Metapopulation Assessment System
Software Design Document

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1. INTRODUCTION

All fishery resources are distributed in space and time. As such, informed assessments of fish stocks require some capacity for understanding and predicting spatiotemporal patterns in resource abundance and distribution. The importance of spatial distribution, scale, and connectivity is a general paradigm in ecology (Levin 1992) and fisheries stock assessment (Quinn and Deriso 1999, Cadrin 2020). This provides a strong rationale to focus on metapopulations, or sets of distinct populations linked through source-sink dynamics, as the basic unit of population ecology in fisheries science. Ignoring population spatial structure and movement or treating a metapopulation as a set of isolated spatial management stocks can lead to approximation errors. This can increase the risk of overfishing, stock depletion and misperceptions of stock status (Hilborn and Walters 1992, Stephenson 1999, Fields et al. 2006, Cope and Punt 2011, Ying et al. 2011, Hurtado et al. 2013, Spies et al. 2015, Cadrin 2020). To understand and predict human impacts on a metapopulation, stock assessment models need to be able to characterize the effects of spatial variation on the fishery system, including population movement. The development and application of metapopulation models for fisheries management will generally require a shift towards hierarchically structured spatial models with greater complexity than typical single-area, single-stock assessment models.

The object-oriented programming paradigm provides many flexible features and extensibility options (Jana 2005, Stroustrup 2013) for developing metapopulation models from the perspective of software design. These include more natural and precise design specifications, shorter development times, and easier-to-maintain software. Precise specifications of objects and their natural relationships can improve the accuracy, interpretability, and maintainability of the computational model of the metapopulation. Assessment scientists can develop new models using existing templates in the MAS model library that have been previously tested and verified to be accurate and reliable. Maintenance of existing software can be streamlined with general definitions of extendable classes, adaptable object data interfaces, and the capacity to add new analytic features without redesigning the system. Of particular importance for modeling fishery systems, the use of an object-oriented design provides a natural way to implement complex hierarchical population models in a structured manner, noting that some object-oriented features have implemented in existing assessment software platforms, e.g. Stock Synthesis 3 (Methot and Wetzel 2013) and CASAL (Bull et al. 2005). Nonetheless, over a period longer than an individual assessment scientist's career (~ 30 years) it seems important to maintain an ongoing process of software maintainability as well as total quality improvement for assessment model development and continuity. This includes the capacity for model selection, uncertainty quantification, and testing (Morgan and Henrion 1990, Burnham and Anderson 2002, NRC 2012), as well as the creation of model ensembles for understanding and predicting how fishery systems will respond to alternative management approaches. In this context, the capacity for rapid model prototyping, development, and testing for fishery systems that account for spatio-temporal variation in populations, fleets, and ecosystem processes is an important goal.

We envision that rapid prototyping, development, and testing of models can be achieved through the ongoing development of a metapopulation assessment system consisting of a library of tested modules with extensible templates that implement various types of population dynamics. The capacity to build new models from existing assessment model templates with just-in-time compilation will encourage the ongoing development and improvement of structured stock assessment models. This, in turn, will help to avoid the life cycle issue of maintaining an up-to-date assessment package as science and technology improves through time.

1.1 Purpose

The goal of this software design document is to describe the construction and maintenance of a metapopulation assessment modeling system that incorporates up-to-date modeling capabilities and ongoing technological improvements and is readily extensible to adapt to diverse stock assessment situations. This includes assessments of both large-scale populations comprised of millions of individuals modeled with continuous variables and small-scale populations comprised of hundreds of individuals modeled as discrete individuals. That is, the general system could be applied to model both commercial fishery and protected species resources. The software design document presented here provides a preliminary model design, which will be iteratively refined to produce a living design document, which will include detailed data and model structures along with computational procedures. The paradigm for this system is that modeling the spatial dynamics of fishery resource and the fishing fleets that harvest it are essential for improved understanding and predictive capacity. An inherent design to handle the spatial structure and its impacts on population dynamics and the fishery system exploiting the stock is a necessary condition for metapopulation stock assessment. In this context, the preliminary design document focuses on spatial population dynamics as approximated by a box-transfer model, noting that other models of spatial dynamics can be implemented as needed (e.g., Goethel et al. 2011). Accounting for spatial structure can have substantial impacts on fishery selectivity and relative abundance indices. As a result, structured assessment models need to be able to approximate spatially structured population dynamics. As a result, the new modeling system is named a **Metapopulation Assessment System**, or **MAS**, to reflect this design element.

In MAS, each instance of a metapopulation model consists of one or more structured populations and one or more habitat areas (or locations or patches, depending upon the context). We use the term population to mean an intraspecific group of randomly mating individuals whose demographic and genetic trajectories are mostly independent of other such groups. This definition of population is analogous to the concept of a fish stock (e.g., Carvalho and Hauser 1994, Waples 1998) and allows for models where metapopulations are comprised of several distinct genetic subpopulations. Here a metapopulation is defined as "*a system of interacting biological populations, termed subpopulations, that exhibit a degree of independence in local* *population dynamics as well as connectivity between subpopulations* (Cardin 2020)". This definition accommodates spatially explicit models to represent a single population whose individuals move among areas and that exhibits geographic variation in life history parameters (e.g., Goethel et al. 2014) with some degree of phenotypic plasticity, or a set of management units or harvest stocks that are defined by geographic location. Overall, we want to be able to model situations where natural genetic differences primarily drive differences among populations and also to model situations where spatial variation in environmental forcing leads to spatial differences among fish inhabiting different areas. This capacity to handle metapopulation models where either nature or nurture is the primary determinant of population dynamics is an important feature for dealing with different species with different life history types.

