated with each location	n_s	Data
σ_c^2	Variance for positive catch for each species	n_i	Fixed effect
$\mu_{\beta 1}(c_i)$	Intercept for 1st linear predictor	n_i	Fixed effect
$\mu_{\beta 2}(c_i)$	Intercept for 2nd linear predictor	n_i	Fixed effect
$L_{\beta 1}(c_i, f)$	Loadings matrix for temporal covariation for 1st linear predictor	$n_c \times n_{\beta 1}$	Fixed effect
$L_{\beta 2}(c_i, f)$	Loadings matrix for temporal covariation for 2nd linear predictor	$n_c \times n_{\beta 2}$	Fixed effect
$L_{\omega 1}(c_i, f)$	Loadings matrix for spatial covariation for 1st linear predictor	$n_c \times n_{\omega 1}$	Fixed effect
$L_{\omega 2}(c_i, f)$	Loadings matrix for spatial covariation for 2nd linear predictor	$n_c \times n_{\omega 2}$	Fixed effect
$\beta_1(t_i, f)$	Temporal factors for 1st linear predictor	$n_t \times n_{\beta 1}$	Random effect
$\beta_2(t_i, f)$	Temporal factors for 2nd linear predictor	$n_t \times n_{\beta 2}$	Random effect
$\omega_1(s_i, f)$	Spatial factors for 1st linear predictor	$n_s \times n_{\omega 1}$	Random effect
$\omega_2(s_i, f)$	Spatial factors for 2st linear predictor	$n_s \times n_{\omega 2}$	Random effect
$p_1(s_i, c_i, t_i)$	1st linear predictor	n_i	Internally derived

$p_2(s_i, c_i, t_i)$	2st linear predictor	n_i	Internally derived
$r_1(s_i, c_i, t_i)$	1st link-transformed predictor that follows Poisson process	n_i	Internally derived
$r_2(s_i, c_i, t_i)$	2nd link-transformed predictor	n_i	Internally derived
$\mathbf{R_1}$	Spatial correlation matrix for 1st linear predictor	$n_s \times n_s$	Internally derived
$\mathbf{R_2}$	Spatial correlation matrix for 2nd linear predictor	$n_s \times n_s$	Internally derived
$\mathbf{V_{total}}$	Joint covariance matrix calculated for temporal and spatial component separately	$n_c \times n_c$	Externally derived
$v_{total}(c_1, c_2)$	Total variance between species c_1 and c_2	1	Externally derived
$\mathbf{L_1}$	Loadings matrix from either temporal or spatial covariation from 1st linear predictor	$n_c \times n_c$	Externally derived
$\mathbf{L_2}$	Loadings matrix from either temporal or spatial covariation from 2nd linear predictor	$n_c \times n_c$	Externally derived
$I(c, t)$	Index of abundance	$n_c \times n_t$	Externally derived
$d(s, c, t)$	Predicted density	$n_s \times n_c \times n_t$	Externally derived
$\gamma(c_1, c_2)$	Distance between a set of species c_1 and c_2 based on covariance matrix	1	Externally derived
$\omega_1(c, s)$	Spatial component estimates from 1st linear predictor	$n_c \times n_s$	Externally derived
$\omega_2(c, s)$	Spatial component estimates from 2nd linear predictor	$n_c \times n_s$	Externally derived
$\omega_{total}(c, s)$	Total spatial component estimate	$n_c \times n_s$	Externally derived
$\omega_{total}(g, s)$	Total average spatial value for each cluster	$n_g \times n_s$	Externally derived
$\beta_1(c, t)$	Temporal component estimates from 1st linear predictor	$n_c \times n_t$	Externally derived
$\beta_2(c, t)$	Temporal component estimates from 2nd linear predictor	$n_c \times n_t$	Externally derived
$\beta_{total}(c, t)$	Total temporal component estimate	$n_c \times n_t$	Externally derived
$\Delta\beta_{total}(c, t)$	Difference between total temporal estimates from t-1 and t	$n_c \times (n_t - 1)$	Externally derived
$\Delta\beta_{total}(g, t)$	Total average difference between temporal estimates from t-1 and t for each cluster	$n_g \times (n_t - 1)$	Externally derived

Table SM2. Life history characteristics for rockfish borrowed from a literature review in Omori et al. (in review).

	Max age	Age at maturity	Length at maturity	Max length
canary	71	9	480	580
harlequin	34	9	230	323
redbanded	106	4	420	698
redstripe	55	8	290	420
sharpchin	58	10	270	350
silvergray	75	10	460	623
yelloweye	117	22	475	644
yellowmouth	99	11	380	469
yellowtail	64	9	410	530

Table SM3. Scaled harvest fractions for each rockfish species used for Ward's hierarchical cluster analysis.

	1996	1999	2001	2003	2005	2007	2009	2011	2013	2015	2017	2019
canary	1	0.936	0.488	0.584	0.109	0.084	0.16	0.104	0.614	0.142	0.162	0.232
harlequin	0.013	0.089	0.126	0.721	0.788	0.598	0.911	0.61	0.53	1	0.807	0.624
redbanded	0.574	0.371	0.477	0.484	0.372	0.444	0.434	0.726	0.996	0.722	1	0.857
redstripe	0.031	0.034	0.017	0.211	0.056	0.212	0.228	0.506	0.188	0.374	0.571	1
sharpchin	0.203	0.078	0.077	0.183	0.036	0.058	0.051	0.094	0.038	0.088	0.102	0.056
silvergray	0.127	0.156	0.078	0.23	0.047	0.215	0.296	0.932	0.267	0.642	0.732	1
yelloweye	0.95	0.729	0.816	1	0.573	0.684	0.764	0.741	0.929	0.612	0.688	0.589
yellowmouth	0.001	0.001	0.001	0.278	0	0.037	0.009	0	0	0	0	1
yellowtail	0.112	0.177	1	0.146	0.035	0.041	0.039	0.041	0.048	0.076	0.04	0.031

Table SM4. Total and first three eigenvalues associated with each linear predictor and total spatial (ω) and temporal (β) model components.

	Total	1	2	3
ω	204.24	147.96	19.06	14.77
β	4.58	3.06	0.74	0.53
ω_1	165.72	-	-	-
ω_2	38.5172	-	-	-
β_1	0.87	-	-	-
β_2	3.72	-	-	-

Table SM5. Combined rotated factor loading values for the spatial components.

	1	2	3	4	5	6	7	8	9
canary	2.034	2.873	-0.829	0.191	-1.295	0.068	0.567	-0.002	-0.252
harlequin	4.453	-1.131	-1.443	1.069	-0.240	0.453	0.064	0.820	0.196
redbanded	2.755	0.620	2.147	1.465	1.013	0.580	0.306	-0.094	-0.164
redstripe	5.475	-0.835	0.120	-1.122	0.789	-0.761	0.782	0.211	-0.144
sharpchin	6.247	-0.564	-0.021	1.001	-0.642	-0.854	-0.328	-0.643	0.142
silvergray	3.958	0.826	0.375	-0.495	0.152	-0.096	-1.008	0.420	-0.417
yelloweye	4.280	-0.855	-1.143	-0.854	0.143	1.187	-0.030	-0.624	-0.108
yellowmouth	3.166	0.394	2.206	-1.040	-0.990	0.382	-0.017	0.187	0.417
yellowtail	1.843	2.562	-1.034	-0.208	1.368	-0.085	-0.181	-0.058	0.427

Table SM6. Combined rotated factor loading values for the temporal components.

	1	2	3	4	5	6	7	8	9
canary	1.221	0.001	-0.119	-0.021	0.020	-0.022	-0.032	0.000	0.000
harlequin	0.404	0.290	-0.367	0.027	-0.162	0.038	0.010	0.000	0.000
redbanded	0.069	0.027	0.004	0.091	0.130	-0.021	0.037	0.000	0.000
redstripe	0.398	0.223	0.205	0.088	-0.097	-0.079	0.006	0.000	0.000
sharpchin	0.315	0.416	-0.219	-0.060	0.192	0.001	0.002	0.000	0.000
silvergray	0.199	0.088	0.287	0.223	0.054	0.045	-0.032	0.000	0.000
yelloweye	0.107	0.089	-0.094	0.222	-0.014	0.012	0.028	0.000	0.000
yellowmouth	0.614	0.230	0.450	-0.147	-0.025	0.038	0.027	0.000	0.000
yellowtail	0.843	-0.603	-0.051	0.017	0.020	0.012	0.020	0.000	0.000

Table SM7. Fixed effect estimates from species distribution model (i.e., VAST model).

Estimates		canary	harlequin	redbanded	redstripe	sharpchin	silvergray	yelloweye	yellowmouth	yellowtail
σ_c^2		1.19	1.47	1.07	1.41	1.51	1.19	0.78	1.37	1.21
$\mu_{\beta 1}(c_i)$		-6.05	-2.43	-2.11	-4.38	-4.48	-2.83	-4.30	-5.40	-4.83
$\mu_{\beta 2}(c_i)$		0.38	1.08	0.41	0.72	1.07	0.47	1.24	0.19	0.27
$L_{\beta 1}(c_i, f)$	$f = 1$	-0.341	0.197	-0.084	-0.040	0.124	-0.080	0.028	-0.164	-0.606
	$f = 2$	0.000	-0.190	-0.119	-0.098	-0.201	-0.146	-0.241	0.130	0.206
	$f = 3$	0.000	0.000	0.028	-0.174	0.098	-0.029	-0.012	-0.052	0.066
	$f = 4$	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	$f = 5$	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	$f = 6$	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	$f = 7$	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	$f = 8$	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	$f = 9$	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
$L_{\beta 2}(c_i, f)$	$f = 1$	-1.179	-0.508	-0.047	-0.378	-0.389	-0.151	-0.124	-0.544	-0.702
	$f = 2$	0.000	-0.278	0.054	0.135	-0.127	0.321	0.006	0.244	0.057
	$f = 3$	0.000	0.000	0.072	-0.048	0.327	-0.073	-0.050	-0.021	-0.238
	$f = 4$	0.000	0.000	0.000	-0.262	-0.144	-0.159	0.042	-0.505	0.335
	$f = 5$	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	$f = 6$	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	$f = 7$	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	$f = 8$	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	$f = 9$	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
$L_{\omega 1}(c_i, f)$	$f = 1$	-3.282	-1.797	-1.468	-2.637	-2.627	-2.082	-2.020	-1.621	-2.714
	$f = 2$	0.000	3.758	1.956	4.259	4.943	2.865	4.109	2.237	0.403
	$f = 3$	0.000	0.000	2.973	0.239	1.076	0.646	-0.963	1.357	-0.015
	$f = 4$	0.000	0.000	0.000	-1.093	-0.283	-0.712	-0.240	-1.028	-0.249
	$f = 5$	0.000	0.000	0.000	0.000	0.619	0.279	0.117	0.308	1.109
	$f = 6$	0.000	0.000	0.000	0.000	0.000	-1.082	0.203	0.201	-0.971
	$f = 7$	0.000	0.000	0.000	0.000	0.000	0.000	0.579	0.415	-0.686
	$f = 8$	0.000	0.000	0.000	0.000	0.000	0.000	0.000	1.922	-1.288
	$f = 9$	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000

$L_{\omega2}(c_i, f)$									
$f = 1$	2.099	0.781	0.004	-0.394	1.536	1.198	0.148	0.674	0.491
$f = 2$	0.000	2.711	-0.010	1.173	1.589	0.110	0.570	-0.680	-0.198
$f = 3$	0.000	0.000	1.184	0.743	0.301	0.615	0.271	0.428	0.531
$f = 4$	0.000	0.000	0.000	2.323	1.399	1.030	0.159	1.215	-0.052
$f = 5$	0.000	0.000	0.000	0.000	-1.462	0.411	0.327	0.220	0.790
$f = 6$	0.000	0.000	0.000	0.000	0.000	-0.600	0.160	-0.551	0.292
$f = 7$	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
$f = 8$	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
$f = 9$	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
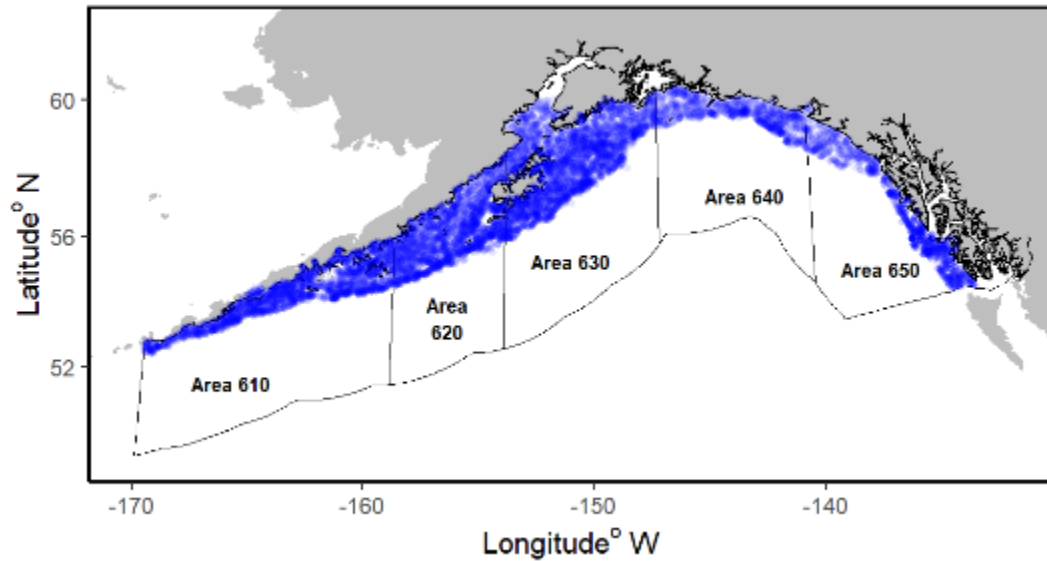
Fig. SM1. Map of the Gulf of Alaska (GOA) with points indicating each haul of the fisheries-independent trawl survey from 1984- 2019 and NMFS management areas outlined in black. The GOA Other Rockfish complex of species covers species in each of these bounded areas, however, the seven species associated with the Demersal Shelf Rockfish complex are managed separately only in Area 650.
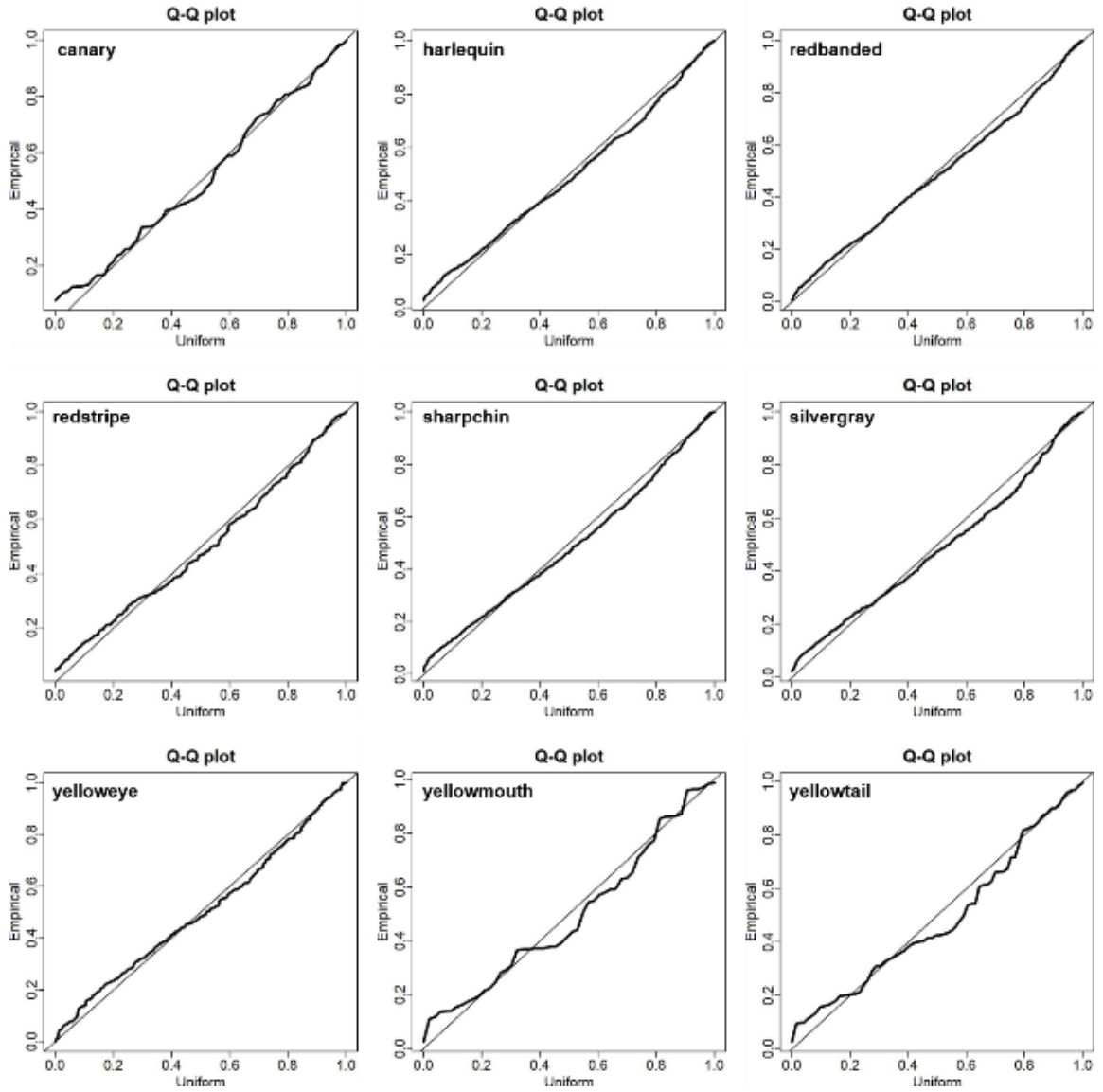
Fig. SM2. Q-Q plots comparing the empirical vs. simulated distributions for each species.
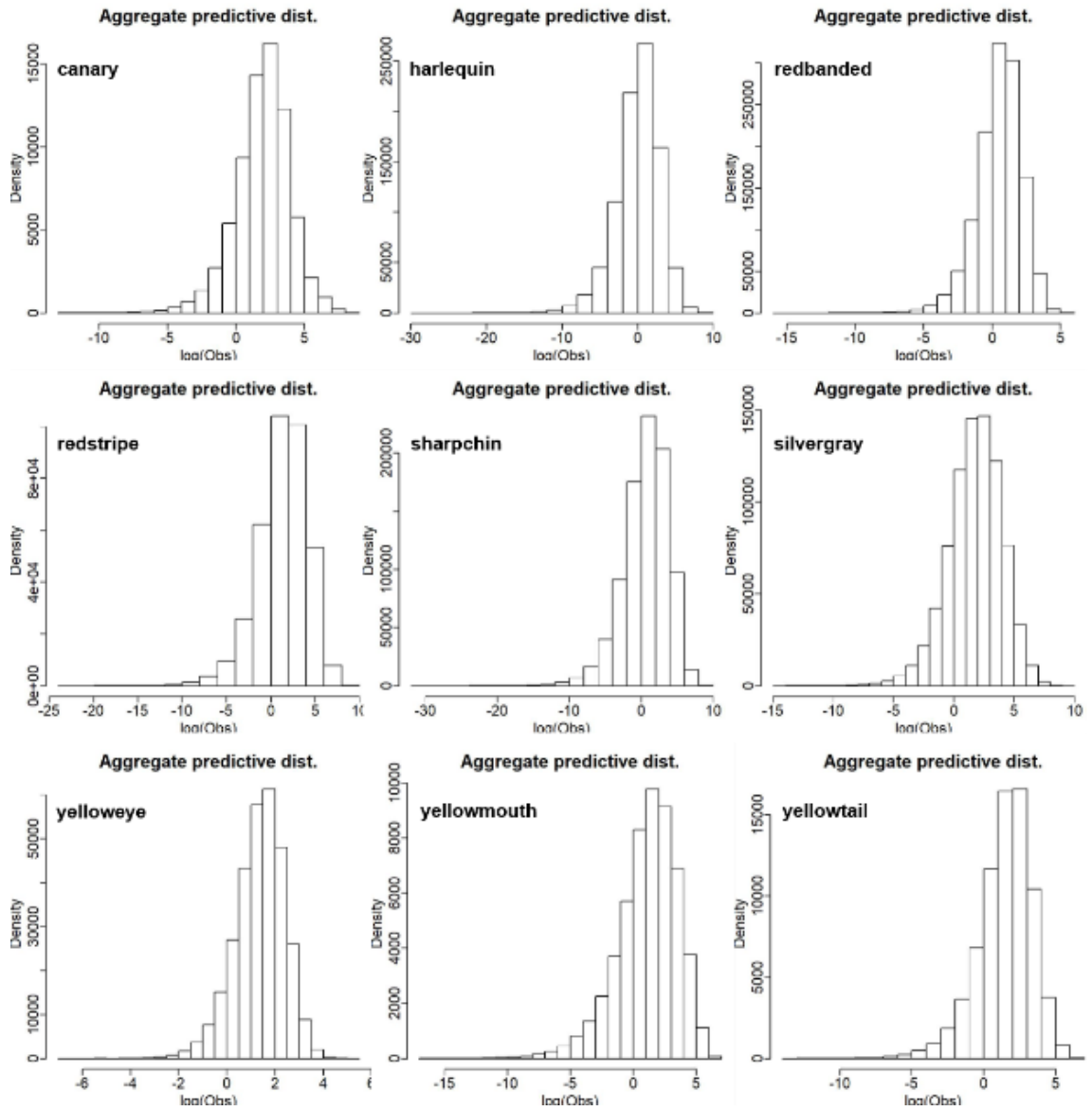
Fig. SM3. Predictive density distributions for each species.
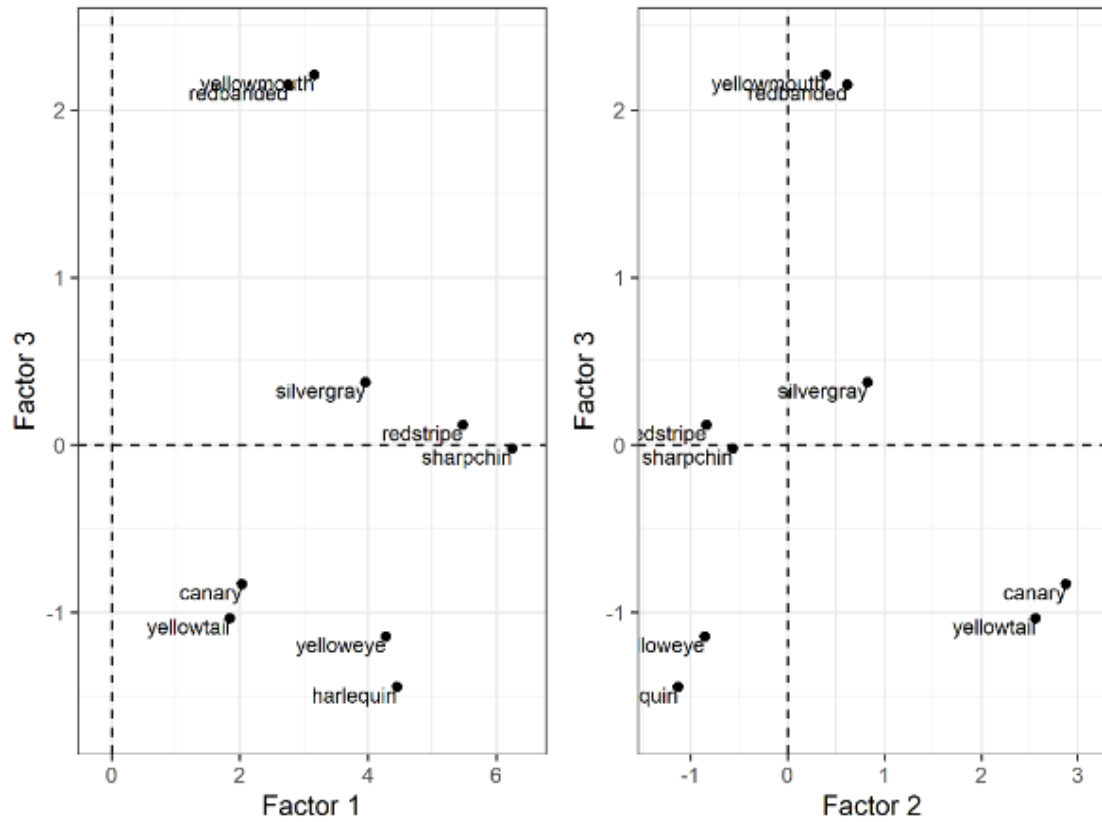
Fig. SM4. Factor loadings with 1st and 3rd (left panel) and 2nd and 3rd (right panel) factors after PCA rotation on the combined spatial covariance matrix.

