# Appendix A. Movement Model of the Dover Sole in the Gulf of Alaska 

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## Introduction

This appendix demonstrates the advantages and challenges of using a two-area statistical catch-at-age model including a shallow area $(0-500 \mathrm{~m})$ and a deep area $(500 \mathrm{~m}-1000 \mathrm{~m})$ to assess Gulf of Alaska (GOA) Dover sole (Microstomus pacificus).This population exhibits ontogenetic movement to deeper water with age. Evidence suggests that fish do not appear in deeper water until older ages. In addition, older cohorts in the population (generally pre-1977 cohorts) did not appear to grow as large as more recent cohorts (Figure 1). The models presented here are "research-phase" models meant to explore the data and hypotheses about the growth and movement dynamics of the stock.

One challenge of assessing GOA Dover sole using a single-area model is that survey coverage was inconsistent over time. In particular, in 1990, 1993, and 1996, the GOA trawl survey covered only depths up to 500 m . This sampling scheme likely missed a disproportionate amount of older Dover sole. This inconsistency is currently taken into account in single area models by using a random walk, random effects model that fills in the gaps in the $500-1000 \mathrm{~m}$ biomass index data. Under this approach, models are set up such that 1990, 1993, and 1996 length- and conditional age-at-length data are associated with a separate set of selectivity curves than for the other survey years. The separate set of selectivity curves is then only informed by three years of data, where in reality, composition data exist for all years of data for the $0-500 \mathrm{~m}$ depths.

A second challenge for this assessment is the clear cohort-specific growth pattern affecting the maximum length of fish. The 2017 GOA rex sole assessment (McGilliard et al. 2017) showed that a lack of accounting for spatially-varying growth can lead to major bias in the assessment, especially when one or more sources of age-composition data are unavailable. As for GOA rex sole before 2017, there are no fishery age data for GOA Dover sole. The cohort-specific growth pattern for Dover sole appears also as a spatial pattern in growth because of the ontogenetic movement dynamics of the stock. In addition, it appears that Dover sole in the Eastern GOA are smaller and younger than Dover sole in the Western and Central GOA (Figure 2, Figure 3, and Figure 4).

A movement model of GOA Dover Sole has the potential to address both of these challenges. By partitioning the data into a 'shallow' $(0-500 \mathrm{~m})$ and 'deep' ( $501-1000 \mathrm{~m}$ ) strata, the information from the shallow region of the survey can be used across all survey years to inform estimation of selectivity for 0500 m depths (rather than depending only on data from 1990, 1993, and 1996 where only $0-500 \mathrm{~m}$ depths were sampled). In addition, partitioning the stock into two areas and allowing estimation of ontogenetic movement parameters within the model allows for estimation of growth by area, where newer cohorts (that appear larger at their current age than old fish from the older cohorts) are more abundant in $0-500 \mathrm{~m}$ depths and older cohorts (which appear smaller at old ages).

Ideally, assessment models attempting to estimate movement parameters would be fit to tagging data (in addition to other typical data sources), but tagging data are unavailable for Dover sole and are unlikely to be available in the future. McGilliard et al. 2014 show that it may still be possible to estimate movement
parameters when a clear ontogenetic movement pattern exists between areas, as these parameters are informed by length and age data. Small sample size, however, limits the information needed to estimate parameters associated with movement, selectivity, and growth, as well as natural mortality.

The models presented here require further research before they can be used for management purposes. This appendix presents results to date, discusses benefits and shortcomings of these models, and makes recommendations for future work.

## Data

# The movement model partitioned fishery catch, fishery length composition, survey index, survey length composition, and survey conditional age-at-length data into two strata: 'shallow' (0-500m) and 'deep' (501-1000m). See Tables 

Table 1 and Figure 5 for data source details.

## Fishery Data

Bottom depth data from the observer program have been recorded consistently since 1987 and values were extracted from the observer database (NORPAC) for each haul record. The retained extrapolated catch weights from each haul were partitioned into a shallow $(0-500 \mathrm{~m})$ or deep $(501-1000 \mathrm{~m})$ category according to the record's associated bottom depth. Partitioned data were used to calculate a proportion of shallow versus deep catch retained each year. These proportions were then applied to catch data from the AlasKa Fisheries Information Network (AKFIN) database to calculate shallow versus deep annual catch. Prior to 1986, catch information from the NORPAC database included bottom depth measurements, but records were sporadic. Locations of fishery hauls to the nearest arc minute were therefore used to extract depth values from a Gulf of Alaska Bathymetric grid (Figure 7) using the NOAA National Centers for Environmental Information (NCEI) Southern Alaska Coastal Relief Model
(https://www.ngdc.noaa.gov/mgg/coastal/s_alaska.html). The same steps were then repeated for the pre1987 data. Extrapolated catch weights were partitioned into shallow and deep strata and used to calculate annual depth strata proportions which were applied to historical catch records, resulting in catch data partitioned into shallow versus deep strata for 1978 to 2019 (Figure 6).