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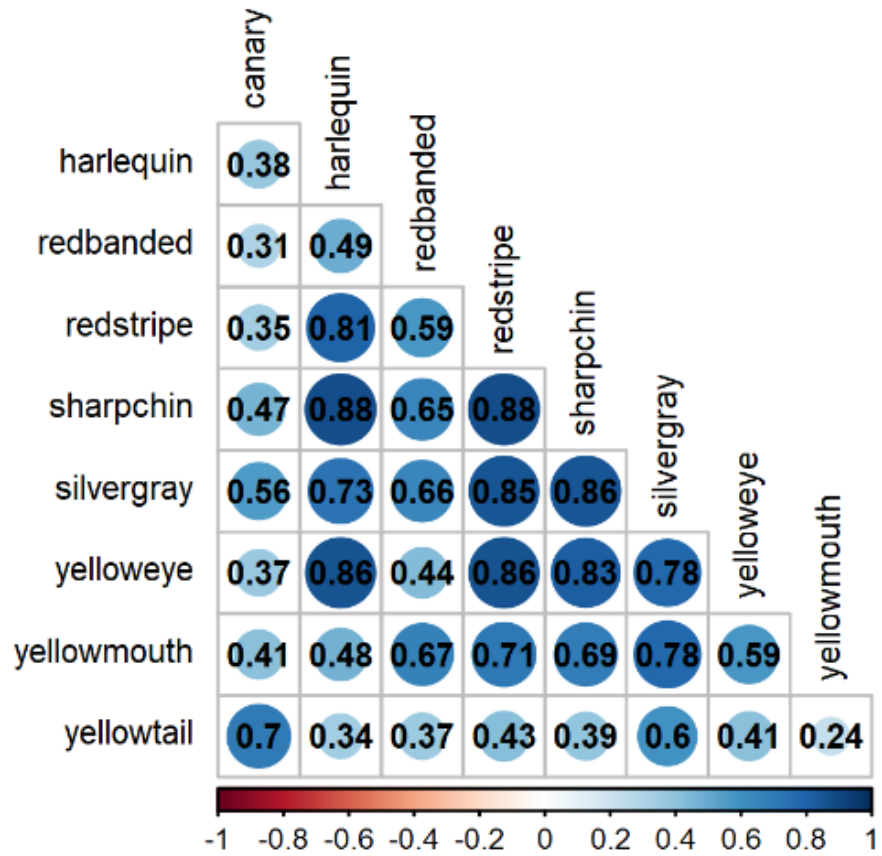
Fig. SM5. Correlation estimates among the nine GOA rockfish from the spatial component of the VAST model. Size of circle and printed value indicate correlation estimate for each pair of species.
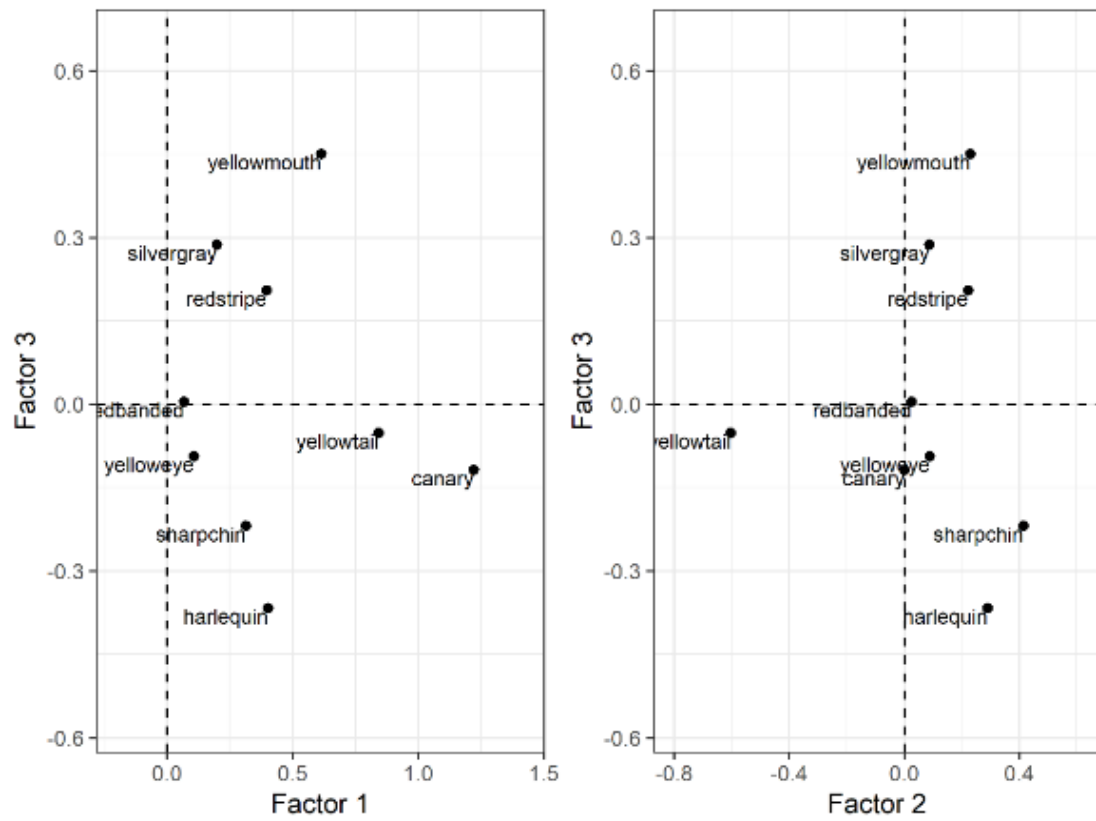
Fig. SM6. Factor loadings with 1st and 3rd (left panel) and 2nd and 3rd (right panel) factors after PCA rotation on the combined temporal covariance matrix.
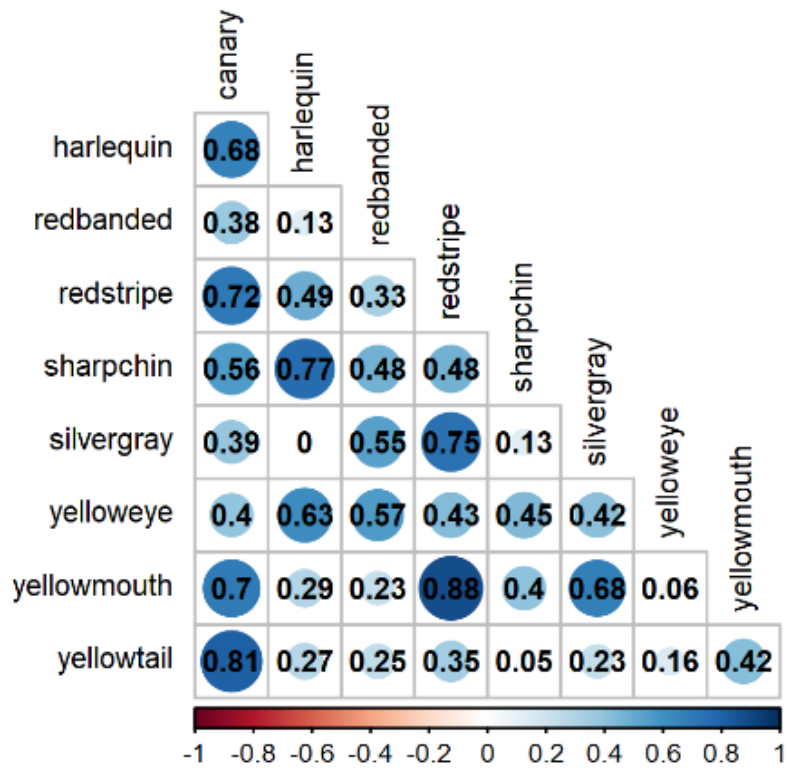
Fig. SM7. Correlation estimates among the nine GOA rockfish from the temporal component of the VAST model. Size of circle and printed value indicate correlation estimate for each pair of species.

Fig. SM8. Standardized indices of abundance from the trawl survey (Index_raw) compared to the JDSDM model biomass estimates (Index_VAST).

CHAPTER 4

A comparison of two stock assessment methods for a non-target rockfish complex in the Gulf of Alaska

Abstract

There are over twenty non-target rockfish species in the Gulf of Alaska that are assessed and managed as a single unit within the "Other Rockfish" complex. Currently, a random effects model is used to estimate the biomass for the complex based on a smoothing algorithm applied to the design-based estimator of survey biomass. However, we develop and apply a spatio-temporal species distribution (i.e., the Vector Autoregressive Spatio-Temporal, VAST) model as an alternative assessment method, which may better account for unknown factors affecting species' abundance and spatial autocorrelation in the estimation of species biomass. We compare the results of the random effects model with the spatio-temporal model for assessing the data-limited Other Rockfish species. We use Mohn's ρ and the coefficient of variation to examine the retrospective pattern (i.e., consistency in model outputs as new years of data are incorporated) and biomass uncertainty, respectively, for each of four main assessment model types: 1) the random effects model implemented on individual species, 2) the spatio-temporal model implemented on individual species, 3) the random effects model implemented on species aggregated by natural mortality (M) groupings, and 4) the spatio-temporal model implemented on species aggregated by M groupings. Results demonstrate that the spatio-temporal model returns biomass estimates with less uncertainty, but has similar stability compared to the random effects model for both the individual and M group models. Additionally, the spatio-temporal model applied to M groups gives the highest biomass estimates, which lead to increased acceptable biological catch (ABC) estimates and could have important implications for management of the directed fisheries that catch these rockfish species as bycatch. Although we recommend that the spatio-

temporal model be considered for management, careful examination is warranted when

selecting the model framework used for assessing data limited, non-target species given

the implications for resultant harvest control rules and catch quotas.

4.1 Introduction

The majority of non-targeted rockfishes (*Sebastes spp.*) in the Gulf of Alaska (GOA) are grouped together as a single unit: the GOA "Other Rockfish" stock complex. Although the complex consists of up to 27 species depending on the management area, only 6 species constitute > 95% of the total estimated catch (Tribuzio and Echave, 2019). Other Rockfish species are grouped in a complex due to their low catch and economic value, and because there is insufficient data for conventional age-structured assessment models. The species belonging to the complex are incidentally caught in lucrative groundfish fisheries, primarily by trawling and longline gear. The complex has a high average annual discard rate of 56% that has decreased to 22- 43% in recent years (Tribuzio and Echave, 2019). The Other Rockfish species vary in their distribution, habitat selection, behavior, and life history characteristics. With the exception of harlequin (*S. variegatus*), these rockfish are at the northern extent of their distribution in the GOA, which spans from southern California to Alaska (Love et al., 2002). Rockfish are typically found near the seabed in a variety of benthic substrates, including high relief rocks, reefs, and boulders, to low relief rocky substrate and mudflats (Johnson et al., 2003; Conrath et al., 2019). Adults can inhabit depths up to 800 m, but are typically found from 100 to 275 m (Love et al., 2002). Rockfish species tend to have late-maturity, are long-lived, and have the ability to bear live young (Love et al. 2002), but species-specific life history values are often not measured for the GOA rockfish. The low productivity characteristics tend to place rockfish into a high vulnerability category compared to other groundfish species in the GOA (Ormseth and Spencer, 2011), requiring careful management.

The species belonging to the Other Rockfish complex are assigned to three data-level tiers: Tier 4 (survey data and age-at-maturity estimates for catch limits), Tier 5 (survey data and fishing mortality proxies for catch limits), and Tier 6 (fisheries catch data and maximum catch for catch limits). Sharpchin (*S. zacentrus*) is categorized as Tier 4, because it is the only species with sufficient maturity and growth data, which are used to set harvest recommendations. The majority of the rockfish (16 total) are assigned to Tier 5 with another species, yelloweye (*S. ruberrimus*), being discussed as a potential additional Tier 5 species (it is currently assigned to Tier 6; assignments listed in Tribuzio and Echave, 2019). Tier 4 and 5 species are assessed throughout the entire GOA area using a fishery-independent trawl survey. Within Tier 5, species are further divided into five (or six with yelloweye) natural mortality (*M*) groups (Table 1). The *M* group assignments are based on a variety of life history invariant methods including Hoenig (1983) and Alverson and Carney (1975). The *M* values range from 0.02 (yelloweye; O'Connell and Brylinsky, 2003) to 0.10 (redstripe, *S. proriger*; Archibald et al., 1981). The biomass for each *M* group for Tiers 4 and 5 are estimated and smoothed using a random effects model, which accounts for both process and observation error (further details in Methods and Appendix A; Hulson et al., 2021). Similar to other complexes in the GOA and Bering Sea- Aleutian Islands, allowable biological catches (ABCs) are then calculated for each Tier then summed for a single ABC for the Other Rockfish complex based on the North Pacific Fishery Management Council's harvest control rule (e.g., fishing mortality that corresponds to 40% of the unfished spawning stock biomass [$F_{40\%}$] for Tier 4 and 0.75**M for Tier 5; DiCosimo et al., 2010).

A spatio-temporal model using a Vector Autoregressive Spatio-Temporal model (VAST; Thorson, 2019) has been suggested as an alternative assessment model for the GOA Other Rockfish complex. The VAST model has become a popular tool for developing abundance indices and estimating spatial dynamics of marine species (e.g., Thorson et al., 2015), and has been adapted to help identify species complexes in the GOA (Omori et al., *in review*; Chapter 3). Spatio-temporal models have been able to produce more precise indices of abundance than other model approaches (e.g., Thorson et al., 2015; Johnson et al., 2019) and estimate sub-area abundance for use in spatial management. The models can account for known and unknown factors that affect the abundance or catchability of species. The VAST framework accounts for observed and latent factors by having the possibility of including spatial autocorrelation and spatio-temporal random effects, and the option of adding known covariates. Spatio-temporal density estimates at each location and time step can then be scaled to produce annual biomass or count estimates that can be integrated into stock assessments (Thorson et al., 2015; Cao et al., 2017).

In this study, we compare the current random effects assessment model and the newly proposed spatio-temporal (VAST) model for the Tier 4 and 5 GOA Other Rockfish species. Specifically, we examine the retrospective patterns and biomass uncertainty using Mohn's ρ, mean-absolute-relative-difference, and the coefficient of variation to compare the performance of the models for single species and M groups. Recommendations from the model comparison can be used directly for management advice for Tier 4 and 5 GOA Other Rockfish species and methods can be adapted to other data-limited stock complexes.