Fishery length composition data were partitioned by first portioning the data into shallow and deep depth strata prior to calculating the proportions of males/females for each 2 cm length bin for each fishery year.

## Survey Data

Trawl survey indices (Figure 8) were partitioned by depth (shallow: <500m and deep: >500m). A random effects model was used to fill in missing area-depth gaps for each year as was done for the 2019 assessment, but for each separate shallow and deep depth categories. Original survey biomass index values were left unchanged when records were complete for a particular depth/area stratum and were only replaced with values and variances from the random effects model for missing strata. Data were then aggregated by year and the two depth strata $(0-500 \mathrm{~m}$ and $501-1000 \mathrm{~m})$.

Length composition data (Figure 9) and conditional age-at-length data (Figure 1) were partitioned into shallow and deep strata. Data were first partitioned by depth strata followed by calculations to determine the age distribution of male/females within each 2 cm length bin for each survey year.

Marginal age data (Figure 10) were excluded from the objective function (ghosted), but plotted along with predicted marginal age composition from the model for the purpose of comparison to assess model fits.

## Analytic Approach

## General Model Structure

The models in this appendix were implemented in Stock Synthesis (SS) version 3.30.13o (SS3.3) using a maximum likelihood approach, as for the 2019 Dover sole assessment model. The SS equations can be found in Methot and Wetzel (2013), and further technical documentation is outlined in Methot et al. (2019).

The GOA Dover sole movement models were based on a two-area model structure that partitioned the GOA into shallow ( $0-500 \mathrm{~m}$ ) and deep ( $501-1000 \mathrm{~m}$ ) areas. Recruitment was defined to occur only in the shallow area and movement was defined to occur only from shallow to deep. Two sex-specific growth patterns were defined such that only fish associated with the second growth pattern moved to the deep strata.

## Accounting for time-varying, cohort-specific growth within the movement models

Several models were run to explore hypotheses about GOA Dover sole ontogenetic movement characteristics, time-varying cohort-specific growth, and the interaction of the two. In the SS framework, it is possible to model more than one sub-population, each with a different growth curve, along with a parameter defining the proportion of fish that recruit to each sub-population. A sub-population may move among areas or may be associated with a particular area, but growth parameters are specific to subpopulations, not areas, even if movement occurs.

Older GOA Dover sole cohorts in the deep strata are thought to exhibit lower maximum lengths (they are smaller at age) than their younger counterparts in the shallow strata. It is unclear whether growth rates slow as fish move to the deep strata or if older cohorts are smaller at age for reasons extraneous to the model. The constraints in SS, however, limit the framework with which movement and growth can be defined, as growth is assigned to a sub-population, not an area. Therefore, it was necessary in SS to define sub-populations such that fish that moved to the deep area belonged to a separate sub-population than fish that remained in the shallow region. The proportion of the overall population that moved to the deep area could be estimated in two ways: 1) recruitment into the two growth patterns were held equal and movement rates from the shallow to the deep were estimated for the second growth pattern; or 2 ) the proportion of fish that recruited to the second growth pattern was estimated relative to the first growth pattern and all fish within this second growth pattern were required to move to the deep by age ten.

## Parameters Estimated Outside the Movement Models

The GOA bottom trawl survey catchability was set to 1 , female natural mortality was fixed at 0.085 , and the recruitment standard deviation was set equal to 0.49 . The weight-length and maturity-at-age relationships were defined using methods outlined in the 2019 assessment.

## Parameters Estimated Inside the Movement Model

Parameters estimated within the movement models were the log of unfished recruitment ( $R_{o}$ ), log-scale recruitment deviations, yearly fishing mortality, sex-specific parameters of the von-Bertalanffy growth curve, CV of length-at-age for ages 2 and 59, male natural mortality, and selectivity parameters for the fishery and survey. A two parameter double normal function without the descending limb was used to
define length-based selectivity in the fishery; an additional set of parameters were used to define male selectivity as an offset to females. A set of length-based selectivity parameters were estimated separately for the shallow and deep fishery. A two parameter double normal function without the descending limb was used to define age-based selectivity in the survey; an additional set of parameters were used to define male selectivity as an offset to females. A set of age-based selectivity parameters were estimated separately for the shallow and deep survey.