4.2 Methods

The National Marine Fisheries Service (NMFS) bottom trawl survey in the GOA, further referred to as the trawl survey, is used as the primary data input for both modeling frameworks. The trawl survey is used as the main biomass data source in the current assessment, covers the largest spatial extent of any survey in the GOA, and samples species-specific biomass data for the GOA Other Rockfish species (Tribuzio and Echave, 2019). The trawl survey uses a stratified-random design, sampling from May to August (von Szalay and Raring, 2018). There are on average 725 tows per year covering an average of 0.031 km^2 swept per tow. The trawl survey operated on a triennial basis from 1984 to 1996, then on a biennial cycle from 1999 to present. There are 16 surveyed years from 1984 to 2019 used in this model comparison study.

A random effects time-series model was developed to ensure consistency in methods among data-limited assessments for biomass estimates and apportionment for species managed by the North Pacific Fisheries Management Council (NPFMC), which includes the GOA and Bering Sea/Aleutian Islands regions (SAWG, 2012). The random effects model implemented in this research is the same model currently used in the assessment for the Other Rockfish complex. The model accounts for variability in biomass over time through a process error term, which follows a random walk. The random walk allows the model to estimate relative biomass for missing survey years. The precision of fit between the model estimates and observed trawl survey data is modeled by the observation error, which uses a log-normal distribution. Relative biomass is estimated for each species or species *M* group for the GOA area. The model is implemented in AD-Model Builder (Fournier et al., 2012) and the R programming

language (R Core Team, 2021). For further model details see Appendix A and Hulson et al. (2021).

The framework of the proposed VAST model is designed as a delta-model with components for encounter (i.e., presence) and positive catch given presence probabilities to accommodate the numerous zero catch observations. A Poisson-link delta-model is implemented with the positive catch modeled using a Gamma distribution. The specifications of the VAST model align with other VAST models being explored for GOA species (e.g., Pacific ocean perch [*S. alutus*] Hulson et al., 2020) and VAST model configurations are available in Table SM1. Both temporal and spatial components initially are included in the VAST models, but may be excluded depending on the species or M group models due to insufficient data to estimate each component (Table SM2). The spatial variation in the spatial component is modeled as an auto-correlated stochastic process using a Gaussian Markov Random Field. The spatial correlation matrix is modeled using a Matérn correlation function. Three versions of VAST are implemented with different temporal processes (Appendix B): 1) VAST using a random walk (VAST-RW), 2) VAST with an autoregressive (AR(1)) process, where the AR coefficient, φ, is freely estimated (VAST-free), and 3) VAST with an AR process, where φ is fixed at a value calculated from the fishing mortality corresponding to the spawner-per-recruit (SPR) proxy value (VAST-fixed). Thorson et al. (2019) demonstrate that the $F_{40\%}$ estimated from SPR levels (F_{SPR}) can be converted to the φ parameter in the AR process by:

$$\varphi = 1 + \frac{F_{SPR}}{1*\log(0.4)} \ , \tag{1}$$

where F_{SPR} is approximated for the GOA Other Rockfish species by the linear relationship between M (natural mortality) and F_{SPR} from similar GOA rockfish species where SPR estimates are available (Table SM2). M values are assigned for GOA Other Rockfish species based on Tier 5 M groupings (Tribuzio and Echave 2019). The final models include fits with a maximum absolute gradient of $< 1e^{-6}$ and a positive definite Hessian matrix as the convergence criteria. Q-Q normal plots are used as a model diagnostic to determine model fit. VAST computations are performed using the VAST model (available at: www.github.com/james-thorson-NOAA/VAST) in Microsoft R Open 3.5.3 (https://mran.microsoft.com/). Further details of the VAST model structure, description, and implementation are described in Thorson (2019).

The random effects model and VAST models (VAST-RW, VAST-free, and VAST-fixed) are applied to eighteen individual species as well as seven M groups (Table 1). Model performance is examined by three metrics: Mohn's ρ, mean-absolute-relative-difference ($\overline{ARD}$), and the coefficient of variation (CV). Mohn's ρ is used to investigate retrospective bias in the models (i.e., systematic inconsistency occurring in the biomass estimates when subsequent years of data are added; Mohn, 1999). Mohn's ρ is calculated using the relative differences between biomass estimated in the base model ($\hat{B}_{Y-y,base}$; model with all years of data) and the terminal year biomass estimated ($\hat{B}_{Y-y,n}$) with fewer years of data (i.e., with subsequent years of data "peeled" or removed) by:

$$\hat{\rho} = \overline{\frac{\hat{B}_{Y-y,n} - \hat{B}_{Y-y,base}}{\hat{B}_{Y-y,base}}} \ , \tag{2}$$

where Y is the final year in the base model and y is the terminal year of the given nth "peel" in the subsequent models. The terminal years for the retrospective analysis include: 2009, 2011, 2013, 2015, and 2017. $\overline{ARD}$ measures the variation on peels in the retrospective analysis, or in other words, is the mean relative bias between the base model and each peel (i.e., when fewer years of data are modeled). $\overline{ARD}$ is calculated by:

$$\overline{ARD} = \overline{\frac{\left| \hat{B}_{Y-y,n} - \hat{B}_{Y-y,base} \right|}{\hat{B}_{Y-y,base}}} \ . \tag{3}$$

The annual CV and average CV across each time series ($\overline{CV}$) from the base models are used to investigate the relative fit of the random effects and VAST models using the biomass estimate ($\widehat{B_y}$) and estimated standard error ($\widehat{SE_y}$) for each year in the survey. The $\overline{CV}$ is derived using:

$$\overline{CV} = \overline{\left(\frac{\widehat{SE_y}}{\widehat{B_y}} \right)} \ . \tag{4}$$

Large average CV and $\overline{CV}$ values (i.e., > 1) can indicate that a model demonstrated poor performance and should not be considered permissible to use.

Lastly, the overfishing limit (OFL) and acceptable biological catch (ABC) are calculated for the Tier 4 and 5 species in the Other Rockfish complex by tier for each model type (random effects, VAST-RW, VAST-free, and VAST-fixed). The NPFMC harvest control rule is utilized for each tier by multiplying the total estimated biomass by the exploitation fraction corresponding to the OFL (F_{OFL}) and ABC (F_{ABC}). The estimated biomass is calculated based on the stratified random design of the trawl survey and then

expanded for the GOA for the random effects model. The VAST model estimates biomass at each grid location in the GOA. The F_{OFL} and F_{ABC} are equivalent to $F_{35\%}$ and $F_{40\%}$ for Tier 4, respectively, which are based on age-at-maturity obtained from the current assessment (Tribuzio and Echave, 2019). The harvest recommendations for Tier 5 are calculated based on M group values as a proxy, where $F_{OFL} \sim M$ and $F_{ABC} = 0.75*$ F_{OFL} (DiCosimo et al., 2010; Tribuzio and Echave 2019). Two harvest control rules for Tier 5 are implemented to calculate the OFL and ABC: 1) the current NPFMC approach where a single, average M value of 0.073 is used to calculate harvest limits for the entire Tier 5, and 2) the M value is used to calculate the OFL and ABC for each corresponding M group before summing together for a total OFL and ABC). The R programming language (R Core Team, 2021) is used to run and compare all models.

4.3 Results

A total of 9 out of 18 individual species models converged using the random effects model compared to 9 species models for VAST-RW, 5 for VAST-free and 11 for the VAST-fixed models (Table 1 and Fig. SM4a-c). The remaining individual species have insufficient survey data to adequately run the models. For example, chilipepper (*S. goodie*) is not caught in any sample of trawl survey. All the individual species that have on average > 3% encounter rate (i.e., average annual proportion of positive catch in a trawl sample) yield abundance results from at least three models. The relative biomass estimates from the random effects, VAST-RW, VAST-free, and VAST-fixed individual species models generally follow the trawl survey catch trends well (Fig. 1). The $\overline{CV}$s from the random effects model are similar or higher than the $\overline{CV}$s from the three configurations

of VAST, whereas the VAST-RW and VAST-fixed models typically have similar $\overline{CV}$s

that are lower than the $\overline{CV}$s from VAST-free (Table 1). There are no consistent

retrospective patterns based on Mohn's ρ (Table 1; Fig. SM4a-c). However, the $\overline{ARD}$

results suggest that the individual species random effects models are more stable or have

similar stability when years of data are added compared to the VAST models (Table 1).

Similar to the individual species results, all four models applied to each M group

provide abundance estimate trends that generally follow the trawl survey catch trends

(Fig. 2), except VAST-free models did not converge for three M groups (M= 0.05, M=

0.06, M= 0.092; Table 1). The random effects models generally produce smoother trends

(i.e., less steep biomass changes from year to year), whereas the VAST models generate

more variable trends (Fig. 2). It is worth noting that because sharpchin is the only Tier 4

species, it is modeled in its own M group; thus, the results in Table 1 for individual and M

group values along with the sharpchin panel in Figure 1 and the M=SC panel in Figure 2

represent identical model outputs. Similarly, yelloweye, harlequin, and redstripe are

represented by single species Tier 5 M group (i.e., M groups for 0.02, 0.092, and 0.10,

respectively). In addition, widow rockfish is grouped with silvergray within the 0.05 M

group did not lead to many differences between the silvergray single species models and

the M group 0.05 models (Table 1), due to the low and infrequent catch of widow

rockfish in the trawl survey. The $\overline{CV}$s from the M group runs for the VAST models range

from 17 to 39%, while the $\overline{CV}$s from the random effects model range from 19 to 79%

(Table 1). The random effects models consistently have small, positive Mohn's ρ values,

but the VAST models demonstrate no consistent retrospective bias (Table 1).

Additionally, the retrospective analysis from the VAST-free model for M= 0.02 (same as

the yelloweye individual VAST-free model), demonstrates that VAST model can be unstable with fewer years of data (Fig. SM4e). Based on the $\overline{ARD}$ results, there is no clear model that outperforms the other models. For example, the random effects model for M= 0.10 (i.e., redstripe) has a lower $\overline{ARD}$ value than all VAST models, whereas the VAST models have lower $\overline{ARD}$ values for M= 0.07 than the random effects model (Table 1). As more species are added to the VAST models within the M groups framework, the resulting magnitude of Mohn's ρ and $\overline{ARD}$ tend to decrease significantly (e.g., the 0.06 and 0.07 M groups; Table 1).

Overall, the VAST-RW model for both individual and *M* groups provide the highest total biomass estimate for 2019 for Tier 5 rockfish, followed by the VAST-fixed, random effects model, and finally the VAST-free (Table 2). The estimated total biomass for Tier 5 species from the VAST-free model is significantly lower than the estimated biomass from all the other models due to model convergence challenges for both individual and *M* group models. The models from the *M* groups produce slightly higher biomass estimates ($< 2\%$) compared to the associated summed values from the individual species model runs (Table 2). The two OFL calculation methods, using a single average *M* value for the entire Tier 5 group and *M* specific values corresponding to each *M* group, provide similar harvest recommendations for the random effects model, but different OFL and subsequent ABC recommendations for the three VAST models; using *M* specific values for each *M* group for the OFL calculation generated larger OFL and ABC values (Table 2). Including yelloweye to the Tier 5 group (it is currently listed as a Tier 6 species) adds between 1,700 to 2,800 metric tons (mt) in total biomass and between 25 to 150 mt to the ABC (Table 2). For the only Tier 4 species, sharpchin, the random effects

model generates the lowest total biomass estimates and subsequent OFL and ABC recommendations compared to the VAST models.

4.4 Discussion

The results from this study demonstrate that the assessment model type, decision to assess species individually or as an M group, and harvest control rule approach (i.e., using M group values compared to a single average M value) have important impacts on the harvest limit recommendations. Here, the proposed VAST models (VAST-RW and VAST-fixed) have the potential to be used as an alternative assessment model for the species in the Tier 4 and 5 Other Rockfish complex. No models produced highly variable and unprecise results (i.e., CVs < 1) suggesting that the model choices provided reasonable results. The input configuration (temporal process choice and spatial components) for the VAST models allow the model to be flexible, but can be unstable in the retrospective analyses, suggesting that VAST models for indices of abundance are feasible, but may be impracticable with short time series or too few data points. In comparison, the random effects model smoothed the time series and provided more stable and consistent results when years of data were excluded in the retrospective analyses. Here in this research, the VAST models produce larger biomass estimates compared to the random effects model. Additionally, the results demonstrate that modeling by M groups led to higher total biomass estimates than the summed biomass estimates from the individual species models because there were insufficient data to run some individual species models. The ability to include more species (and thus increased total survey catch) in the grouped models led to the higher biomass estimates compared to summing

the individual species models, because non-converged individual models led to no biomass being added to the complex for that species. Conversely, ability to examine changes in species specific biomass trends and how they change over time when running individual species models can be equally as important as scientists continue to see shifts in populations (e.g., Pinsky et al., 2013; Thorson and Barnett, 2017).

The application of alternative harvest control rules (i.e., OFL calculation method) provides different harvest limits for the VAST models, but not for the random effects model. We recommend using OFL and ABC calculations that apply the M value for each associated M group as a proxy for F_{OFL} for each of the M group models for the Tier 4 and 5 Other Rockfish. The weighting of biomass estimates from the M groups better reflects the proportion of biomass that can be harvested as a whole compared to a single M value for the entire stock complex. Therefore, applying individual M group values in the development of harvest recommendations should provide a more biologically realistic approach to setting harvest recommendations.

The differences in ABCs from each model and F_{OFL} calculation method could alter fishing practices if these non-target species are limiting the catch of target species (i.e., if any are 'choke' species; Schrope, 2010; Batsleer et al., 2015). Additionally, because the VAST models can provide fine-scale spatiotemporal maps of abundance, they can be used to identify potential areas of high concentration for a given species. If any species are deemed to be particularly vulnerable or exhibiting high bycatch rates, abundance maps can be provided to fishermen to help identify potential areas of bycatch hotspots, which can then be used to avoid areas of high non-target catch or to inform managers of areas to implement spatio-temporal fishery closures (Dolder et al., 2018;

NPFMC, 2021). Fortunately, the total fishery catch for the GOA Other Rockfish are typically below the set catch limits (Tribuzio and Echave, 2019), but the high vulnerability to overfishing of *Sebastes* species necessitates precautions (Cope et al., 2011; Ormseth and Spencer, 2011). As noted by the NPFMC Science and Statistical Committee (NPFMC, 2021), it may be useful to set lower ABCs for vulnerable, non-target stocks, such as the Other Rockfish complex, to increase awareness of potential challenges and consequences if the stock becomes overfished.

Previous comparisons of VAST and alternative design- or model-based estimators have typically involved more "data-rich" species than those explored here (Cao et al., 2017; Thorson et al., 2015, 2021). Our results illustrate the need to explore alternative model structures for data-poor cases like sharpchin where the scale is radically different between model and design-based estimators. Exploration could focus upon, e.g., the consequence of including covariates, identifying and exploring fit in subareas with large discrepancies between methods, and diagnostics for model suitability.

We note that the random effects model explored here is also used to recommend total catches for subareas within the Gulf of Alaska. Similar to this study, the random effects model is applied to survey catch data for each management area separately. The proportion of biomass estimated in each management area then is used to apportion the ABCs to each area (Tribuzio and Echave, 2019). VAST is being explored for use in apportionment, similar to its use for Tier-4/5/6 OFL estimates that we propose here.

The tier designations used here are based on those of the most recent full assessment, conducted in 2019 (Tribuzio and Echave 2019). One important consideration is that some of the species within the complex may change tier category. Both harlequin

and yelloweye rockfish are being considered for moving up tiers. Further, species with little data that are currently Tier 5 (e.g., chilipepper) could be downgraded to Tier 6, which could reduce some of the non-convergence issues. Lastly, for at least one species, yelloweye rockfish, hook-and-line surveys may provide more useful information for the species and alternate surveys need to be considered.

The selection of assessment model and harvest control rules requires further discussion with regional management entities, because there is a large range in resulting harvest limit recommendations (i.e., OFLs and ABCs) based on the model and harvest control rule selection. Likewise, the advantages and caveats of each model does not produce a clear best model choice. While the results and application are specific to the GOA Other Rockfish, similar methods and lessons from this research can provide guidance to other studies comparing assessment models. Although the VAST and random effects models implemented in this study provided similar results and performance, we would suggest that the VAST models might be a useful alternative modeling tool moving forward. VAST, as applied in this research, included spatial and temporal components, but can include a spatio-temporal term if spatial changes are known to occur over time. From prior investigation, we excluded the spatio-temporal component to reduce the model complexity for these data-limited species and to not over fit the model because there was no indication that spatial changes occurred over time. Future models can include a spatio-temporal component if necessary when more data are available. As the survey time series continues to expand, survey protocols will continue to improve to better account for non-target rockfish in both trawlable and untrawlable habitat by incorporating additional or alternative surveys (e.g., other survey gears and fishery

catch), and identifying and reporting other environmental variables. It is expected that a spatio-temporal modeling framework will continue to improve, resulting in more robust biomass estimates for the data-limited Other Rockfish species in the Gulf of Alaska.

The spatio-temporal modeling approach, implemented here in the VAST framework, to be a useful method to identify (multivariate approach) and model (univariate approach) species complexes. Although the full range of data and grouping methods available should be implemented and compared when developing species complexes, a spatio-temporal model, such as VAST, provides a useful single tool that can first be used to identify spatio-temporal correlations and changes among species that can help determine which species could be managed as a complex (e.g., Omori et al., *in preview*). Then, the same framework can be utilized to determine the biomass of the entire complex and resultant sustainable harvest levels (univariate approach used in this chapter). The ability to use a single framework for the entire species complex management process could help reduce the time needed to manage non-target and data-limited species, while also improving consistency among modeling assumptions throughout the management process.

4.5 References

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4.6 Tables

Table 4.1. List of Tier 4 and 5 rockfish species, average annual encounter percentage (Enc; encounter percentage range in parentheses), their associated natural mortality (*M*) group, AR *φ* parameter for associated VAST-fixed model, model performance metrics (Mohn's ρ [Eq. 2], absolute relative difference [*ARD;* Eq. 3]) and, average CV [$\overline{CV}$; Eq. 4]) for each individual and *M* group model run of the random effects (RE), VAST-RW, VAST-free, VAST-fixed model. The "-" indicates that the either the model was unable to converge or there were insufficient data to run the model.