A two-parameter logistic function was used to define age-specific, time-invariant movement rates of Dover sole from the shallow to deep areas, with a parameter defining the movement rate at a specified young age (age 3 ) and at a specified older age (age 10). For all models presented in this appendix, the movement rate of age 3 fish was set to 0 and, for two of the three models, the movement rate of age 10 fish was estimated. Movement parameters were not sex-specific. Above the age of 10, the movement rate was held constant through to the maximum fish age of 59 at the value estimated for age 10, and below age 3 , the movement rate was set equal to 0 .

The distribution of recruitment by sub-population and area was estimated as the $\log$ of the proportion calculated for each subpopulation and area. Recruitment in the model was defined to be specific to the shallow strata. Under this model structure, the apportionment of recruitment to the deep strata for both sex-specific growth patterns was set to 0 , meaning that fish occupying the deep strata could only occur through a movement process. The distribution of recruitment was either set to be equal between the two sex-specific growth patterns or estimated inside the model.

## Description of Alternative Models

## Model 0

This model assumes that all fish have the same sex-specific growth pattern (1GP). Parameters of the vonBertalanffy growth curve from the 2015 stock assessment were used and growth was not estimated within the model. This model assumes that all recruitment occurs in the shallow area. Fish movement was defined to occur from the shallow to the deep with a minimum movement rate of 0 at age 3 and maximum movement rate at age 10 , after which the movement rate was held constant at the maximum value until the maximum fish age, 59 . This model represents the hypothesis that the population has one set of sexspecific, time-invariant growth patterns with all recruitment occurring in shallow areas, and some fish moving from shallow to deep as they grow older. Catchability is fixed at 1 for both areas.

## Model 1

This model proposes that two subpopulations occur in the GOA, each with sex-specific growth patterns (2GP), and a proportion of fish from the second sub-population moves to the deep. This model sets up two subpopulations (gp1 and gp2), each with a set of sex-specific parameters of the von-Bertalanffy growth curve, which were estimated inside the model. Recruitment was defined for each subpopulation to occur only in the shallow area. The 2GP model structure is illustrated in Figure 11 and describes a population where all recruitment occurs in the shallow area, all gp1 fish remain in the shallow area, and any gp 2 fish that move to the deep remain in the deep.

This model specifically determines the proportion of fish that move to the deep by estimating the movement rate of age $10+\mathrm{gp} 2$ fish inside the model. The recruitment distribution parameter used to estimate the proportion of the total population that recruited to gp1 versus gp2 was set so that recruitment was evenly distributed between the two sub-populations. Under this model framework, recruitment was equally distributed between the two sub-populations, and a proportion of fish from gp2 moved to the deep. This model represents the hypothesis that the population has two sets of sex-specific growth
patterns with all recruitment occurring in shallow areas, and some fish exhibiting small lengths at older ages move from the shallow to the deep as they grow older. This structure introduces the flexibility that allows an estimable proportion of fish that are smaller at old ages to remain in the shallow strata.

The male, gp2, von Bertalanffy $K$ parameter was inestimable because few data exist for the older, smaller fish when they were young and still growing. Therefore, the male and female $K$ parameters were fixed with values chosen as follows. All growth parameters were first estimated using models configured so that the same selectivity parameters were shared for each depth strata, that is, one set of sex-specific, length-based parameters were estimated for the entire fishery regardless of depth and one set of sexspecific, age-based selectivity parameters were estimated for the entire survey, regardless of depth. This was necessary in order to estimate the male, gp2, von Bertalanffy $K$ parameter (that was not on the bounds). This estimated value was then used for the male, gp2, von Bertalanffy $K$ parameter in Model 1.

## Model 2

This model assumes that the gp2 growth rate is exclusive to depths greater than 500m. Similar to Model 1 , this model sets up two subpopulations (2GP), each with a set of sex-specific parameters of the von Bertalanffy growth curve estimated inside the model. Recruitment was defined for each subpopulation to occur only in the shallow area. This model required all gp2 fish to move to the deep strata. This was achieved by determining the proportion of fish that moved to the deep by estimating the apportionment of recruitment between gp1 and gp2 inside the model, and setting the movement rate of age $10+$ fish in gp2 to 1 (ie. all gp2 fish move to the deep by age 10 ). This model represents the hypothesis that the population has two sets of sex-specific growth patterns with all recruitment occurring in shallow areas, and all fish that exhibit lower maximum size eventually move from the shallow to the deep by the age of 10 .

The male, gp2, von Bertalanffy $K$ parameter was inestimable inside the model (same issue as Model 1). As was done for Model 1, growth parameters were first estimated using models where selectivity parameters were shared among depth strata, that is, one set of sex-specific length-based parameters were estimated for the entire fishery regardless of depth and one set of sex-specific age-based selectivity parameters were estimated for the entire survey, regardless of depth. This resulted in a male, gp2, Bertalanffy $K$ parameter value that was used for the male, gp2, Bertalanffy $K$ parameter in Model 2 (and Model 1, as described above).

## Results

## Biomass Index

The 2019 assessment models and the movement models that assumed constant catchability $(q)$ and/or natural mortality $(M)$ could not capture the downturn in observed indices occurring in 2015 and onward. Time-varying $M$ and $q$ were not estimated in the movement models. It is expected that the estimation of these parameters inside the model would lead to a similar ability to fit the recent trends in survey biomass as for the 2019 assessment candidate models. Standard errors around index values for 2015 and later are likely underinflated due to the lack of information in the random effects model used to inform values for missing deep-area gaps.

## Estimation of growth, movement, and selectivity

Length and conditional age-at-length data are used to inform growth, movement, and selectivity parameters. Simultaneous estimation of these parameters, therefore, is challenging to achieve without tagging data. Dover sole exhibit ontogenetic movement and differences in growth between the shallow and deep areas improve parameter estimation related to these three processes. Due to the longevity of
these fish, however, longer time series are likely required for there to be enough information to estimate all growth parameters in the deep. Sample sizes are small and less frequent in the deep areas, minimizing the information that can be used to inform growth rates, movement, and selectivity simultaneously. Improved ageing error definitions calculated from GOA-specific data could affect the estimation of these three model components as well.

The male von Bertalanffy $K$ parameter for the gp2 growth curve was inestimable, as gp2 is comprised of older cohorts, and the data do not extend backwards in time to capture size-at-age when these cohorts were young, which would inform the growth parameters $\operatorname{Lmin}$ and $K$. It was necessary to estimate the male von Bertalanffy $K$ parameter outside the models. This was done with simplified models where length-based fishery and age-based selectivity parameters were constant across the entire GOA region. Under this constraint, all growth parameters were estimable, however, model fits to the survey biomass index in the deep area was poor, and there were poorer fits to aggregated length-composition and conditional age-at-length data and therefore these models were not reported.

The female peak age survey selectivity parameter in the deep hit the upper bound set for the parameter in Models 0-2. Increasing the bound only improved the estimation of the deep age-based selectivity in Model 2, although this parameter was still close to the upper bound. Within Model 0 and Model 1, this parameter continued to hit the upper bound, regardless of the upper bound value (Figure 18).

Two subpopulations of GOA Dover sole each with sex-specific growth
Results from a comparison of fits to biomass indices (Figure 12), conditional age-at-length data (Figure 16), and length compositions (Figure 17) provide evidence against a single growth pattern for GOA Dover sole. Models 1 and 2, which estimated two sex-specific growth patterns, provided better fits to shallow survey indices compared to Model 0 with a single sex-specific growth pattern.

Additionally, Model 0 overestimated the mean length-at-age of females in the deep


Figure 16) compared with Models 1 and 2. Length composition plots (Figure 17) indicate Model 0 resulted in a higher expected proportion of larger female fish and lower expected proportion of midlength male fish in the deep than was observed in both the fishery and surveys. The best fits to length composition for both the fishery and survey were from Models 1 and 2 (Table 3).

Estimating two sex-specific growth patterns resulted in lower variability in age-at-length estimation. The CV values in length-at-age for young and old fish estimated in Models 1 and 2 were consistently lower for gp1 compared with 2015 stock assessment estimates used in Model 0 (Table 2 and Figure 16). This trend was also seen in the CV of old fish for gp2. The estimated CV values in length-at-age of young gp2 fish were higher than those from the 2015 assessment model in Model 0, however, this result is in line with expectations due to the difficulty in estimating length at age 3 and $K$ in the deep area.

## Ontogenetic movement associated with growth

Model likelihoods and convergence properties, as detailed below, favored Model 2 over Model 1, supporting the hypothesis that slower growth rates are specific to the deep regions. It is not possible, however, to rule out that improvements to convergence issues in Model 1 could reverse this result.

Fits to biomass indices were similar for Models 1 and 2 (Figure 12). Model 2 resulted in better convergence statistics (Table 3). Model 1 estimated three parameters on the bounds: the movement rate at age 10 was estimated on the upper bound, the male offset to the peak fishery selectivity parameter in the deep was estimated on the lower bound, and the peak survey selectivity parameter in the deep was estimated on the upper bound. All Model 2 parameters were estimable.

Comparison of fits to length composition data aggregated over years (Figure 17), demonstrated that Model 1 resulted in an overestimation of the proportion of mid-sized females in both the fishery and survey deep areas, a slight underestimation of the proportion of mid-sized males in the deep area fishery, and a large underestimation of the proportion of mid-sized males in the deep Survey. Model 2 resulted in the best fit to fishery and survey length compositions.