Common name	Sebastes spp.	Enc	M group	AR *φ*		Individual					M Group			
						RE	VAST-RW	VAST-free	VAST-fixed		RE	VAST-RW	VAST-free	VAST-fixed
Yelloweye	S. ruberrimus	3% (1-4)	0.02	0.98	$\overline{CV}$	0.24	0.22	0.22	0.22	$\overline{CV}$	0.24	0.22	0.22	0.22
					ρ	0.06	-0.27	-0.04	-0.05	ρ	0.06	-0.27	-0.04	-0.05
					ARD	0.08	0.28	0.07	0.07	ARD	0.08	0.28	0.07	0.10
Silvergray	S. brevispinis	7% (1-10)			$\overline{CV}$	0.37	0.28	-	0.28					
					ρ	0.02	-0.01	-	-0.02	$\overline{CV}$	0.37	0.28	-	0.28
			0.05	0.94	ARD	0.07	0.04	-	0.04	ρ	0.02	-0.01	-	-0.02
Widow	S. entomelas	0% (0-1)			$\overline{CV}$	-	-	-	-	ARD	0.07	0.04	-	0.04
					ρ	-	-	-	-					
					ARD	-	-	-	-					
Blackgill	S. melanostomus	0% (0-0)			$\overline{CV}$	-	-	-	-					
					ρ	-	-	-	-					
					ARD	-	-	-	-					
Bocaccio	S. paucispinis	0% (0-1)			$\overline{CV}$	-	-	-	-					
					ρ	-	-	-	-					
			0.06	0.92	ARD	-	-	-	-					
Chilipepper	S. goodie	NA			$\overline{CV}$	-	-	-	-					
					ρ	-	-	-	-					
					ARD	-	-	-	-					
Pygmy	S. wilsoni	1% (0-1)			$\overline{CV}$	-	-	-	0.50					
					ρ	-0.66	-	-	0.24					
					ARD	0.94	-	-	0.47					

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Common	Species	% (range)												
Redbanded	S. babcocki	11% (5-13)			$\overline{CV}$	0.18	0.16	-	0.16	$\overline{CV}$	0.19	0.17	-	0.17
					ρ	0.03	0.02	-	0.00	ρ	0.02	0.01	-	0.00
					ARD	0.03	0.04	-	0.03	ARD	0.04	0.04	-	0.03
Splitnose	S. diploproa	0% (0-1)			$\overline{CV}$	-	-	-	-					
					ρ	-	-	-	-					
					ARD	-	-	-	-					
Stripetail	S. saxicola	0% (0-0)			$\overline{CV}$	-	-	-	-					
					ρ	-	-	-	-					
					ARD	-	-	-	-					
Vermilion	S. miniatus	0% (0-0)			$\overline{CV}$	-	-	-	-					
					ρ	-	-	-	-					
					ARD	-	-	-	-					
Yellowmouth	S. reedi	0% (0-1)			$\overline{CV}$	7.67	-	-	0.68					
					ρ	-0.24	-	-	-0.77					
					ARD	0.31	-	-	0.83					
Darkblotched	S. crameri	1% (0-1)			$\overline{CV}$	1.11	0.58	0.61	0.57					
					ρ	0.07	0.33	-0.76	0.20					
					ARD	0.20	0.39	0.84	0.27					
Greenstriped	S. elongates	1% (0-2)	0.07	0.90	$\overline{CV}$	-	0.37	-	0.38	$\overline{CV}$	0.79	0.38	0.39	0.38
					ρ	-	-0.08	-	-0.11	ρ	0.08	0.03	0.00	0.01
					ARD	-	0.15	-	0.16	ARD	0.17	0.08	0.05	0.07
Yellowtail	S. flavidus	1% (0-2)			$\overline{CV}$	-	0.81	0.78	0.81					
					ρ	-	0.07	-0.84	-0.40					
					ARD	-	0.31	0.84	0.55					
Harlequin	S. variegatus	8% (5-14)	0.092	0.87	$\overline{CV}$	0.49	0.29	-	0.29	$\overline{CV}$	0.49	0.29	-	0.29
					ρ	0.13	-0.02	-	-0.02	ρ	0.13	-0.02	-	-0.02
					ARD	0.13	0.09	-	0.08	ARD	0.13	0.09	-	0.08
Redstripe	S. proriger	3% (1-6)	0.1	0.85	$\overline{CV}$	0.63	0.36	0.41	0.37	$\overline{CV}$	0.63	0.36	0.41	0.37
					ρ	0.05	-0.12	-0.50	-0.15	ρ	0.05	-0.12	-0.50	-0.15
					ARD	0.12	0.16	0.50	0.15	ARD	0.12	0.16	0.50	0.15
Sharpchin	S. zacentrus	7% (3-13)	SC (0.060)	0.92	$\overline{CV}$	0.50	0.30	0.31	0.30	$\overline{CV}$	0.50	0.30	0.31	0.30
					ρ	0.03	-0.01	-0.01	-0.02	ρ	0.03	-0.01	-0.01	-0.02
					ARD	0.08	0.07	0.02	0.07	ARD	0.08	0.07	0.02	0.07

Table 4.2. Estimated total biomass, overfishing limit (OFL), and acceptable biological catch (ABC) in metric tons (mt) for the GOA region in 2019 for Tier 4 and 5 rockfish by model type (random effects [RE] and VAST models). Results are provided with and without yelloweye rockfish (YE) included in the Tier 5 total biomass and subsequent harvest recommendations (see text for more details). The 'M=0.07' signifies the average M value used as a proxy for F_{OFL} and the associated F_{ABC} ($F_{ABC} = 0.75 * M$). The harvest recommendations with 'M per grp' indicates that each M for each M group or individual was used as a proxy for F_{OFL} and associated F_{ABC} ($F_{ABC} = 0.75 * M$).

Tier	YE	Model	Total Biomass	OFL M=0.07	OFL M per grp	ABC M=0.07	ABC M per grp
4	-	RE	10,826		855		704
	-	VAST- RW	19,636		1,551		1,276
	-	VAST- free	19,995		1,580		1,300
	-	VAST- fixed	19,316		1,526		1,256
5	✘	RE	56,318	3,942	3,950	2,957	2,963
	✘	VAST- RW	85,506	5,985	6,595	4,489	4,946
Individual	✘	VAST- free	36,825	2,578	3,587	1,933	2,691
	✘	VAST- fixed	83,345	5,834	6,385	4,376	4,789
	✘	RE	59,862	4,190	4,192	3,143	3,144
	✘	VAST- RW	86,313	6,042	6,642	4,531	4,982
M Group	✘	VAST- free	37,314	2,612	3,622	1,959	2,716
	✘	VAST- fixed	83,693	5,859	6,405	4,394	4,804
	✔	RE	58,021	4,061	3,984	3,046	2,988
	✔	VAST- RW	88,255	6,178	6,650	4,633	4,987
Individual	✔	VAST- free	39,705	2,779	3,645	2,085	2,734
	✔	VAST- fixed	86,098	6,027	6,440	4,520	4,830
	✔	RE	61,565	4,310	4,226	3,232	3,170
	✔	VAST- RW	89,063	6,234	6,697	4,676	5,023
M Group	✔	VAST- free	40,194	2,814	3,679	2,110	2,759
	✔	VAST- fixed	86,446	6,051	6,460	4,538	4,845

4.7 Figures
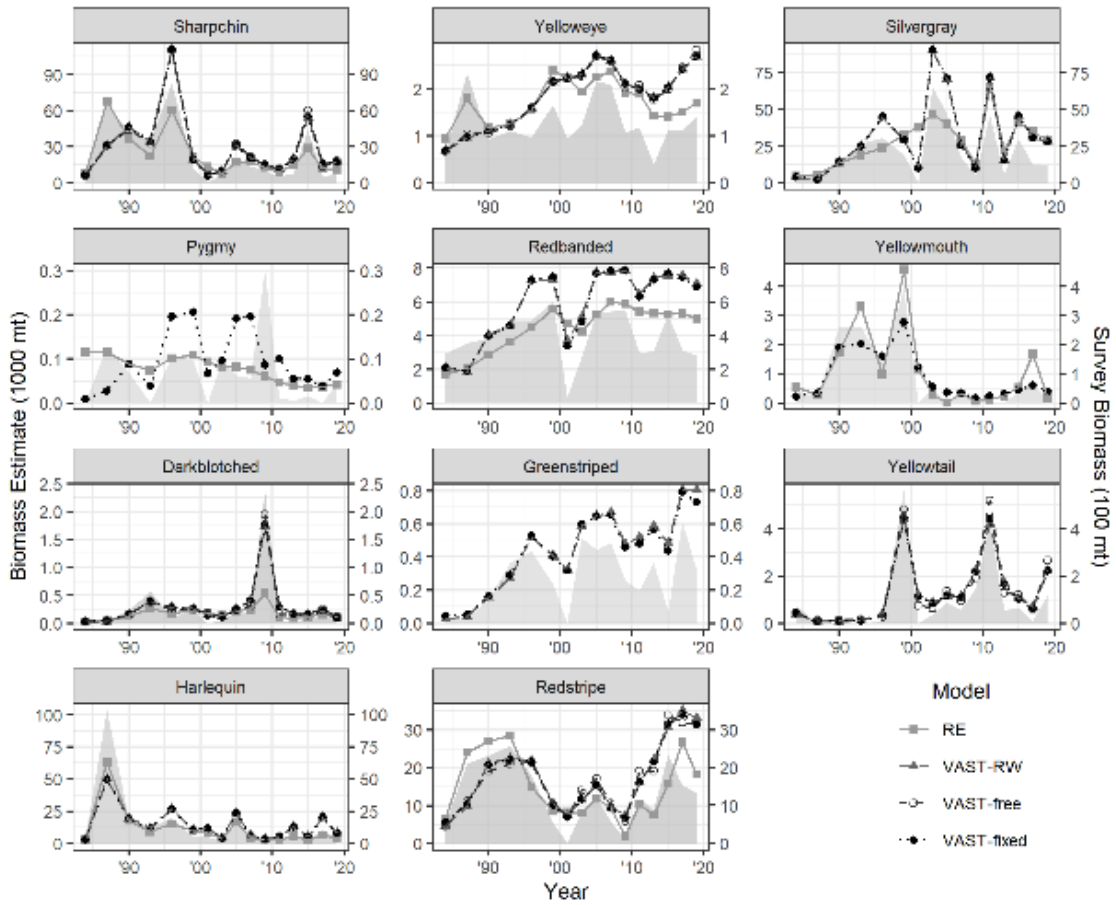
Fig. 1. Estimated biomass trends for each individual GOA Tier 4 and 5 rockfish species from each model type (line type and color for each model are provided in legend for the random effects [RE] and VAST models; observed survey catch values are represented by the grey shaded region and corresponding right-hand y-axis).
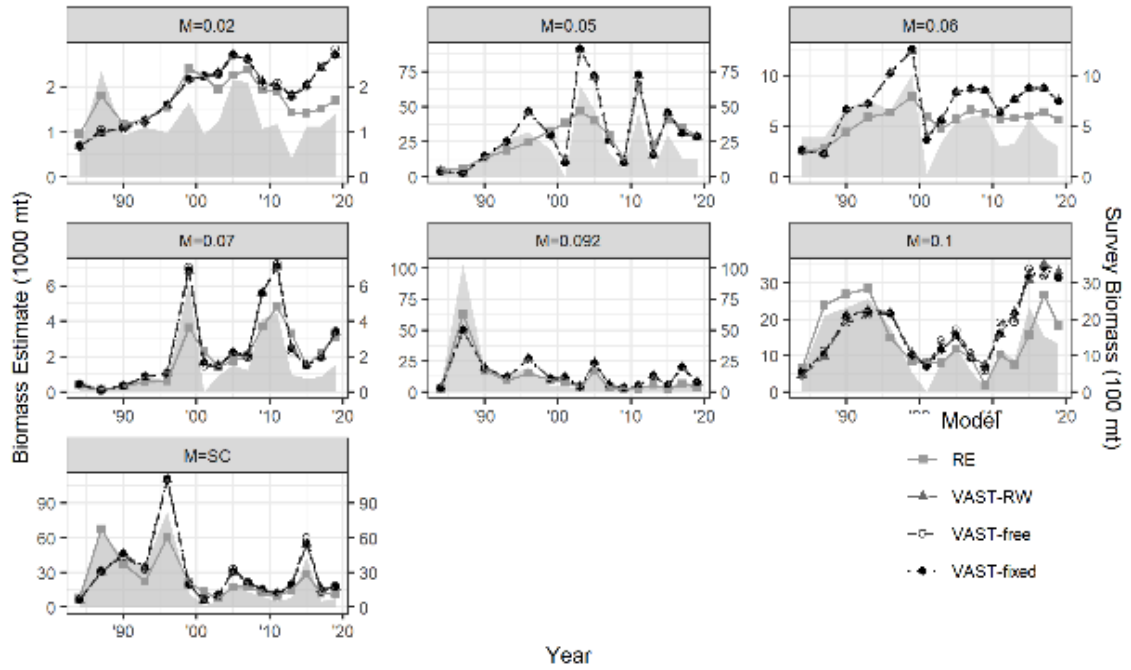
Fig. 4.2. Estimated biomass trends for each natural mortality (*M*) group of GOA Tier 4 (Sharpchin; *M= SC*) and 5 rockfish from each model type (line type and color for each model are provided in legend random effects [RE] and VAST models; observed survey catch values are represented by the grey shaded region and corresponding right-hand y-axis).

4.8 Appendices

Appendix A. Random effects time series model

The random effects model for estimating biomass in a time series was developed by the North Pacific Stock Assessment Working Group (SAWG, 2013) and recent updates to the model are found in Hulson et al. (2021). The estimated biomass, $\hat{B}_y$, for year y, is estimated by:

$$\hat{B}_y = \sum_R e^{\hat{\epsilon}_{r,y}},$$

where each region, r, is modeled separately and summed for the total estimated biomass. The random effects parameters, $\hat{\epsilon}_{r,y}$, for each region and year are estimated using two components, the process and observational errors, that are summed and minimized in the negative log-likelihood functions.

The process error, which accounts for the changes of biomass over time, follows a random-walk process, which is constrained by the estimated process error variance, $\hat{\sigma}_{\epsilon,r}^2$. The negative log-likelihood for the process error component, p, is:

$$-\ln L_p = \sum_{y=2}^{Y} \sum_R \frac{1}{2} \ln(\pi \hat{\sigma}_{\epsilon,r}^2) + \left(\hat{\epsilon}_{r,y} - \hat{\epsilon}_{r,y-1}\right)^2 / \hat{\sigma}_{\epsilon,r}^2$$

The observational error, which accounts for the difference between the estimated and observed survey biomass ($B_{r,y}$), follows a log-normal distribution with the variance as the trawl survey biomass variance, $\sigma_{B,r,y}^2$. The negative log-likelihood for the observational error, o, is:

$$-\ln L_o = \sum_Y \sum_R \frac{1}{2} \left[\ln\left(2\pi\sigma_{B,r,y}^2\right) + \frac{1}{\sigma_{B,r,y}^2} \left(\hat{\epsilon}_{r,y} - \ln B_{r,y}\right)^2 \right]$$

Appendix B. VAST temporal process

Temporal process (β), where the "φ" dictates the difference between the three VAST models, is as follows:

$$\beta_*(t) \sim \begin{cases} Normal(0, \sigma_{\beta_*}^2) & if \ t = 1 \\ Normal\left(\phi_{\beta_*}\beta(t-1), \sigma_{\beta_*}^2\right) & if \ t > 1 \end{cases}.$$

$\beta_*(t)$ represents $\beta_1(t)$ and $\beta_2(t)$ for the first and second linear predictors and $\sigma_{\beta_*}^2$ is the conditional covariance for the temporal component in the first ($\sigma_{\beta_1}^2$) and second ($\sigma_{\beta_2}^2$) linear predictors. Similarly, ϕ_{β_*} is the coefficient in the autoregressive (AR) process in the temporal component for the first and second linear predictor. If $\phi = 1$, the temporal process follows a random walk (VAST-RW). If ϕ is estimated freely, the temporal process follows an AR (1) process (VAST-free). If ϕ is fixed at a calculated value based on F_{SPR}, the temporal process also follows an AR (1) process, but ϕ is not estimated in the model.

4.9 Supplementary Material

Supplementary Tables

Table SM1. Starting input configuration for each VAST model. See Table SM3 for unique inputs for each model.

Model	VAST-RW	VAST-free	VAST-fixed
No. knots	750	750	750
Use anisotrophy	TRUE	TRUE	TRUE
ObsModel	(2,1)= Poisson-link Gamma	(2,1)= Poisson-link Gamma	(2,1)= Poisson-link Gamma
Overdispersion	Eta1= 0, Eta2= 0	Eta1= 0, Eta2= 0	Eta1= 0, Eta2= 0
Fine scale	TRUE	TRUE	TRUE
AR φ	NA	Free	Species-specific
Bias correct	TRUE	TRUE	TRUE
FieldConfig	Beta1= "IID", Beta2= "IID" Omega1=0, Omega2= 0 Epsilon1= 0, Epsilon2= 0	Beta1= "IID", Beta2= "IID" Omega1=0, Omega2= 0 Epsilon1= 0, Epsilon2= 0	Beta1= "IID", Beta2= "IID Omega1= 0 Omega2= 0 Epsilon1= 0, Epsilon2= 0
RhoConfig	Beta1= 2, Beta2= 2 Epsilon1= 0, Epsilon2= 0	Beta1= 2, Beta2= 4 Epsilon1= 0, Epsilon2= 0	Beta1= 2, Beta2= 4 Epsilon1= 0, Epsilon2= 0

Table SM2. List of GOA rockfish species that have fishing mortality that corresponds to 40% of the unfished spawning stock biomass (F_{40}) estimated from spawner-per-recruit levels, M (natural mortality) values, year of the F_{SPR} and M estimates, and source.

Rockfish	Year	F_{40}	M	Source
Dusky	2020	0.093	0.070	Fenske, K. H., Hulson, P.-J.F., Williams, B., and O'Leary, C.A.. 2020. Assessment of the dusky rockfish stock in the Gulf of Alaska. In Stock Assessment and Fishery Evaluation Report for the Groundfish Resources of the Gulf of Alaska, North Pacific Fishery Management Council, 605 W 4th Ave, Suite 306. Anchorage, AK 99501. 85pp.
Northern	2020	0.061	0.059	Williams, B.C., Hulson, P.-J.F., Lunsford, C.R., and Cunningham, C.J. 2020. Assessment of the northern rockfish stock in the Gulf of Alaska. In Stock Assessment and Fishery Evaluation Report for the Groundfish Resources of the Gulf of Alaska, North Pacific Fishery Management Council, 605 W 4th Ave, Suite 306. Anchorage, AK 99501. 77pp.
Pacific Ocean Perch	2020	0.10	0.076	Hulson, P.-J.F., Lunsford, C.R., Fissel, B., and Jones, D. 2020. Assessment of the Pacific ocean perch stock in the Gulf of Alaska. In Stock Assessment and Fishery Evaluation Report for the Groundfish Resources of the Gulf of Alaska, North Pacific Fishery Management Council, 605 W 4th Ave, Suite 306. Anchorage, AK 99501. 79pp.
Rougheye/ Blackspotted	2019	0.04	0.036	Shotwell, S.K. and Hanselman, D.H. 2019. Assessment of the rougheye and blackspotted rockfish stock complex in the Gulf of Alaska. In Stock Assessment and Fishery Evaluation Report for the Groundfish Resources of the Gulf of Alaska, North Pacific Fishery Management Council, 605 W 4th Ave, Suite 306. Anchorage, AK 99501. 115pp.