## Movement rates versus Numbers at age at equilibrium

Model 0 , estimated a movement rate that increased from 0 at age 3 to 0.012 at age 10 and remained constant at 0.012 until age 59 (Figure 19). This movement rate resulted in a slow increase in numbers at age at equilibrium for males and females with a peak near age 20 followed by a slow decline to age 59 . Figure 20 illustrates the possible identifiability (i.e. the theoretical property of a model that states all parameters are estimable) issues between movement and selectivity. The left panel of Figure 20 shows the Model 1 movement rate at age 10 on the upper bound of 1 . The right panel shows numbers-at-age at equilibrium, which demonstrates how this high movement rate leads to equal proportions of fish in the shallow versus deep area at equilibrium from age 10 onward. This high movement rate is assumed to be in error due to the smaller proportion of fish observed from deep versus shallow Surveys (Figure 8). In Model 1, the peak survey selectivity parameter in the deep area is also on the upper bound (Figure 17). As the movement rate increases, the model may be accommodating for the discrepancy between model expectation and observation by increasing the peak age and/or length of selectivity.

While movement at age 10 in Model 2 was set to the value of 1 and held constant to age 59, numbers at age at equilibrium did not show as high of a spike at age 10 as Model 1 (Figure 21). This was because the recruitment apportionment in Model 2 was estimated inside the model and the value apportioned to gp2 was 0.291 (Table 3), lower than the 50/50 recruitment distribution used in Model 1.

## Data weighting considerations

Data weighting using both McAllister-Ianelli (1997) and Francis (2011) tuning methods, however, resulted in convergence issues. Conditional age-at-length data were always downweighted compared to other data components in the tuning step. It is possible that because estimating movement relies on age data, down weighting conditional age-at-length data improves fits to indices, yet leads to instabilities in the movement component of the model resulting in convergence failure.

## Detailed results for Model 2

Model 2 was used to detail yearly fits to length and conditional age-at-length data as it had the best fits to survey indices and length compositions, did not have any convergence issues in the final model, and had the lowest total negative log likelihood (Table 3).

## Fishery Length Composition

While a number of years in the fishery demonstrated a lack of fit to expected length compositions, no discernable temporal trends were detected in the shallow area (Figure 24, Figure 25). Fits to annual length compositions in the deep, however, did suggest temporal patterns where clusters of years shared similar lack of fit relationships (Figure 26). In years 1993-1995, 2002-2003, and 2017, fits to annual length compositions underestimated the proportion of $30-40 \mathrm{~cm}$ male fish. In years 1998, 2002, 2004, 2012, and 2014, fits to annual length compositions underestimated the proportion of $40-60 \mathrm{~cm}$ female fish.

Survey length composition data fits
No noticeable temporal trends in fits to survey length compositions were detectable in the shallow area (Figure 27). Most fits to annual length composition data in the deep underestimated the proportion of 3050 cm male fish (Figure 28).

Conditional age-at-length plots
Plots comparing mean age-at-length in the shallow area (Figure 29, Figure 30) illustrate how the model underestimated the age of large fish in the shallow area in three years $(2007,2009,2017)$ and overestimated the age of large fish in the shallow in one year (1993). The model also likely underestimated the age of mid-sized fish in four years (1999, 2003, 2005, 2011). Overall, the uncertainty intervals in the age-at-length are smaller than those from the shallow area model in the 2019 assessment.

Conditional age-at-length plots in the deep demonstrate the lack of data informing the growth parameter fits (Figure 31, Figure 32). In general, model fits are capturing data trends, yet large standard deviations communicate the uncertainty in these results.

## Marginal Survey Age Data

Marginal survey age data are sparse and do not conform to smooth distributions. The data were included here for comparison between the model and the data, but were excluded from the model's objective function. Fits to annual marginal age composition data suggest a temporal trend, to the extent that it is possible to see a trend in sparse age data. As the time series progresses, the model exhibits a lack of fit for an increasing proportion of shallow older male and female fish and a decreasing proportion of shallow middle-aged male and female fish (Figure 22). Marginal age data in the deep are too sparse to detect any temporal patterns (Figure 23).

## Discussion

## Recommendations for Future Model Development

## Exploration of identifiability between growth, movement, and depth-specific selectivity

Some von Bertalanffy growth parameters were not estimable due to the lack of data available for the older cohorts. In particular, the male von Bertalanffy $K$ parameter for the gp2 growth curve was estimated at upper parameter bounds. It was necessary to first estimate this value from models with constant lengthbased fishery selectivity and age-based survey selectivity throughout the GOA.

To explore identifiability issues in greater depth, it is recommended to set specific values for growth, selectivity, and movement parameters to observe how other parameters change. In addition, there is not strong evidence to support that age 10 is the optimum age to use for the maximum movement rate. Adjusting this age may shift the distribution of gp2 ages that move to the deep, thereby affecting the age-
based selectivity parameters. Exploring different ages of maximum movement rate may provide insight into the interaction between movement and selectivity. Ideally, the two ages at which movement rates are defined would be estimated within the assessment model, but SS currently doesn't have this ability.

## Additional Future Directions

This exercise does not explore the possible differences in movement or growth between Eastern, Central, and Western GOA. While differences likely exist between these areas, difficulties may arise due to lack of sufficient information once data is partitioned at this level (Figure 2, Figure 3, and Figure 4).

Improvement to the SS movement model structure could result in better model design of ontogenetic movement in Dover sole. Specifically, assigning growth parameters to areas would allow for exploration of area associated rather than cohort-specific growth. Hunter et al. (1990) suggested a mechanism explaining the disparate growth rates in Dover sole at shallow versus deeper depths. The study, conducted in central California, noted slower growth rates at depth were associated with fish ontogenetically moving into cooler, oxygen minimum zones. If a similar process occurs in the GOA, a model that estimated areaspecific growth would better align with the biological system. Additionally, allowing for sex-specific movement would allow models to explore the differences observed between the youngest age of male versus female appearance in the deep strata or account for possible female movement back to the shallow for recruitment.

The random effects model was used in this exercise to fill in biomass area-depth gaps. Another possible approach to account for missing data in the GOA is to use model-based estimates via Vector Autoregressive Spatio-Temporal (VAST) models. An initial exploration of model-based indices for the GOA Dover sole is detailed in Appendix B.

Lastly, it is recommended to update the ageing error matrix with GOA specific data. Given the reliance of growth, movement, and survey selectivity on ageing data, this update could result in improvements to identifiability issues encountered in this modeling exercise.

## Literature Cited

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## Tables

Table 1. Sources and years of data used in the Movement models.

| Source | Data | Years |
| :--- | :--- | :--- |
| NMFS Groundfish survey | Survey biomass | $1984-1999$ (triennial), 2001-2019 (biennial) |
|  | Age Composition | $1993,1996,1999,2003,2005,2007,2009,2011$, |
|  |  | $2013,2015,2017,2019$ |
|  | Length Composition | $1990,1993,1996,1999,2003,2005,2007,2009$, |
|  |  | $2011,2013,2015,2017,2019$ |
| U.S. trawl fisheries | Catch | $1978-2019$ |
|  | Length Composition | $1991-2019$ |

Table 2. Growth parameter estimates and standard deviation (St Dev) of GOA Dover Sole.

|  | Model 0 |  | Model 1 |  | Model 2 |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | Value | St.Dev | Value | St.Dev | Value | St.Dev |
| Length at Min Age, Female, gp1 | 25.366 | - | 25.798 | 0.962 | 25.596 | 0.725 |
| Length at <br> Max Age, <br> Female, gp1 | 52.101 | - | 52.188 | 0.287 | 52.115 | 0.279 |
| VonBert K, Female, gp1 | 0.113 | - | 0.127 | 0.006 | 0.129 | 0.006 |
| CV young, <br> Female, gp1 | 0.150 | - | 0.133 | 0.010 | 0.140 | 0.008 |
| CV old, Female, gp1 | 0.107 | - | 0.098 | 0.003 | 0.097 | 0.003 |
| Length at <br> Min Age, Female, gp2 | 25.366 | - | 22.500 | 1.251 | 21.081 | 1.887 |
| Length at <br> Min Age, Female, gp2 | 52.101 | - | 46.903 | 0.785 | 47.498 | 0.760 |
| VonBert K, Female, gp2 | 0.113 | - | 0.207 | 0.028 | 0.201 | 0.040 |
| CV young, Female, gp2 | 0.150 | - | 0.189 | 0.021 | 0.207 | 0.036 |
| CV old, Female, gp2 | 0.107 | - | 0.104 | 0.012 | 0.103 | 0.012 |
| Male Natural Mortality, gp1 | 0.085 | - | 0.079 | 0.002 | 0.079 | 0.002 |
| Length at <br> Min Age, <br> Male, gp1 | 27.110 | - | 22.064 | 0.764 | 25.922 | 0.922 |
| Length at <br> Max Age, <br> Male, gp1 | 43.968 | - | 44.595 | 0.179 | 44.614 | 0.199 |
| VonBert K, Male, gp1 | 0.158 | - | 0.186 | 0.008 | 0.166 | 0.010 |
| CV young, <br> Male, gp1 | 0.151 | - | 0.144 | 0.010 | 0.144 | 0.008 |
| CV old, <br> Male, gp1 | 0.090 | - | 0.082 | 0.002 | 0.081 | 0.002 |
| Male Natural Mortality, gp2 | 0.085 | - | 0.087 | 0.003 | 0.068 | 0.006 |
| Length at <br> Min Age, | 27.110 | - | 27.063 | 0.783 | 27.020 | 1.944 |