Table SM3. VAST input settings for final converged VAST models for each species and species group

Model	Species/ *M* Group	Use aniso	AR φ	RhoConfig	FieldConfig	Converged
VAST-RW	Silvergray	T	RW	Beta1 = IID, Beta2 = IID, Omega1 = 0 , Omega2 = 0, Epsilon1 = 0 , Epsilon2 = 0	Beta1 = 2 , Beta2 = 2, Epsilon1 = 0 , Epsilon2 = 0	T
VAST-RW	Darkblotched	T	RW	Beta1 = IID, Beta2 = IID, Omega1 = 0 , Omega2 = 0, Epsilon1 = 0 , Epsilon2 = 0	Beta1 = 2 , Beta2 = 2, Epsilon1 = 0 , Epsilon2 = 0	T
VAST-RW	Splitnose	-	-	-	-	F
VAST-RW	Greenstriped	T	RW	Beta1 = IID, Beta2 = IID, Omega1 = 0 , Omega2 = 0, Epsilon1 = 0 , Epsilon2 = 0	Beta1 = 2 , Beta2 = 2, Epsilon1 = 0 , Epsilon2 = 0	T
VAST-RW	Widow	-	-	-	-	F
VAST-RW	Yellowtail	T	RW	Beta1 = IID, Beta2 = IID, Omega1 = 0 , Omega2 = 0, Epsilon1 = 0 , Epsilon2 = 0	Beta1 = 2 , Beta2 = 2, Epsilon1 = 0 , Epsilon2 = 0	T
VAST-RW	Chilipepper	-	-	-	-	F
VAST-RW	Blackgill	-	-		-	F
VAST-RW	Vermilion	-	-	-	-	F
VAST-RW	Bocaccio	-	-	-	-	F
VAST-RW	Redstripe	T	RW	Beta1 = IID, Beta2 = IID, Omega1 = 0 , Omega2 = 0, Epsilon1 = 0 , Epsilon2 = 0	Beta1 = 2 , Beta2 = 2, Epsilon1 = 0 , Epsilon2 = 0	T
VAST-RW	Redbanded	T	RW	Beta1 = IID, Beta2 = IID, Omega1 = 0 , Omega2 = 0, Epsilon1 = 0 , Epsilon2 = 0	Beta1 = 2 , Beta2 = 2, Epsilon1 = 0 , Epsilon2 = 0	T
VAST-RW	Stripetail	-	-	-	-	F
VAST-RW	Harlequin	T	RW	Beta1 = IID, Beta2 = IID, Omega1 = 0 , Omega2 = 0, Epsilon1 = 0 , Epsilon2 = 0	Beta1 = 2 , Beta2 = 2, Epsilon1 = 0 , Epsilon2 = 0	T
VAST-RW	Pygmy	T	RW	Beta1 = IID, Beta2 = IID, Omega1 = 0 , Omega2 = 0, Epsilon1 = 0 , Epsilon2 = 0	Beta1 = 2 , Beta2 = 2, Epsilon1 = 0 , Epsilon2 = 0	F
VAST-RW	Yellowmouth	-	-	-	-	F
VAST-RW	Yelloweye	T	RW	Beta1 = IID, Beta2 = IID, Omega1 = 0 , Omega2 = 0, Epsilon1 = 0 , Epsilon2 = 0	Beta1 = 2 , Beta2 = 2, Epsilon1 = 0 , Epsilon2 = 0	T
VAST-RW	Sharpchin	T	RW	Beta1 = IID, Beta2 = IID, Omega1 = 0 , Omega2 = 0, Epsilon1 = 0 , Epsilon2 = 0	Beta1 = 2 , Beta2 = 2, Epsilon1 = 0 , Epsilon2 = 0	T
VAST-free	Silvergray	T	free	Beta1 = IID, Beta2 = IID, Omega1 = 0 , Omega2 = 0, Epsilon1 = 0 , Epsilon2 = 0	Beta1 = 2 , Beta2 = 4, Epsilon1 = 0 , Epsilon2 = 0	F

VAST-free	Darkblotched	T	free	Beta1 = IID, Beta2 = IID, Omega1 = 0 , Omega2 = 0, Epsilon1 = 0 , Epsilon2 = 0	Beta1 = 2 , Beta2 = 4, Epsilon1 = 0 , Epsilon2 = 0	T
VAST-free	Splitnose	-	-	-	-	F
VAST-free	Greenstriped	T	free	Beta1 = IID, Beta2 = IID, Omega1 = 0 , Omega2 = 0, Epsilon1 = 0 , Epsilon2 = 0	Beta1 = 2 , Beta2 = 4, Epsilon1 = 0 , Epsilon2 = 0	F
VAST-free	Widow	-	-	-	-	F
VAST-free	Yellowtail	T	free	Beta1 = IID, Beta2 = IID, Omega1 = 0 , Omega2 = 0, Epsilon1 = 0 , Epsilon2 = 0	Beta1 = 2 , Beta2 = 4, Epsilon1 = 0 , Epsilon2 = 0	T
VAST-free	Chilipepper	-	-	-	-	F
VAST-free	Blackgill	-	-	-	-	F
VAST-free	Vermilion	-	-	-	-	F
VAST-free	Bocaccio	-	-	-	-	F
VAST-free	Redstripe	T	free	Beta1 = IID, Beta2 = IID, Omega1 = 0 , Omega2 = 0, Epsilon1 = 0 , Epsilon2 = 0	Beta1 = 2 , Beta2 = 4, Epsilon1 = 0 , Epsilon2 = 0	T
VAST-free	Redbanded	T	free	Beta1 = IID, Beta2 = IID, Omega1 = 0 , Omega2 = 0, Epsilon1 = 0 , Epsilon2 = 0	Beta1 = 2 , Beta2 = 4, Epsilon1 = 0 , Epsilon2 = 0	F
VAST-free	Stripetail	-	-	-	-	F
VAST-free	Harlequin	T	free	Beta1 = IID, Beta2 = IID, Omega1 = 0 , Omega2 = 0, Epsilon1 = 0 , Epsilon2 = 0	Beta1 = 2 , Beta2 = 4, Epsilon1 = 0 , Epsilon2 = 0	F
VAST-free	Pygmy	T	free	Beta1 = IID, Beta2 = IID, Omega1 = 0 , Omega2 = 0, Epsilon1 = 0 , Epsilon2 = 0	Beta1 = 2 , Beta2 = 4, Epsilon1 = 0 , Epsilon2 = 0	F
VAST-free	Yellowmouth	-	-	-	-	F
VAST-free	Yelloweye	T	free	Beta1 = IID, Beta2 = IID, Omega1 = 0 , Omega2 = 0, Epsilon1 = 0 , Epsilon2 = 0	Beta1 = 2 , Beta2 = 4, Epsilon1 = 0 , Epsilon2 = 0	T
VAST-free	Sharpchin	T	free	Beta1 = IID, Beta2 = IID, Omega1 = 0 , Omega2 = 0, Epsilon1 = 0 , Epsilon2 = 0	Beta1 = 2 , Beta2 = 4, Epsilon1 = 0 , Epsilon2 = 0	T
VAST-fixed	Silvergray	T	0.937	Beta1 = IID, Beta2 = IID, Omega1 = 0 , Omega2 = 0, Epsilon1 = 0 , Epsilon2 = 0	Beta1 = 2 , Beta2 = 4, Epsilon1 = 0 , Epsilon2 = 0	T
VAST-fixed	Darkblotched	T	0.903	Beta1 = IID, Beta2 = IID, Omega1 = 0 , Omega2 = 0, Epsilon1 = 0 , Epsilon2 = 0	Beta1 = 2 , Beta2 = 4, Epsilon1 = 0 , Epsilon2 = 0	T
VAST-fixed	Splitnose	-	-	-	-	F
VAST-fixed	Greenstriped	T	0.903	Beta1 = IID, Beta2 = IID, Omega1 = 0 , Omega2 = 0, Epsilon1 = 0 , Epsilon2 = 0	Beta1 = 2 , Beta2 = 4, Epsilon1 = 0 , Epsilon2 = 0	T
VAST-fixed	Widow	-	-	-	-	F

VAST-fixed	Yellowtail	T	0.903	Beta1 = IID, Beta2 = IID, Omega1 = 0 , Omega2 = 0, Epsilon1 = 0 , Epsilon2 = 0	Beta1 = 2 , Beta2 = 4, Epsilon1 = 0 , Epsilon2 = 0	T
VAST-fixed	Chilipepper	-	-	-	-	F
VAST-fixed	Blackgill	-	-	-	-	F
VAST-fixed	Vermilion	-	-	-	-	F
VAST-fixed	Bocaccio	-	-	-	-	F
VAST-fixed	Redstripe	T	0.853	Beta1 = IID, Beta2 = IID, Omega1 = 0 , Omega2 = 0, Epsilon1 = 0 , Epsilon2 = 0	Beta1 = 2 , Beta2 = 4, Epsilon1 = 0 , Epsilon2 = 0	T
VAST-fixed	Redbanded	T	0.92	Beta1 = IID, Beta2 = IID, Omega1 = 0 , Omega2 = 0, Epsilon1 = 0 , Epsilon2 = 0	Beta1 = 2 , Beta2 = 4, Epsilon1 = 0 , Epsilon2 = 0	T
VAST-fixed	Stripetail	-	-	-	-	F
VAST-fixed	Harlequin	T	0.867	Beta1 = IID, Beta2 = IID, Omega1 = 0 , Omega2 = 0, Epsilon1 = 0 , Epsilon2 = 0	Beta1 = 2 , Beta2 = 4, Epsilon1 = 0 , Epsilon2 = 0	T
VAST-fixed	Pygmy	F	0.92	Beta1 = IID, Beta2 = IID, Omega1 = 0 , Omega2 = 0, Epsilon1 = 0 , Epsilon2 = 0	Beta1 = 2 , Beta2 = 4, Epsilon1 = 0 , Epsilon2 = 0	T
VAST-fixed	Yellowmouth	T	0.92	Beta1 = IID, Beta2 = IID, Omega1 = 0 , Omega2 = 0, Epsilon1 = 0 , Epsilon2 = 0	Beta1 = 2 , Beta2 = 4, Epsilon1 = 0 , Epsilon2 = 0	T
VAST-fixed	Yelloweye	T	0.987	Beta1 = IID, Beta2 = IID, Omega1 = 0 , Omega2 = 0, Epsilon1 = 0 , Epsilon2 = 0	Beta1 = 2 , Beta2 = 4, Epsilon1 = 0 , Epsilon2 = 0	T
VAST-fixed	Sharpchin	T	0.92	Beta1 = IID, Beta2 = IID, Omega1 = 0 , Omega2 = 0, Epsilon1 = 0 , Epsilon2 = 0	Beta1 = 2 , Beta2 = 4, Epsilon1 = 0 , Epsilon2 = 0	T
VAST-RW	M=0.1	T	RW	Beta1 = IID, Beta2 = IID, Omega1 = 0 , Omega2 = 0, Epsilon1 = 0 , Epsilon2 = 0	Beta1 = 2 , Beta2 = 2, Epsilon1 = 0 , Epsilon2 = 0	T
VAST-RW	M=0.092	T	RW	Beta1 = IID, Beta2 = IID, Omega1 = 0 , Omega2 = 0, Epsilon1 = 0 , Epsilon2 = 0	Beta1 = 2 , Beta2 = 2, Epsilon1 = 0 , Epsilon2 = 0	T
VAST-RW	M=0.07	T	RW	Beta1 = IID, Beta2 = IID, Omega1 = 0 , Omega2 = 0, Epsilon1 = 0 , Epsilon2 = 0	Beta1 = 2 , Beta2 = 2, Epsilon1 = 0 , Epsilon2 = 0	T
VAST-RW	M=0.06	T	RW	Beta1 = IID, Beta2 = IID, Omega1 = 0 , Omega2 = 0, Epsilon1 = 0 , Epsilon2 = 0	Beta1 = 2 , Beta2 = 2, Epsilon1 = 0 , Epsilon2 = 0	T
VAST-RW	M=0.05	T	RW	Beta1 = IID, Beta2 = IID, Omega1 = 0 , Omega2 = 0, Epsilon1 = 0 , Epsilon2 = 0	Beta1 = 2 , Beta2 = 2, Epsilon1 = 0 , Epsilon2 = 0	T
VAST-RW	M=0.02	T	RW	Beta1 = IID, Beta2 = IID, Omega1 = 0 , Omega2 = 0, Epsilon1 = 0 , Epsilon2 = 0	Beta1 = 2 , Beta2 = 2, Epsilon1 = 0 , Epsilon2 = 0	T
VAST-RW	M=SC	T	RW	Beta1 = IID, Beta2 = IID, Omega1 = 0 , Omega2 = 0, Epsilon1 = 0 , Epsilon2 = 0	Beta1 = 2 , Beta2 = 2, Epsilon1 = 0 , Epsilon2 = 0	T

VAST-free	M=0.1	T	free	Beta1 = IID, Beta2 = IID, Omega1 = 0 , Omega2 = 0, Epsilon1 = 0 , Epsilon2 = 0	Beta1 = 2 , Beta2 = 4, Epsilon1 = 0 , Epsilon2 = 0	T
VAST-free	M=0.092	T	free	Beta1 = IID, Beta2 = IID, Omega1 = 0 , Omega2 = 0, Epsilon1 = 0 , Epsilon2 = 0	Beta1 = 2 , Beta2 = 4, Epsilon1 = 0 , Epsilon2 = 0	F
VAST-free	M=0.07	T	free	Beta1 = IID, Beta2 = IID, Omega1 = 0 , Omega2 = 0, Epsilon1 = 0 , Epsilon2 = 0	Beta1 = 2 , Beta2 = 4, Epsilon1 = 0 , Epsilon2 = 0	T
VAST-free	M=0.06	T	free	Beta1 = IID, Beta2 = IID, Omega1 = 0 , Omega2 = 0, Epsilon1 = 0 , Epsilon2 = 0	Beta1 = 2 , Beta2 = 4, Epsilon1 = 0 , Epsilon2 = 0	F
VAST-free	M=0.05	T	free	Beta1 = IID, Beta2 = IID, Omega1 = 0 , Omega2 = 0, Epsilon1 = 0 , Epsilon2 = 0	Beta1 = 2 , Beta2 = 4, Epsilon1 = 0 , Epsilon2 = 0	F
VAST-free	M=0.02	T	free	Beta1 = IID, Beta2 = IID, Omega1 = 0 , Omega2 = 0, Epsilon1 = 0 , Epsilon2 = 0	Beta1 = 2 , Beta2 = 4, Epsilon1 = 0 , Epsilon2 = 0	T
VAST-free	M=SC	T	free	Beta1 = IID, Beta2 = IID, Omega1 = 0 , Omega2 = 0, Epsilon1 = 0 , Epsilon2 = 0	Beta1 = 2 , Beta2 = 4, Epsilon1 = 0 , Epsilon2 = 0	T
VAST-fixed	M=0.1	T	0.853	Beta1 = IID, Beta2 = IID, Omega1 = 0 , Omega2 = 0, Epsilon1 = 0 , Epsilon2 = 0	Beta1 = 2 , Beta2 = 4, Epsilon1 = 0 , Epsilon2 = 0	T
VAST-fixed	M=0.092	T	0.867	Beta1 = IID, Beta2 = IID, Omega1 = 0 , Omega2 = 0, Epsilon1 = 0 , Epsilon2 = 0	Beta1 = 2 , Beta2 = 4, Epsilon1 = 0 , Epsilon2 = 0	T
VAST-fixed	M=0.07	T	0.903	Beta1 = IID, Beta2 = IID, Omega1 = 0 , Omega2 = 0, Epsilon1 = 0 , Epsilon2 = 0	Beta1 = 2 , Beta2 = 4, Epsilon1 = 0 , Epsilon2 = 0	T
VAST-fixed	M=0.06	T	0.92	Beta1 = IID, Beta2 = IID, Omega1 = 0 , Omega2 = 0, Epsilon1 = 0 , Epsilon2 = 0	Beta1 = 2 , Beta2 = 4, Epsilon1 = 0 , Epsilon2 = 0	T
VAST-fixed	M=0.05	T	0.937	Beta1 = IID, Beta2 = IID, Omega1 = 0 , Omega2 = 0, Epsilon1 = 0 , Epsilon2 = 0	Beta1 = 2 , Beta2 = 4, Epsilon1 = 0 , Epsilon2 = 0	T
VAST-fixed	M=0.02	T	0.987	Beta1 = IID, Beta2 = IID, Omega1 = 0 , Omega2 = 0, Epsilon1 = 0 , Epsilon2 = 0	Beta1 = 2 , Beta2 = 4, Epsilon1 = 0 , Epsilon2 = 0	T
VAST-fixed	M=SC	T	0.92	Beta1 = IID, Beta2 = IID, Omega1 = 0 , Omega2 = 0, Epsilon1 = 0 , Epsilon2 = 0	Beta1 = 2 , Beta2 = 4, Epsilon1 = 0 , Epsilon2 = 0	T
VAST-fixed	M=SC	T	0.92	Beta1 = IID, Beta2 = IID, Omega1 = 0 , Omega2 = IID, Epsilon1 = 0 , Epsilon2 = 0	Beta1 = 2 , Beta2 = 4, Omega1 = 0 , Omega2 = 0	T

Table SM4. VAST model fixed parameter estimates

VAST model	Group	Con-verged	Beta_mean1_c	L_beta1_z	Beta_mean2_c	L_beta2_z	Beta_rho2_f	Log SigmaM
RW	Silvergray	T	0.265	0.297	2.268	0.647	NA	0.458
RW	Darkblotched	T	-2.789	-0.262	0.222	0.596	NA	0.19
RW	Splitnose	F	NA	NA	NA	NA	NA	NA
RW	Greenstriped	T	-2.482	-0.314	0.05	0.163	NA	0.087
RW	Widow	F	NA	NA	NA	NA	NA	NA
RW	Yellowtail	T	-1.825	0.513	2.088	0.634	NA	0.322
RW	Chilipepper	F	NA	NA	NA	NA	NA	NA
RW	Blackgill	F	NA	NA	NA	NA	NA	NA
RW	Vermilion	F	NA	NA	NA	NA	NA	NA
RW	Bocaccio	F	NA	NA	NA	NA	NA	NA
RW	Redstripe	T	-0.267	0.231	3.02	0.333	NA	0.611
RW	Redbanded	T	0.767	0.196	1.152	-0.116	NA	0.252
RW	Stripetail	F	NA	NA	NA	NA	NA	NA
RW	Harlequin	T	0.397	0.159	1.872	0.731	NA	0.658
RW	Pygmy	F	NA	NA	NA	NA	NA	NA
RW	Yellowmouth	F	NA	NA	NA	NA	NA	NA
RW	Yelloweye	T	-1.082	-0.14	1.906	0.1	NA	-0.083
RW	Sharpchin	T	0.411	0.296	2.659	0.579	NA	0.671
free	Silvergray	F	NA	NA	NA	NA	NA	NA
free	Darkblotched	T	-2.788	0.262	0.906	0.783	0.296	0.186
free	Splitnose	F	NA	NA	NA	NA	NA	NA
free	Greenstriped	F	NA	NA	NA	NA	NA	NA
free	Widow	F	NA	NA	NA	NA	NA	NA
free	Yellowtail	T	-1.826	0.513	2.706	0.874	0.155	0.305
free	Chilipepper	F	NA	NA	NA	NA	NA	NA
free	Blackgill	F	NA	NA	NA	NA	NA	NA
free	Vermilion	F	NA	NA	NA	NA	NA	NA
free	Bocaccio	F	NA	NA	NA	NA	NA	NA
free	Redstripe	T	-0.267	-0.231	3.845	0.529	0.261	0.61
free	Redbanded	F	NA	NA	NA	NA	NA	NA
free	Stripetail	F	NA	NA	NA	NA	NA	NA
free	Harlequin	F	NA	NA	NA	NA	NA	NA
free	Pygmy	F	NA	NA	NA	NA	NA	NA
free	Yellowmouth	F	NA	NA	NA	NA	NA	NA
free	Yelloweye	T	-1.082	-0.14	1.87	0.145	0.646	-0.086
free	Sharpchin	T	0.411	0.296	3.354	0.674	0.335	0.671
fixed	Silvergray	T	0.414	-0.319	2.47	0.649	NA	0.458
fixed	Darkblotched	T	-2.789	-0.262	0.51	0.596	NA	0.19
fixed	Splitnose	F	NA	NA	NA	NA	NA	NA
fixed	Greenstriped	T	-2.483	0.314	0.711	0.204	NA	0.092
fixed	Widow	F	NA	NA	NA	NA	NA	NA
fixed	Yellowtail	T	-1.825	0.513	2.303	0.654	NA	0.317
fixed	Chilipepper	F	NA	NA	NA	NA	NA	NA
fixed	Blackgill	F	NA	NA	NA	NA	NA	NA
fixed	Vermilion	F	NA	NA	NA	NA	NA	NA
fixed	Bocaccio	F	NA	NA	NA	NA	NA	NA
fixed	Redstripe	T	-0.268	0.231	3.539	0.366	NA	0.611
fixed	Redbanded	T	0.766	0.196	1.255	0.142	NA	0.251
fixed	Stripetail	F	NA	NA	NA	NA	NA	NA
fixed	Harlequin	T	0.397	-0.159	2.247	0.707	NA	0.658
fixed	Pygmy	T	-3.917	0.607	0.278	0	NA	0.417

|								
fixed	Yellowmouth	T	-1.922	0	1.934	0.612	NA	0.389
fixed	Yelloweye	T	-1.082	-0.14	1.904	0.101	NA	-0.083
fixed	Sharpchin	T	0.41	-0.296	2.858	0.57	NA	0.671
RW	M=0.1	T	-0.267	0.231	3.02	0.333	NA	0.611
RW	M=0.092	T	0.397	0.159	1.872	0.731	NA	0.658
RW	M=0.07	T	-1.284	0.303	1.58	0.556	NA	0.328
RW	M=0.06	T	0.855	0.206	1.284	0.199	NA	0.317
RW	M=0.05	T	0.265	0.303	2.268	0.651	NA	0.458
RW	M=0.02	T	-1.082	-0.14	1.906	0.1	NA	-0.083
RW	M=SC	T	0.411	0.296	2.659	0.579	NA	0.671
free	M=0.1	T	-0.267	-0.231	3.845	0.529	0.261	0.61
free	M=0.092	F	NA	NA	NA	NA	NA	NA
free	M=0.07	T	-1.284	0.303	1.716	0.604	0.666	0.328
free	M=0.06	F	NA	NA	NA	NA	NA	NA
free	M=0.05	F	NA	NA	NA	NA	NA	NA
free	M=0.02	T	-1.082	-0.14	1.87	0.145	0.646	-0.086
free	M=SC	T	0.411	0.296	3.354	0.674	0.335	0.671
fixed	M=0.1	T	-0.268	0.231	3.539	0.366	NA	0.611
fixed	M=0.092	T	0.397	-0.159	2.247	0.707	NA	0.658
fixed	M=0.07	T	-1.284	0.303	1.65	0.546	NA	0.328
fixed	M=0.06	T	0.854	0.206	1.379	0.211	NA	0.317
fixed	M=0.05	T	0.417	0.325	2.469	0.652	NA	0.458
fixed	M=0.02	T	-1.082	-0.14	1.904	0.101	NA	-0.083
fixed	M=SC	T	0.41	-0.296	2.858	0.57	NA	0.671

Supplementary Figures
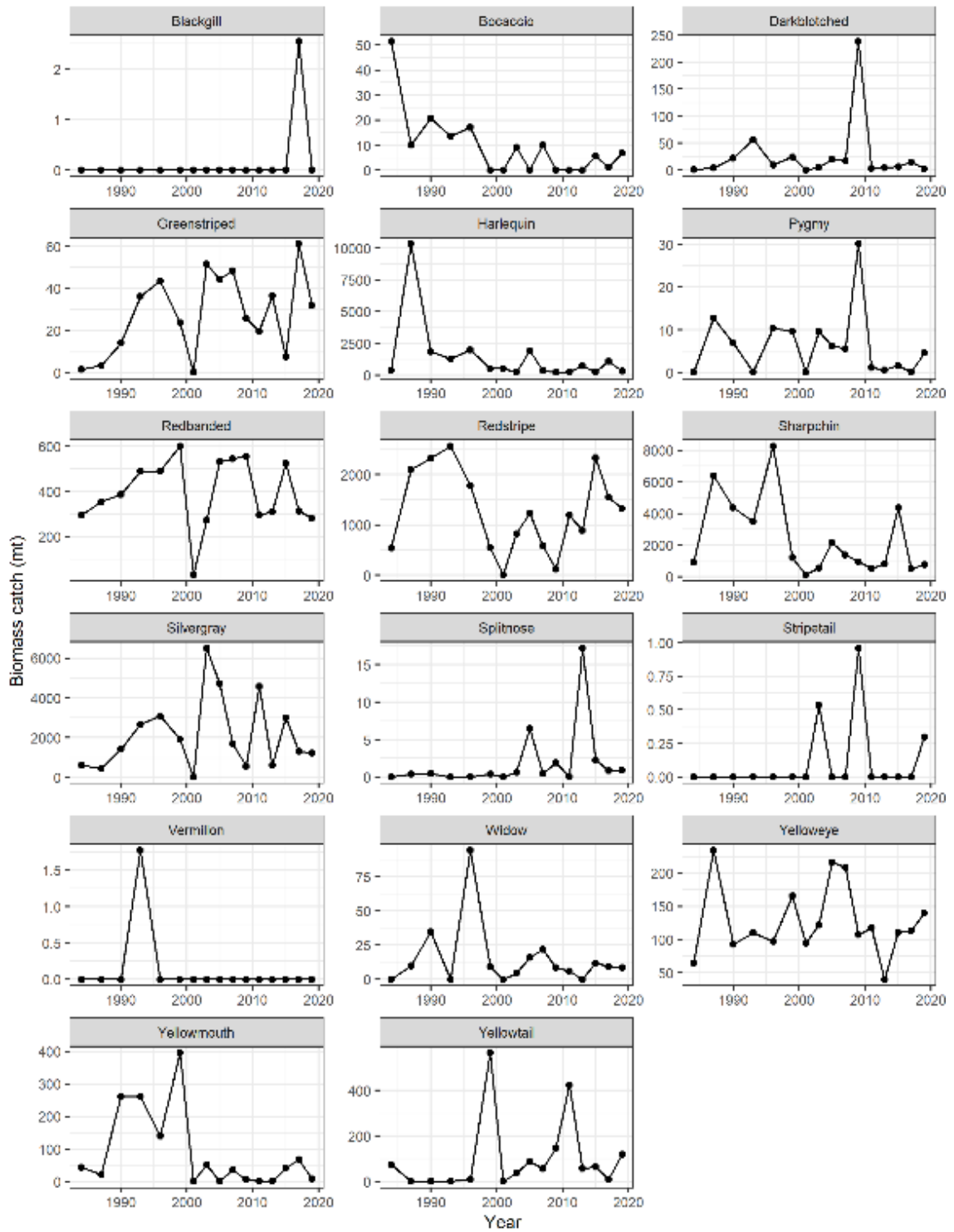
Fig. SM1. Raw total biomass (metric tons, mt) caught in the NMFS bottom trawl survey for each species.
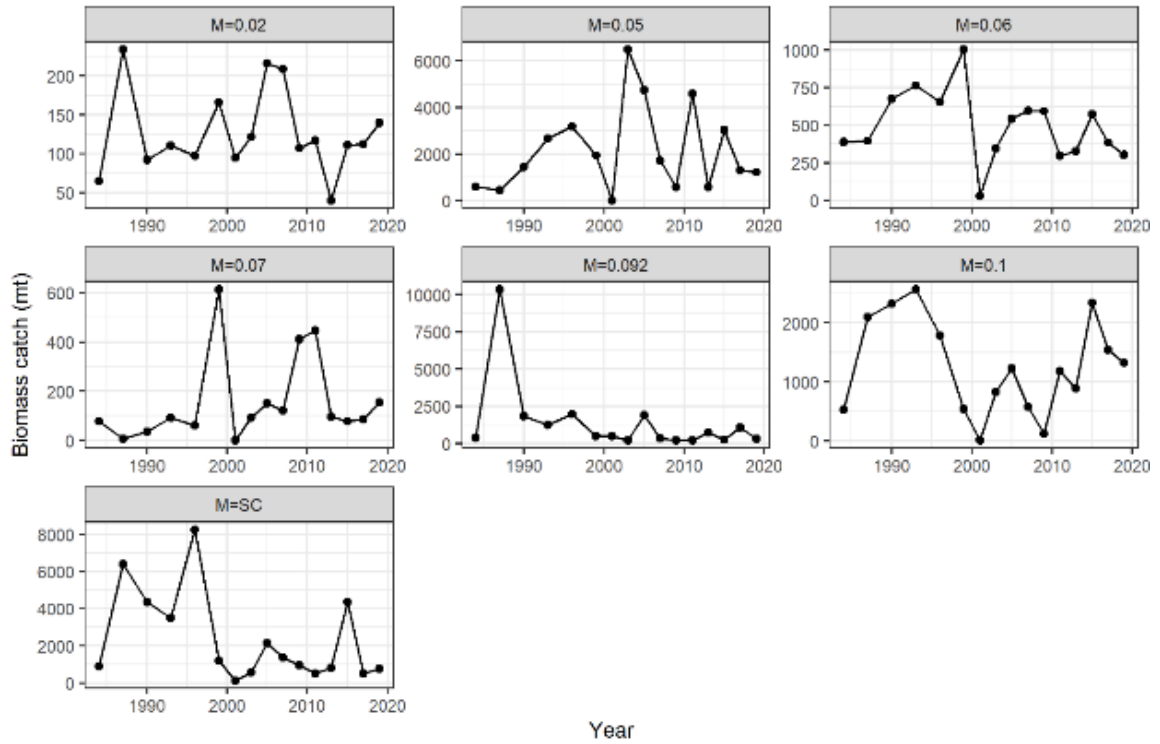
Fig. SM2. Raw total biomass (metric tons, mt) caught in the NMFS bottom trawl survey for each species natural mortality (*M*) group.
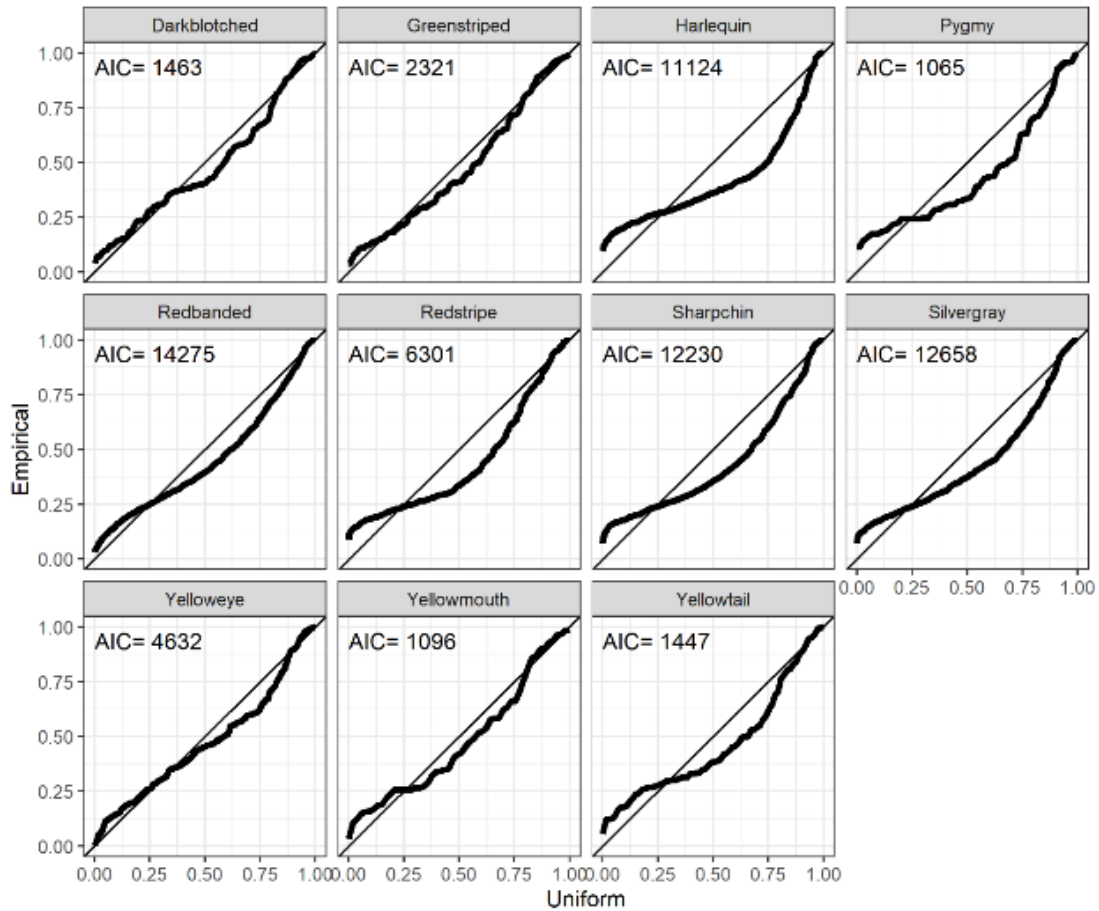
Fig. SM3a. Q-Q plots and AIC values for individual species VAST-RW models from the base 2019 models.
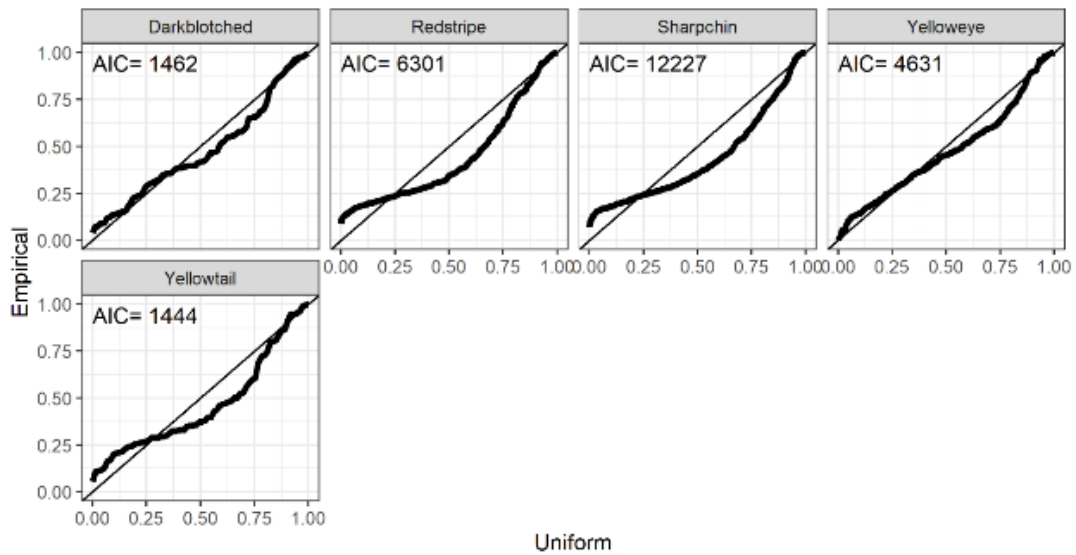

Fig. SM3b. Q-Q plots and AIC values for individual species VAST-free models from the base 2019 models.

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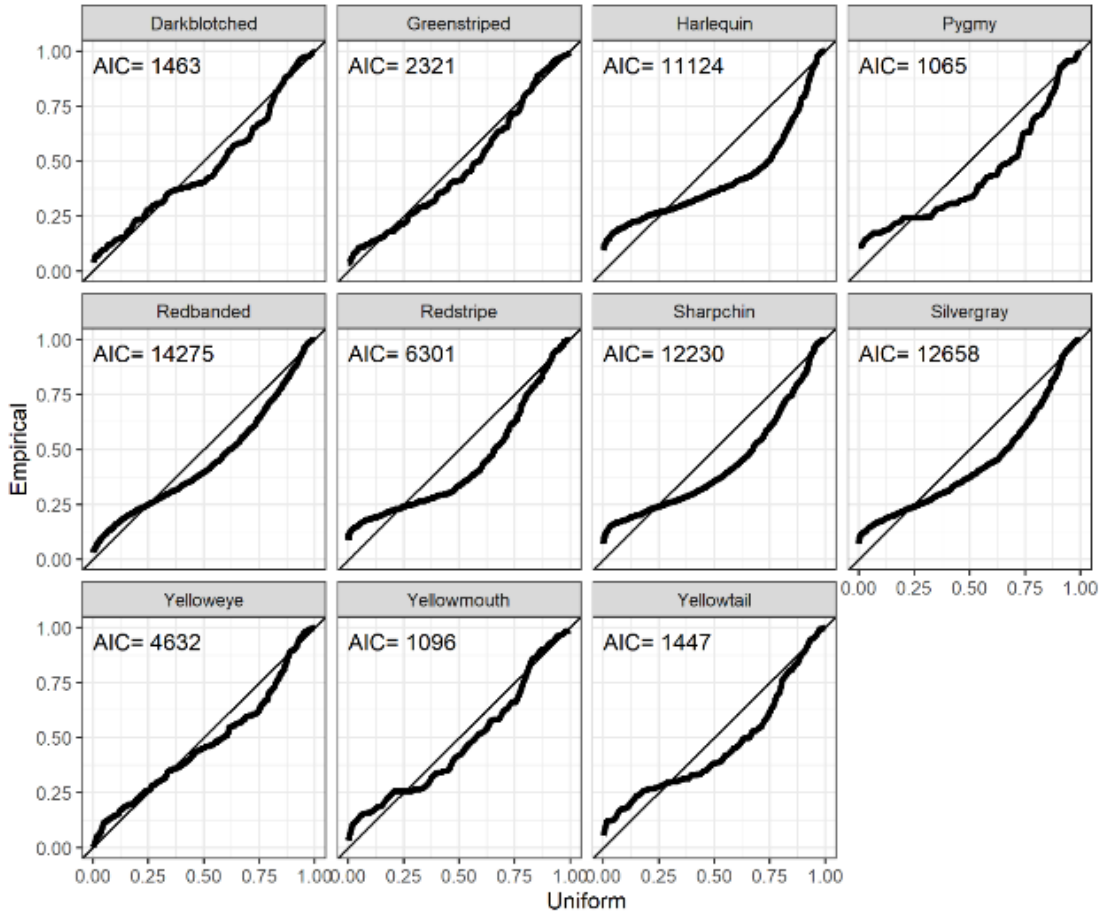**Fig. SM3c.** Q-Q plots and AIC values for individual species VAST- fixed models from the base 2019 models.

Fig. SM3d. Q-Q plots and AIC values for *M* group VAST- RW models from the base 2019 models.
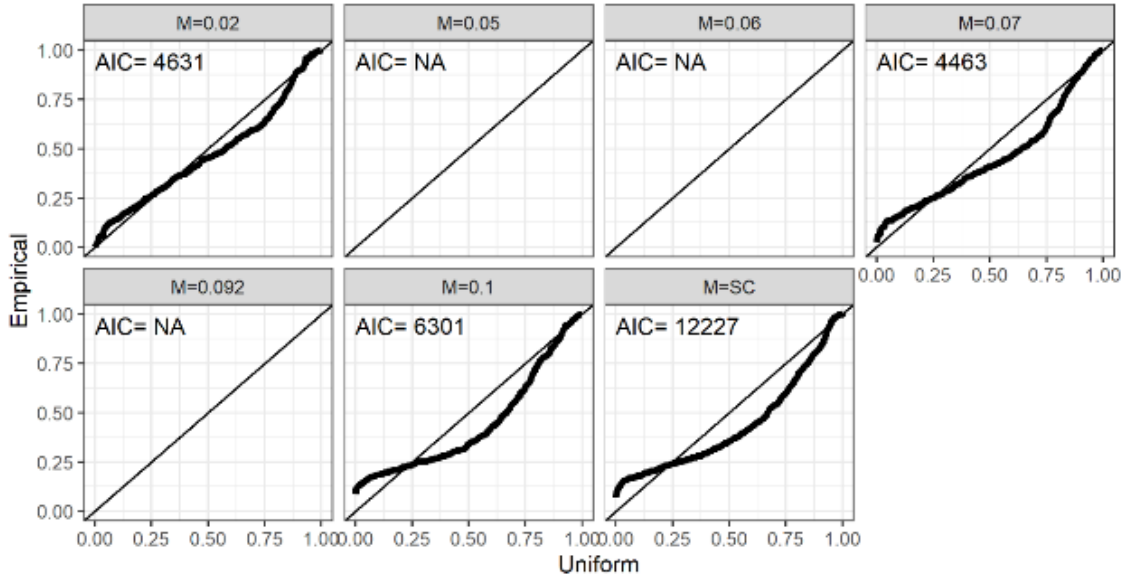
Fig. SM3e. Q-Q plots and AIC values for *M* group VAST- RW models from the base 2019 models.
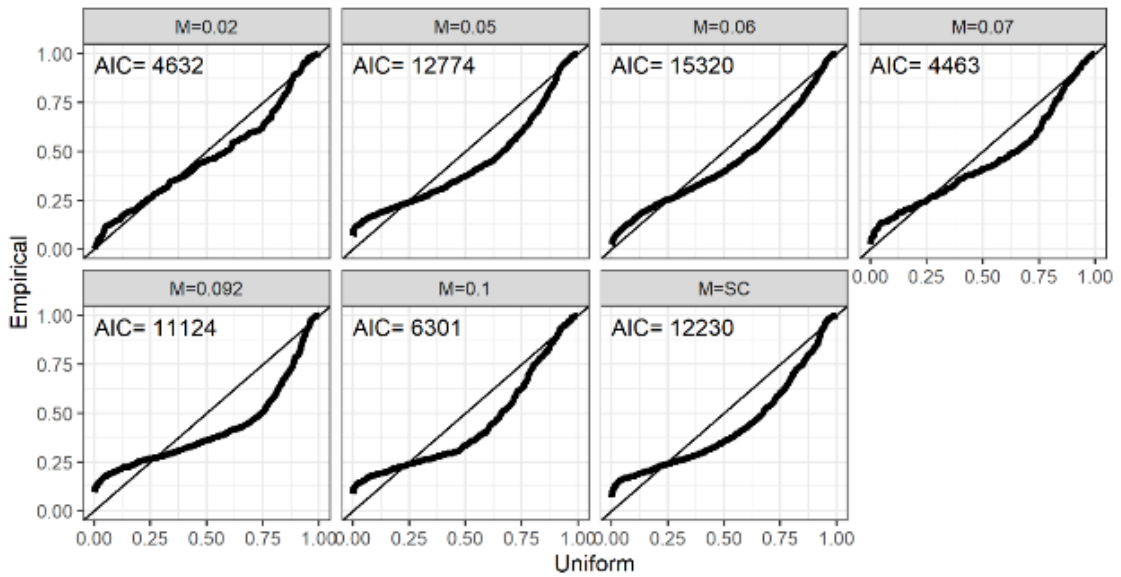
Fig. SM3f. Q-Q plots and AIC values for *M* group VAST- fixed models from the base 2019 models.