| Male, gp2 <br> Length at | 43.968 | - | 42.379 | 0.240 | 42.546 | 0.254 |  |
| :--- | :--- | :--- | :--- | :--- | :--- | :--- | :--- |
| Max Age, <br> Male, gp2 |  |  |  |  |  |  |  |
| VonBert K, <br> Male, gp2 | 0.158 | - | 0.304 | - | $0.199 \neq$ | - |  |
| CV young, <br> Male, gp2 | 0.151 | - | 0.100 | 0.023 | 0.223 | 0.031 |  |
| CV old, <br> Male, gp2 | 0.090 | - | 0.084 | 0.004 | 0.078 | 0.005 |  |

Table 3. Likelihood values, parameters, and derived quantities of the GOA Dover Sole models.

|  |  |  |  |
| :--- | :--- | :--- | :--- |
|  | Model 0 | Model 1 | Model 2 |
| Likelihoods |  |  |  |
| Total Negative Log Likelihood | 5924.34 | 5712.25 | 5687.97 |
| Survey Negative Log Likelihood | 1.38 | -11.40 | -11.83 |
| Length comp Negative Log Likelihood | 528.23 | 429.68 | 415.02 |
| Age comp Negative Log Likelihood | 5386.95 | 5282.69 | 5273.97 |
| Parameters |  |  |  |
| SR LN(R0) | 10.23 | 10.12 | 9.81 |
| SR_BH_steep | 1 | 1 | 1 |
| Derived Quantities | 0 | 0 | 0 |
| gp1 Movement rate at min age 3 | 0 | 0 | - |
| gp1 Movement rate at max age 10 | 0 | 0 | 0.709 |
| gp2 Movement rate at min age 3 | 0 | 0 | 0.291 |
| gp2 Movement rate at max age 10 | 0.012 | 0.5 | 18.208 |
| Recruitment Dist of shallow gp1 | 1 | 0.5 | 46.879 |
| Recruitment Dist of shallow gp2 | - | 0.830 |  |
| Recruitment Virgin (millions) | 27.750 | 71.623 | 61.000 |
| SSB Virgin (1000 mt) | 0.894 | 0.866 | 0.031 |
| Bratio, 2017 | 0.026 | 0.023 |  |
| SPRratio, 2016 |  |  | 0 |

Figures


Figure 1. Length age data for GOA Dover sole by sex, depth strata, and cohort from the GOA bottom trawl survey.


Figure 2. Length age data for GOA Dover sole by sex, FMP sub-area, and cohort from the GOA bottom trawl survey.


Figure 3. Length age data for male GOA Dover sole by FMP sub area, depth strata, and cohort from the GOA bottom trawl survey.


Figure 4. Length age data for female GOA Dover sole by FMP sub-area, depth strata, and cohort from the GOA bottom trawl survey.


Figure 5. Sources and years of data used in the assessment. "Shallow" indicates the fishery and survey data from depths $0-500 \mathrm{~m}$ and "Deep" indicates fishery and survey data from depths $501-1000 \mathrm{~m}$. Size of circle for catches indicates the relative magnitude of catches. The size of circles for length-composition data and conditional age-atlength data indicate the relative input sample size by year.


Figure 6. Catch data of GOA Dover sole in metric tons 1978-2019 partitioned into Shallow (0-500m) and Deep (501-1000m) depth strata.


Figure 7. NORPAC Catch Data, 1978-1986. The Gulf of Alaska region bathymetry was extracted from the NCEI Southern Alaska Coastal Relief Model (https://www.ngdc.noaa.gov/mgg/coastal/s_alaska.html).



Figure 8. Survey Biomass Index partitioned into Shallow (top: 0-500m) and Deep (bottom: 501-1000m) depth strata.


Figure 9. Distribution of length compositions from left to right: Fishery, Survey and from top to bottom: Shallow (0500 m ) and Deep ( $501-1000 \mathrm{~m}$ ). Each plot further partitions length compositions by female (top) and male (bottom).


Figure 10. Distribution of age composition by Shallow (top: 0-500m) and Deep (bottom:501-1000m) depth strata. Each plot further partitions age composition by female (top) and male (bottom).


Figure 11. Schematic of two-area model with two growth patterns. All recruitment occurs in the shallow area (0500 m ). Growth pattern 2 moves to the deep (501-1000m) while growth pattern 1 remains in the shallow area.