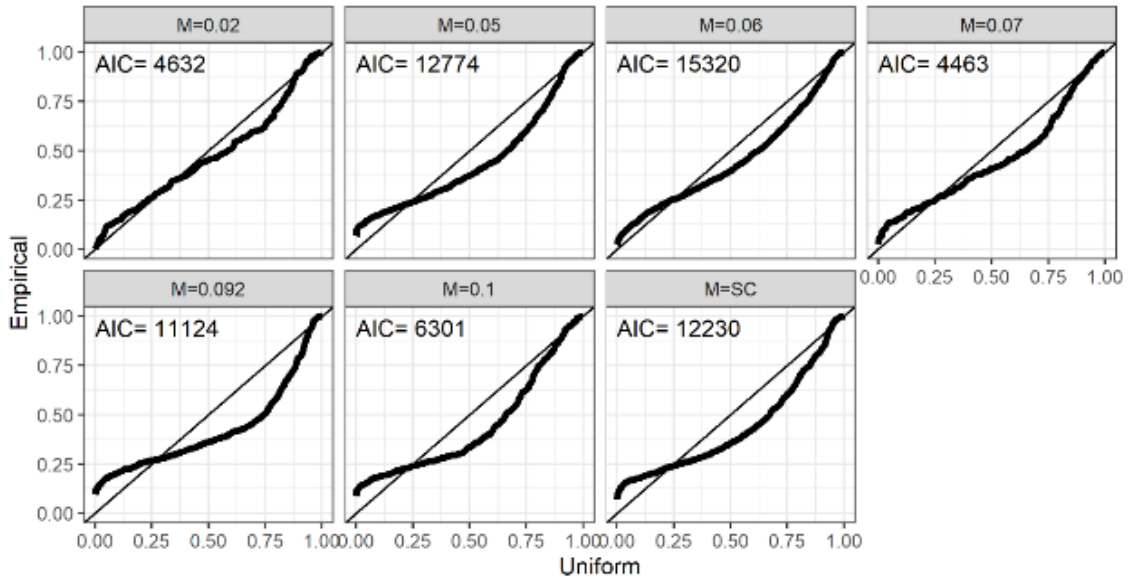**Fig. SM4a.** Biomass estimates (in 1000 metric tons, mt) from each model (random effects [RE], VAST-fixed, VAST-free, and VAST-RW) and individuals, darkblotched, silvergray, splitnose, and widow, showing the retrospective pattern.

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Fig. SM4b. Biomass estimates (in 1000 metric tons, mt) from each model (random effects [RE], VAST-fixed, VAST-free, and VAST-RW) and individuals, harlequin, redbanded, redstripe, and yellowtail, showing the retrospective pattern.

Fig. SM4c. Biomass estimates (in 1000 metric tons) from each model (random effects [RE], VAST-fixed, VAST-free, and VAST-RW) and individuals, greenstriped, pygmy, sharpchin, yelloweye, and yellowmouth, showing the retrospective pattern.

Fig. SM4d. Biomass estimates (in 1000 metric tons, mt) from each model (random effects [RE], VAST-fixed, VAST-free, and VAST-RW) and M groups, M= 0.6, M= 0.07, M= 0.092, and M= 0.1, showing the retrospective pattern.

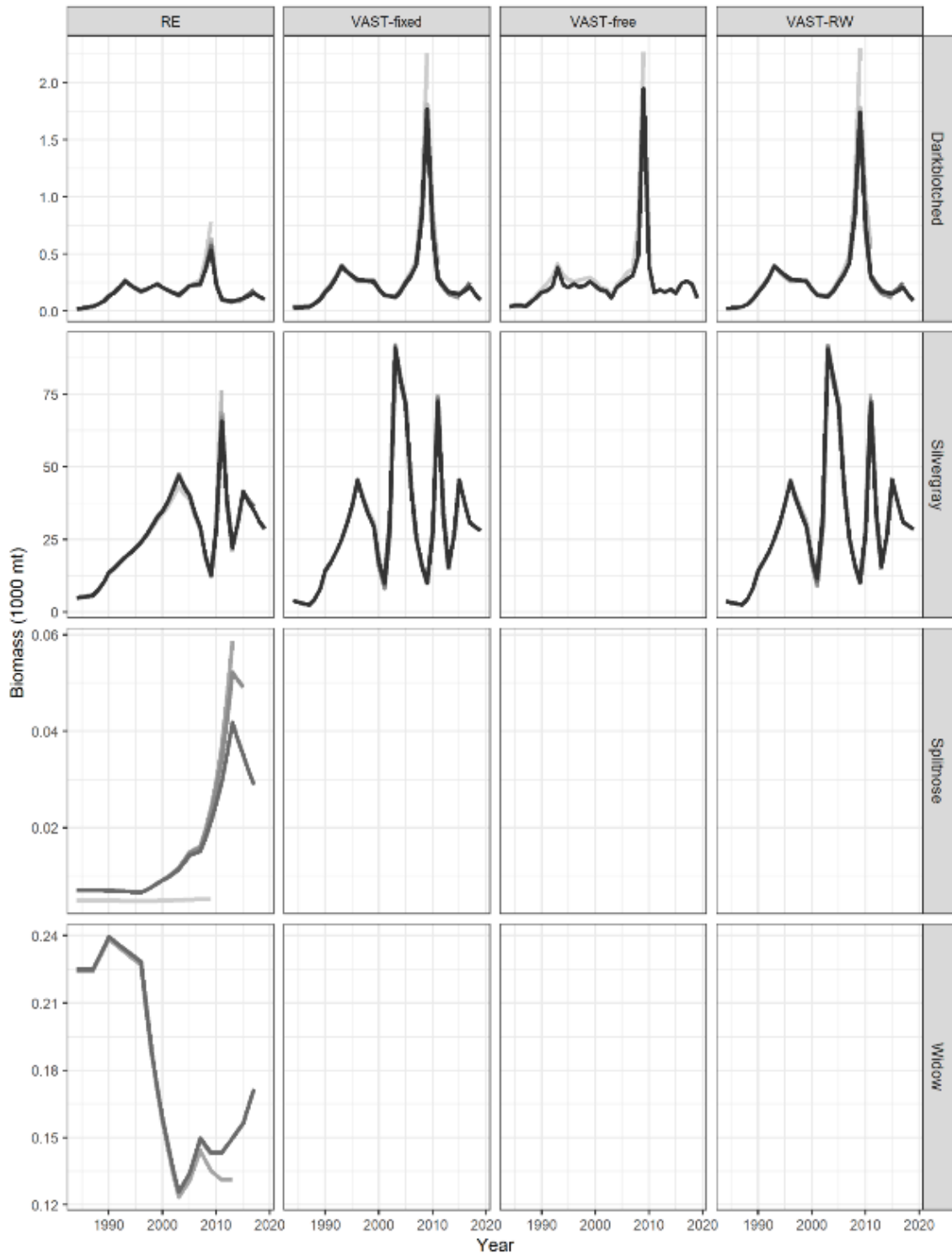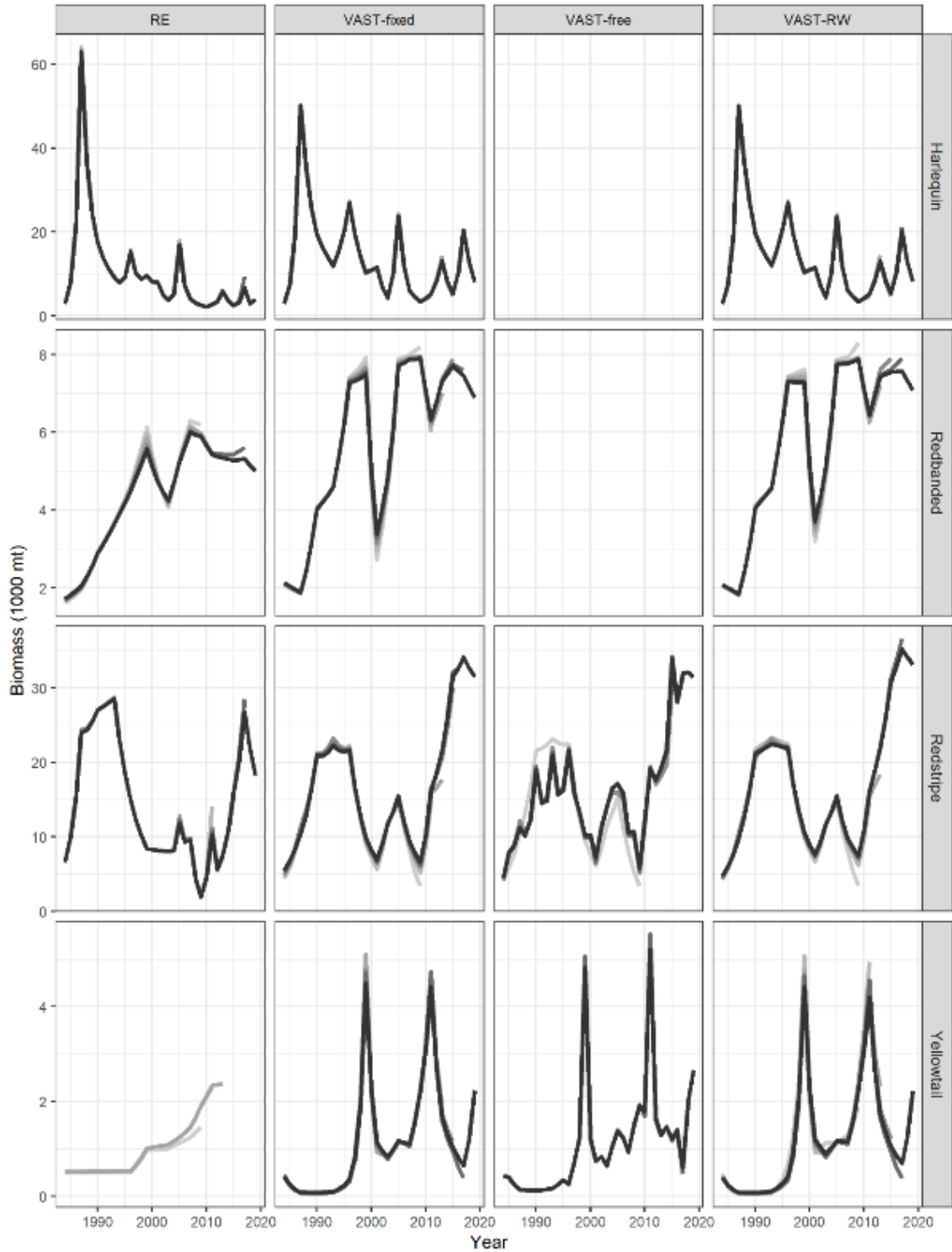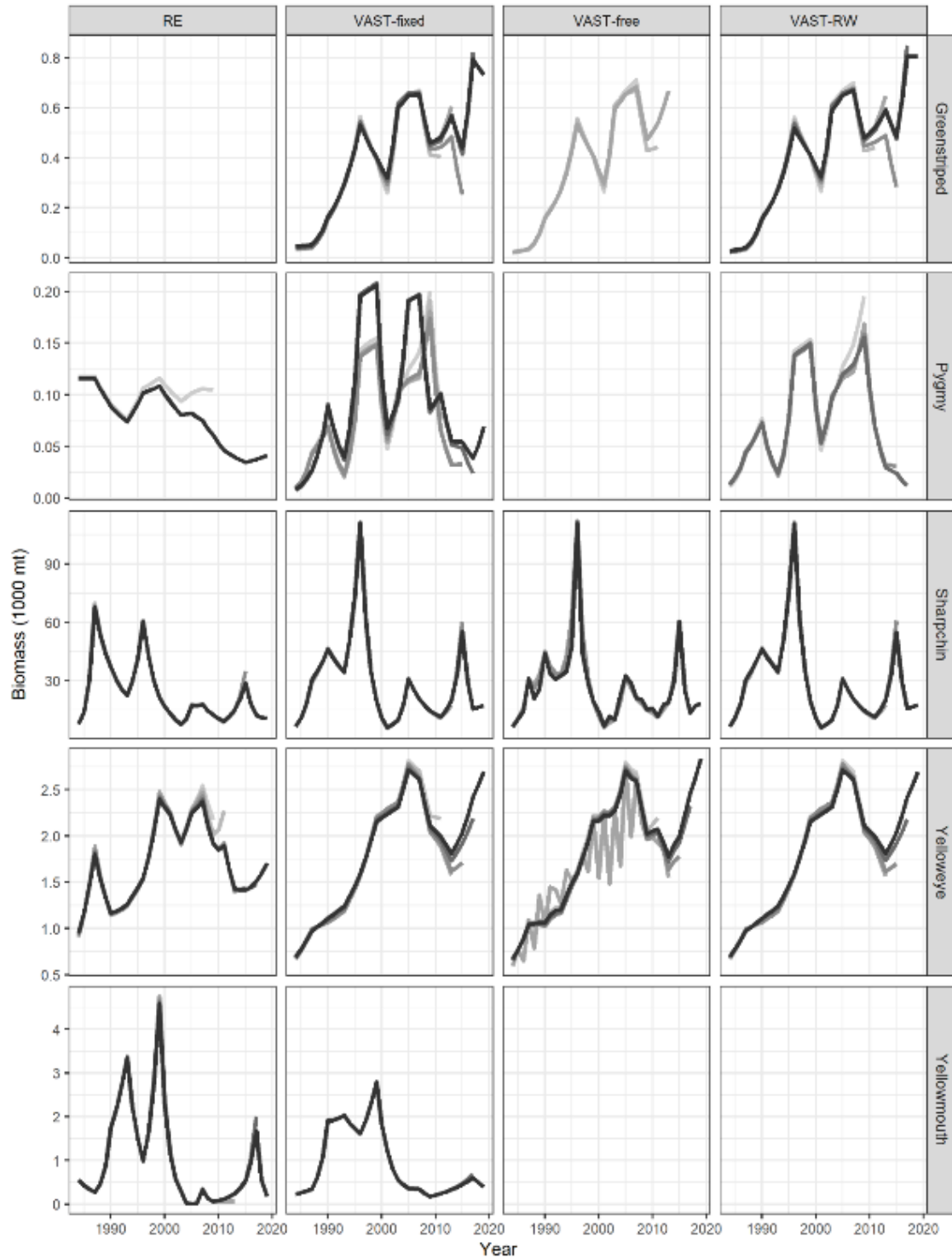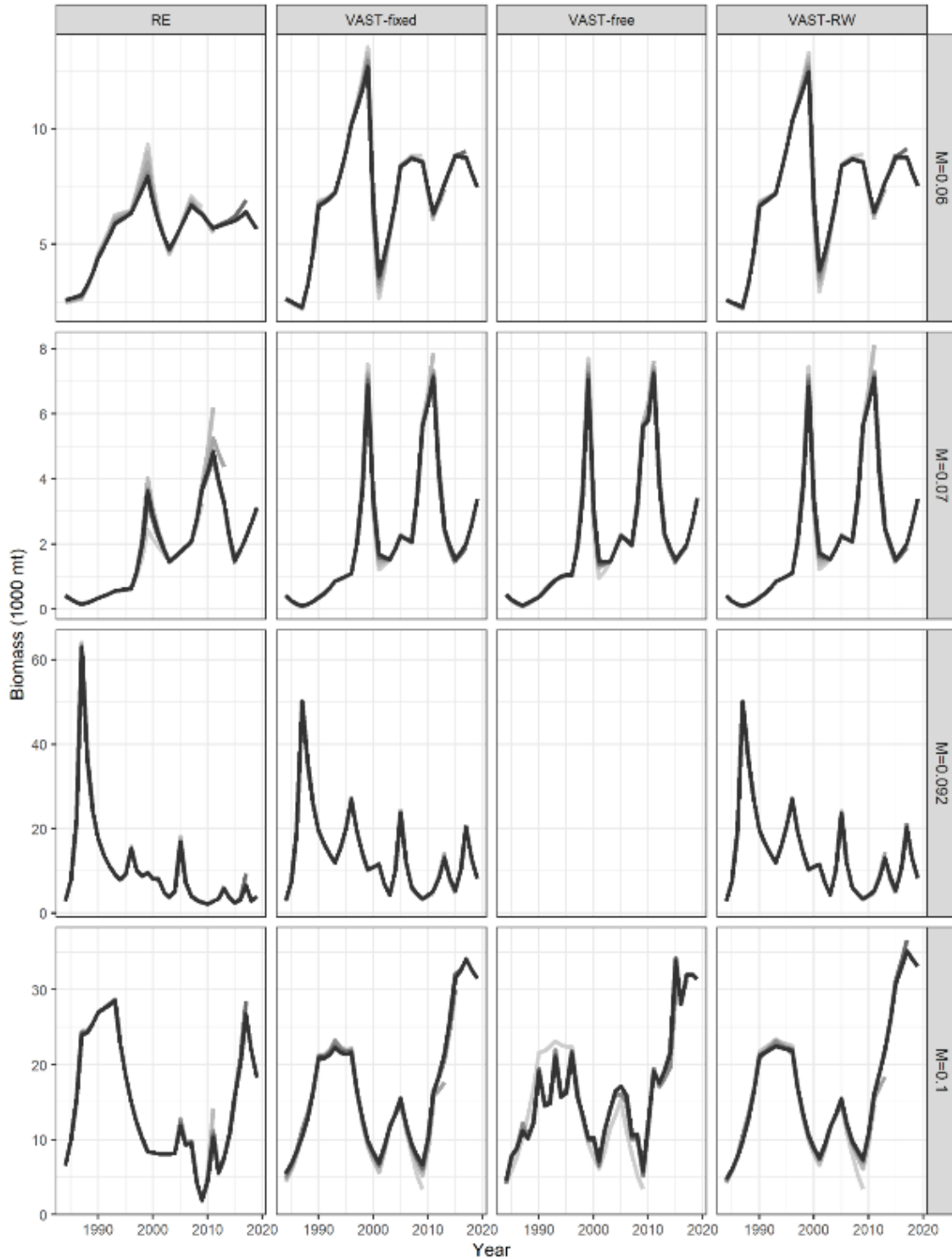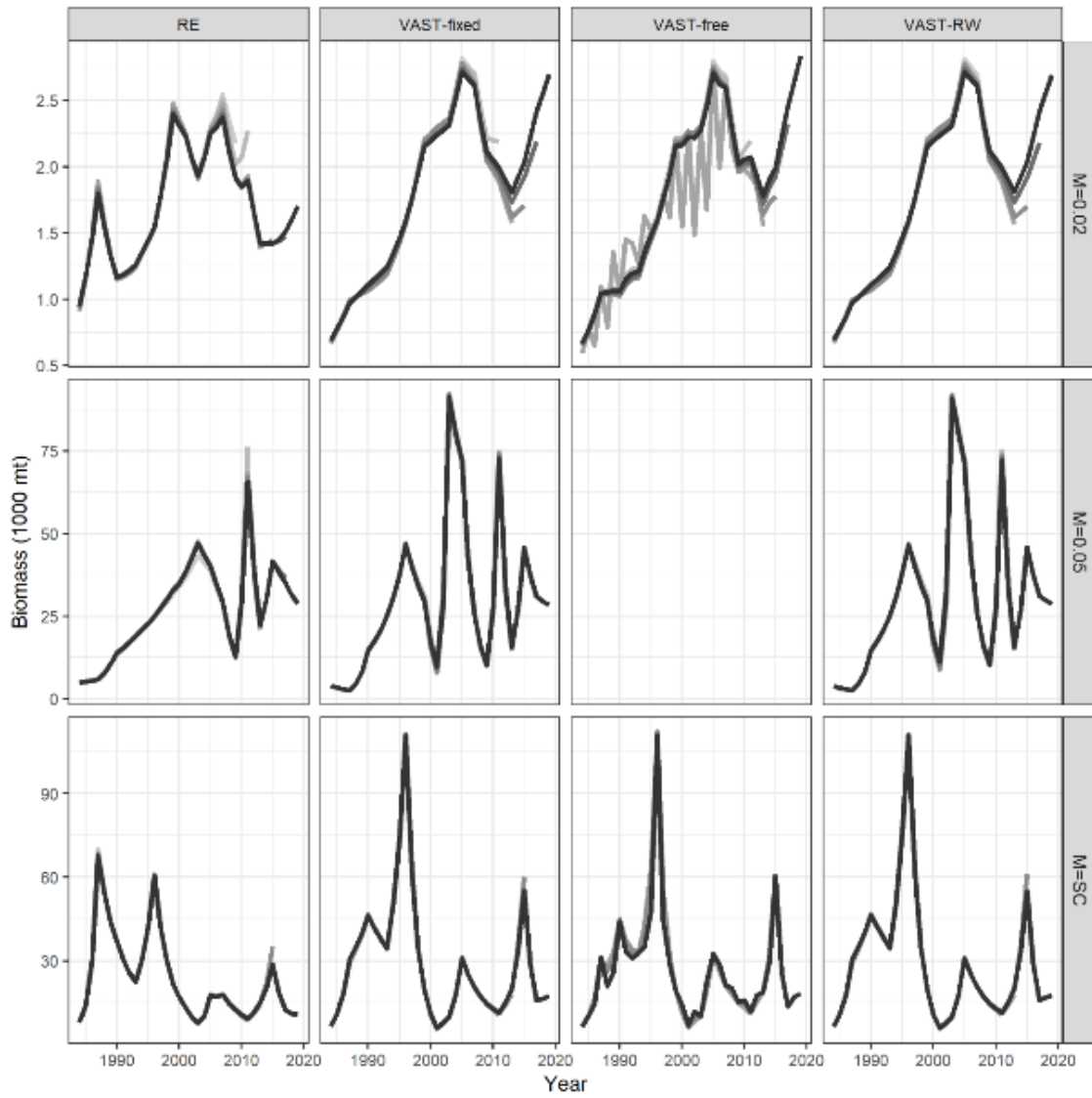**Fig. SM4e.** Biomass estimates (in 1000 metric tons, mt) from each model (random effects [RE], VAST-fixed, VAST-free, and VAST-RW) and M groups, M= 0.02, M= 0.05, and M= SC, showing the retrospective pattern.

CHAPTER 5

Conclusions

The role of stock assessment scientists is to provide the best estimate of sustainable harvest levels possible given the data constraints of the species being assessed and managed. However, for species with limited data or that are not directly targeted, scientists must make recommendations to stakeholders and managers based on limited information. Despite the large number of data-limited stocks worldwide, relatively few analytical methods exist to assign species to complexes and also provide direct management advice. Thus, the development of new approaches that can help fisheries managers make informed decisions on how to best harvest a species complex can be useful for a variety of management situations globally. The methodology developed in this dissertation provides tangible steps towards a robust and integrated framework for identifying species complexes and providing direct management advice.

5.1 Development of Novel Methodology for Grouping and Assessing Species Complexes

Because species are often managed as a complex due to limited data being available or reduced economic value compared to target species, the process of assigning species to complexes is oftentimes not treated as thoroughly as a full stock assessment. Typically, a productivity-susceptibility analysis (PSA; Patrick et al., 2010; Hordyk and Carruthers, 2018) or expert judgement provides a preliminary determination of species assignment, but such assignments should be verified using more thorough analytical approaches. The methodology developed here demonstrates how a variety of multivariate techniques can be combined with species distribution models to provide a more thorough and holistic determination of appropriate species complex groupings compared to using

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only a single analytical or qualitative approach. The explicit demonstration of the importance of using and comparing a variety of species assignment methods, which can help to better elucidate patterns of association that may not be obvious from a single methodology (e.g., looking only at life history characteristics or spatio-temporal patterns in abundance), is, perhaps, the most valuable contribution of the current research. Using both broad-scale (low spatial resolution) and fine-scale (high spatial resolution) methods and incorporating multiple datasets provides a well-rounded assessment on the spatial overlap and fishery susceptibility similarities (or dissimilarities) among species. But, determining the important factors (e.g., gear type, life history characteristics, and habitat preferences) that can be used to group species can be difficult, especially for rare species. In such instances, spatio-temporal overlap of species may be a useful indicator of species that may warrant grouping into a complex, because species that share common distributions often encounter similar biotic, abiotic, and anthropogenic perturbations; although this is not often considered when defining species complexes. Thus, the inclusion of spatio-temporal models into the species complex analytical toolbox can be valuable.

A significant advancement for assigning and assessing species within complexes demonstrated by this study was the application of the spatio-temporal model, 'VAST', to the Gulf of Alaska (GOA) rockfish complex. This work represents one of the first applications of a species distribution model for the purpose of managing species complexes. There are multiple benefits associated with the application of VAST for species complexes, which include identifying spatiotemporal patterns in abundance that can be used to group species with common patterns, validating or comparing groupings

from existing or alternate species assignment approaches, and, ultimately, providing target harvest levels and management advice based on direct biomass estimates (e.g., when fitting to survey abundance data). Thus, the use of spatiotemporal models when developing and assessing species complexes provides a single integrated framework that provides species groupings as well as harvest advice, which can reduce the burden (i.e., need to utilize multiple models to assign then assess species complexes, as is currently required for the GOA Other rockfish complex) on scientists tasked with assessing and managing complexes.

A common problem for development of species complexes is how to treat species with high prevalence (i.e., frequently caught in all gear types in all spatial areas) along with rare species. In the case of species with wide spatial occupancy, spurious correlations can result with other species, simply because they overlap with less frequently observed species. Similarly, rare species may be difficult to assign to a complex, because infrequent observation may prevent identification of overlap with any other species. Although increased data collection, use of novel data (e.g., eDNA), and better emphasis on accurate species identification are always advisable for data-poor species, especially rare species, increased expenditures to improve data collection for these species is not always realistic. Thus, it is important to utilize as many species assignment approaches as possible to ensure consistency, especially for both ubiquitous and rarely observed species, then carefully analyze results across analytical approaches or data sources to determine why complex assignments may have differed. After complexes are identified, researching and testing potential assessment models and harvest control rules is the next critical step for providing catch advice. A variety of models should be

examined that maximize the data available for the species complex. Each assessment model has assumptions and caveats that should be explored to determine its robustness and reliability for determining the stock status of a given species complex. While data limitations can hinder the selection of models, applying models that use the full extent of the available data is important. Once again, the VAST framework can be a useful tool for determining biomass based on survey abundance data, which can then be directly used to set catch advice. Although not the only approach available for estimating the biomass of a species complex, the spatio-temporal modeling framework utilized in VAST is flexible and can be adapted to incorporate a variety of data types (e.g., both fishery-dependent and independent data and habitat covariates). Additionally, as noted previously and demonstrated by the current research, VAST can be used as a single, integrated modeling framework that can determine appropriate species complex groupings (Chapter 3) then be subsequently applied to determine biomass estimates and sustainable catch limits (Chapter 4).

Species are commonly grouped into a complex to reduce administrative or personnel burden when management advice is required for a large number of data-limited and non-target species. The methodology developed here for the GOA Other Rockfish complex provides a novel approach to assign and assess species complexes by thoroughly analyzing existing data using multiple analytical approaches. Although the specific analytical techniques that can be utilized will be context specific (i.e., mainly depending on the available data), the general approach can easily be adapted and should be more widely considered for other species complexes around the world. By using a wider array of clustering methods, more robust species groupings can be developed and

inconsistencies among methods can provide insight into which species may require more careful monitoring. In particular, it is highly recommended that species distribution models be more widely applied to identify species groupings based on consistent spatio-temporal patterns in abundance and to provide direct harvest advice from a single framework. Despite species groupings for GOA rockfish being similar across the methods utilized in this research (i.e., multivariate techniques and spatio-temporal models), it is not expected that this will be a common result for other species complexes. Additionally, the VAST models provided important insight into spatio-temporal patterns of abundance and appropriate harvest levels that could not otherwise be obtained from traditional multivariate grouping methods. Therefore, implementing spatio-temporal models when there is sufficient data represents an important advancement in the analysis of species complexes that can be widely utilized to improve management for non-target species worldwide.

5.2   Improving Species Complex Assignment for Gulf of Alaska Rockfish

The assessment and management of the GOA Other Rockfish complex evolves as new data and research are incorporated into the stock assessment process. Due to their low productivity and high vulnerability to overfishing (Ormeth and Spencer, 2011), the species belonging to the Other Rockfish complex require careful management that assimilates the array of data and analytical techniques available. The focus of this dissertation was to determine whether the species assignments to the Other Rockfish complex, which includes a subset of species that belong to the Demersal Shelf Rockfish complex in all but one management area in the GOA, were appropriate based on

development and application of new analytical techniques. Through the application of a variety of multivariate methods (*Chapter 2*) and fine-scale species distribution models (*Chapter 3*), this research demonstrated that the Other Rockfish complex species assignments were generally robust, but minor adjustments may be warranted to ensure sustainable management of each species. For instance, results suggest that the species comprising the Demersal Shelf Rockfish Complex should be separated from the Other Rockfish complex in all GOA management areas. Although the range of life history characteristics (e.g., maximum age and length at maturity) along with variation in survey biomass and fisheries catch make it challenging to manage the Other Rockfish complex, consistent patterns in species groupings across analytical approaches and data sources suggest that these species can likely be adequately managed as a single complex.

However, as is often the case when comparing species groupings across different data sources and methods, species assignments were not always consistent. While the application of multivariate methods on each fine-scale fisheries and survey catch datasets separately did not yield usable (i.e., stable or meaningful) results, analysis of the aggregated (i.e., combined into a single dataset by year, management sub-area, and gear type) dataset indicated that the species composition was different for each gear type. The combined method also allowed direct comparison of species groupings from the fishery versus survey data across gear types (i.e., trawl compared to longline gear). Here, the results demonstrated that the species composition from the trawl survey was similar to the species composition from the trawl fishery (i.e., non-pelagic trawl) in the GOA, whereas the species composition from the longline survey did not always represent the species composition in the longline fisheries (i.e., longline and jig). These results

demonstrated that the application of multiple multivariate analyses on multiple datasets is very important to capture relationships of all species in the complex. In comparison, the fine-scale species distribution model (i.e., spatio-temporal species distribution model; *Chapter 3*) was only applied to the trawl survey data, where the subset of rockfish from the Other Rockfish complex that were included in the analysis demonstrated spatial structure, but little temporal correlation. Based on the species distribution models, the spatial patterns among species that emerged were similar to those found using the multivariate approaches in *Chapter 2*, but there were no strong temporal relationships among species.

Although each approach provided interesting and slightly different insights into species groupings, the results were influenced by data availability. Thus, the species compositions and identified relationships between species were confined to those rockfish in the Other Rockfish complex that were most frequently caught. As with any data limited species, the ability to manage the Other Rockfish complex would be greatly enhanced by improved or increased data collection. Fortunately, species identification for the species belonging to the complex is not an issue, but little data are collected otherwise. Increased collection of length (or even age) composition data for these species would aid in developing improved life history characteristics, which are not well known for many of these species.

Results from *Chapter 2* and *Chapter 3* suggest that assignments to the Other Rockfish and Demersal Shelf Rockfish are appropriate, but the species comprising the Demersal Shelf Rockfish Complex should be separated from the Other Rockfish complex in all GOA management areas. The species in the Demersal Shelf Rockfish complex are

caught by different gears and occupy different habitats throughout the GOA. In the case of GOA Other Rockfish, yelloweye rockfish provides an interesting example of a ubiquitous species that has important influence on species assignments between the Other Rockfish and Demersal Shelf rockfish complexes. Currently yelloweye is assigned to the Demersal Shelf Rockfish complex, constituting the majority of the catch for the Demersal Shelf Rockfish group, but it is caught in all gear types and is distributed Gulf-wide (Tribuzio and Echave, 2019). Conversely, canary and yellowtail, both infrequently caught, consistently grouped together in all analyses, despite being assigned to separate complexes for the GOA management area 650. Based on the combined results of the variety of analytical species assignment methods (i.e., based on groupings using life history characteristics, harvest levels, and spatiotemporal patterns in abundance), yellowtail rockfish could either be considered for reassignment (i.e., move to the Demersal Shelf Rockfish complex) or remain in the Other Rockfish complex, but it should be closely monitored due to its strong association with canary. The difficulties associated with assigning a species, such as yelloweye and yellowtail, to a complex demonstrates how species complex assignment is an ever-evolving process that warrants periodic reevaluation as new data and new methodology become available. Much like the application of traditional stock assessment models, species complex assignments should be reanalyzed every few years and not treated as long-term static decisions.

The spatio-temporal VAST model proved to be a useful alternative assessment approach for the Other Rockfish complex (*Chapter 4*), but harvest recommendations differed moderately depending on the assessment model used (i.e., VAST versus the currently utilized random effects model) and whether species were modeled individually

or grouped by natural mortality levels (*M* groups). The comparison across assessment approaches undertaken in *Chapter 4* suggested that the Other Rockfish complex should continue to be assessed by grouping species with similar *M* values (i.e., utilizing *M* groups). The grouped assessment approach incorporates the full extent of survey biomass data and allows incorporation of species that would otherwise go unassessed into the total catch advice for similar species groups, given that many of the Other Rockfish species do not have sufficient data for individual species assessments. Likewise, calculating catch limits based on *M* groups, where the average *M* values were calculated across fewer species with more consistent life history characteristics compared to a single average *M* value for the entire complex (i.e., as is currently assumed in the random effects GOA Other Rockfish management advice), was deemed more practical. It is expected that using multiple *M* groupings in which species maintain consistent natural mortality rates better reflects the population dynamics of individual species, thus providing a more accurate estimate of fishable biomass for the complex as a whole and more appropriate catch targets.

The species being considered for inclusion in the Other Rockfish complex present challenges for identifying relationships among species that can be used to develop appropriate groupings and, ultimately, provide sustainable management advice. These non-target rockfish in the GOA occupy a range of habitat types and demonstrate a variety of behaviors and life history characteristics (Johnson et al., 2003; Conrath et al., 2019). Although the range of analyses presented attempted to utilize the full extent of available fishery and fishery-independent data covering the variety of habitat types and spatial areas occupied by these species, there were many species that could not be included in

various analyses because insufficient data was available. Moving forward, the Other

Rockfish assessment can potentially be improved if other fishery-independent survey data

aside from the trawl survey are included in the model. Unfortunately, the trawl survey

only covers low relief, trawlable habitat, whereas the longline surveys (e.g., NOAA

longline survey and the International Pacific Halibut Commission longline survey) cover

untrawlable habitat and would provide increased spatial coverage. The flexible,

integrated nature of the VAST framework allows incorporation of a variety of data

sources, and longline data could be incorporated into the assessment models developed

here, thereby providing more comprehensive data inputs that could be particularly useful

for rare species that could not be included in the models developed in the current

analyses. Additionally, other alternative surveys, such as using automated underwater

vehicles (AUV), could also help fill in spatio-temporal data gaps for the Other Rockfish

complex.

5.3   The Future of Species Complexes

Species will continue to be managed as complexes due to the number of data-

limited species that either do not have sufficient data for single-species assessments, have

species identification issues, or simply due to personnel or funding limitations that

necessitate reducing the number of single species assessments being conducted by a

given institution (Koutsidi et al., 2016). However, the management of a complex is only

as good as the information used to define the groupings (Fujita et al., 1998). The species

within a complex should be periodically monitored to ensure species-specific populations

are not declining due to mis-specified species membership. Additionally, as fish

populations move poleward or to different areas (e.g., deeper waters) due to shifts in climatic conditions (e.g., Perry et al., 2005; Pinsky et al., 2013), species assignment to complexes and the assessment of the complexes must be carefully monitored and refined based on the most current information available. Incorporating new or unused data sets (e.g., life history characteristics along with a variety of fishery-dependent and independent data) will be vital to identifying changes in abundance and distributions for species complexes as well as the appropriateness of species groupings given differential responses to ecological and environmental perturbations.

It is also important to consider that directed fishery species can be impacted by the catch limits set for non-target species complexes. Setting low quotas for non-target species can lead to these species becoming "choke" species that may impede obtaining the full quota for the target species (Schrope, 2010; Batsleer et al., 2015). While setting catch advice for species complexes should not be influenced by catch levels for target species (i.e., the goal should be sustainable catch levels for all species), incorporating socioeconomic considerations into harvest control rules for non-target species complexes can help provide a different management strategy and bridge the goals of sustainable yields with maximizing economic return.

The methodology outlined here, wherein a variety of multivariate and spatiotemporal models were utilized to determine species groupings and then VAST models were used to estimate group biomass, represents a tangible step forward in understanding the dynamics of species complexes despite the limited data available. The flexibility of spatiotemporal models, such as VAST, to incorporate myriad datasets, while also providing descriptions of spatiotemporal changes or overlap (i.e., when comparing

across species) in distribution, will be useful for many situations worldwide where managing species complexes is necessitated by the preponderance of data limited and nontarget species. As national and international legislation continues to urge quantitative catch advice for all species caught in commercial fisheries, including non-target species, the need to define, implement, assess, and manage species complexes will only expand. The methodology and research presented here provides a useful framework that can be easily adapted to assign species to groups, while also providing direct management advice. Although the tools and data utilized to manage species complexes will necessarily expand and be refined, the methods developed here should provide a useful baseline framework to use for researchers endeavoring to define new species complexes or test the robustness of current species complex delineations.

5.4   References

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