Figure 12. Survey Biomass Index (black dots), asymptotic 95\% confidence intervals (vertical black lines), and estimated survey biomass for the model with one growth pattern, Model 0 (blue), the model with two growth patterns that assumes a proportion of gp2 fish remain the the shallow area, Model 1 (red), and the model with two growth patterns that assumes all gp2 fish move to the deep area, Model 2 (green). From top to bottom: Biomass from the shallow $(0-500 \mathrm{~m})$ area and biomass from the deep $(501-1000 \mathrm{~m})$ area.


Figure 13. Comparison of Spawning Biomass with $95 \%$ asymptotic confidence intervals by year for the model with one growth pattern, Model 0 (blue), the model with two growth patterns that assumes a proportion of gp2 fish remain the shallow area, Model 1 (red), and the model with two growth patterns that assumes all gp2 fish move to the deep area, Model 2 (green).


Figure 14. Time series of age 0 recruits for the model with one growth pattern, Model 0 (blue), the model with two growth patterns that assumes a proportion of gp2 fish remain the shallow area, Model 1 (red), and the model with two growth patterns that assumes all gp2 fish move to the deep area, Model 2 (green).


Figure 15. Recruitment deviations for years 1976-2019 and 95\% asymptotic confidence intervals for the model with one growth pattern, Model 0 (blue), the model with two growth patterns that assumes a proportion of gp2 fish remain the shallow area, Model 1 (red), and the model with two growth patterns that assumes all gp2 fish move to the deep area, Model 2 (green).


Figure 16. Comparison of predicted versus observed age by length associations. Top: Model 0 (Left) and Model 1 (Right) Bottom: Model 2.


Figure 17. Comparison of aggregated length compositions over all years. From top to bottom: Model 0, Model 1, Model 2


Figure 18. Left: Comparison of length based fishery selectivities. Right: Comparison of age-based survey selectivities. From top to bottom: Model 0, Model 1, Model 2


Figure 19. Model 0. Top: Comparison of Movement rate of gp2 fish from Area 1 (shallow) to Area 2 (deep).
Bottom: Numbers at age at equilibrium. Male equilibrium curves in area 1 and area 2 are directly underneath female curves and therefore are not visible.


Figure 20. Model 1. Top: Comparison of Movement rate of gp2 fish from Area 1 (shallow) to Area 2 (deep). Bottom: Numbers at age at equilibrium.


Figure 21. Model 2. Top: Comparison of Movement rate of gp2 fish from Area 1 (shallow) to Area 2 (deep). Bottom: Numbers at age at equilibrium.


Figure 22. Model 2: Fits to shallow marginal age data by year. These data were not included in the main objective function.


Figure 23. Model 2: Fits to deep marginal age data by year. These data were not included in the main objective function.


Figure 24. Model 2: Fits to the length composition by year, Fishery Shallow.


Figure 25. Model 2: Fits to the length composition by year, Fishery Shallow.


Figure 26. Model 2: Fits to the length composition by year, Fishery Deep.


Figure 27. Model 2: Fits to the length composition by year, Survey Shallow.


Figure 28. Model 2: Fits to the length composition by year, Survey Deep.


Figure 29. Model 2: Conditional Age at Length, total catch, Shallow (plot 1-2 of 4). These plots show mean age and standard deviation in conditional Age at Length. Left: plots are mean Age at Length by size-class (observed and predicted) with $90 \%$ CIs based on adding 1.64 SE of mean to the data. Right plots in each pair are SE of mean Age at Length (observed and predicted) with $90 \%$ CIs based on the chi-square distribution.


Figure 30. Model 2: Conditional Age at Length, whole catch, Shallow (plot 3-4 of 4). These plots show mean age and standard deviation in conditional Age at Length. Left: plots are mean Age at Length by size-class (observed and predicted) with $90 \%$ CIs based on adding 1.64 SE of mean to the data. Right plots in each pair are SE of mean Age at Length (observed and predicted) with $90 \%$ CIs based on the chi-square distribution.


Figure 31. Model 2: Conditional Age at Length, whole catch, Deep (plot 1-2 of 3). These plots show mean age and std. dev. in conditional Age at Length. Left: plots are mean Age at Length by size-class (observed and predicted) with $90 \%$ CIs based on adding 1.64 SE of mean to the data. Right plots in each pair are SE of mean Age at Length (observed and predicted) with $90 \%$ CIs based on the chi-square distribution.


Figure 32. Model 2: Conditional Age at Length, whole catch, Deep (plot 3 of 3). These plots show mean age and standard deviation in conditional Age at Length. Left: plots are mean Age at Length by size-class (observed and predicted) with $90 \%$ CIs based on adding 1.64 SE of mean to the data. Right plots in each pair are SE of mean Age at Length (observed and predicted) with $90 \%$ CIs based on the chi-square distribution.