Here we also note that the MAS is designed with an emphasis on providing the capacity to construct alternative credible models versus the expectation of being able to create a single model that provides a best approximation to the set of all plausible movement dynamics of the metapopulation. For example, one might wish to compare a single population moving between two areas with an alternative two-population model with feeding migrations and natal homing to a single area. Here we use the term "population" to represent a group of related animals with linked recruitment patterns and similar demographic parameters, including for example, growth characteristics, stock-recruitment resilience, and survival rates. Each population will have a set of movement probabilities (e_{ij}) among areas in a given time step (e_{ij} is the probability of movement from area *i* to area *j*). These probabilities can depend on various population and environmental variables in a dynamic manner, for example movement probabilities may be density-dependent (e.g., Goethel et al. 2014). In this context, a given population could have individuals that are very mobile and potentially can move into any of the modeled areas ($e_{ij} > 0$) or have adults that are mainly sessile and not move at all ($e_{ij} \approx 0 \;\; for \; i \neq j$) from the area where they recruit as juveniles (Figure 1). Information on the local structure and characteristics of each habitat area and associated environmental forcing is to be included in the environment component.

The capacity to accommodate populations that have a clumped distribution in space as well as populations that can move through the entire spatial domain is a key design element of MAS. This design feature allows for the modeling of highly migratory stocks, such as salmon, tunas, or whales, as a metapopulation, comprised of populations that have the capacity to transit through and mix in habitat areas of varying suitability. Similarly, the design also allows for the modeling of sedentary populations, such as sea scallops, surf clams, or abalones, which are comprised of local or area-specific populations with overlapping larval distributions and sessile adult distributions. This design feature allows for a wide variety of movement patterns with interannual and seasonal variability to be modeled. Allowing for diverse movement patterns is one of the basic elements in MAS and is also one of the reasons an object-oriented system design will be needed for organizing the information required to model these diverse patterns.

1.2 Scope

The scope of the MAS design document is to provide mathematical modeling and computer programming specifications for alternative data structures and model parameterizations of metapopulation dynamics using a likelihood-based or integrated modeling approach. In brief, here are some of the design features that are envisioned, noting that how and when these features can be implemented is subject to resource constraints. Movement dynamics among areas can be modeled for highly migratory that move among areas or for relatively sedentary populations with or without exchange of recruitment among areas. The metapopulation size can be a large commercially important fishery resource with millions of individuals or a small bycatch-impacted protected species resource with hundreds of individuals. The spatial resolution of the modeled areas can be coarse or granular and the size of areas can be uniform or irregular. The parameter estimation process can be based on frequentist, simple Bayes, hierarchical Bayes or mixed models with random effects, noting that the Bayesian and random effects approaches are not currently implemented in MAS version 1.0. Metapopulation models can be developed for age- or size-structured populations. Fishery systems can be comprised of single or multiple fleets operating over one or more habitat areas with dynamic characteristics. The environmental characteristics of areas can be stationary or time varying and populations can be subject to local (single-area) or global (multiple-area) environmental forcing. Models can be compared and tested using simulated data sets under alternative operating models and harvest strategies for management strategy evaluation. Best-fitting models or ensembles of credible models can be used for making forecasts of annual catch limits and other quantities of interest under alternative future states of nature. Ideally, models will be able to be extended to include multispecies and socioeconomic components of the fishery system for integrated ecosystem analyses.

1.3 Overview

This software design document provides specifications for the development of a metapopulation assessment system. This system will employ an object-oriented programming paradigm to ensure software maintenance and flexibility and to improve model extensibility through time. The object-oriented paradigm focuses on the development of class structures to represent the assessment data and function objects needed to construct, optimize, compare, and simulation test a set of metapopulation models for stock assessment applications. The class structures will use data encapsulation and will include functions with an internal or private view for acting on variables of the class objects (Figure 2) as well as an external or public view with functions to share processed data sets with other class objects. For example, one public view of an instance of the population component could be the catch biomass by fishing fleet conditioned on the abundance and spatial distribution of the population in relation to a fishing fleet effort and selectivity by subarea within the fishing grounds (Figure 2). Similarly, a private view could be the amount of spawning output produced in a time interval conditioned on the population numbers at age and its private data for maturity ogive, fecundity, and natural mortality, as well as any influences made by changing environmental conditions (Figure 2).

The metapopulation assessment system will consists of a set of libraries of class objects and associated functions to fit fishery system observations. The system will employ just-in-time compilation to produce executable software for specific applications. The system will have the capacity to parallelize some aspects of the model construction, selection and testing, and projection analyses to facilitate large-scale simulations to evaluate model performance under uncertainty. This next section provides an overview of the initial MAS including descriptions of the general system architecture and along with the data and model structure and the design of input and output objects.

2. SYSTEM OVERVIEW

Assessment systems are typically designed to answer management questions using models that approximate nature. Assessment analyses typically produce historic and current estimates of stock abundance, mortality, and productivity and may use a variety of model structures fitted to alternative data inputs. Assessments also need to be able to produce forecasts of future stock conditions and fishery yields and other quantities of interest under alternative harvest scenarios. As a result, there are multiple types of modeling analyses that comprise a stock assessment and these can be generally categorized into analysis layers. In this context, the fundamental system unit for MAS is the metapopulation assessment model. The MAS modeling algorithm consists of four analysis layers, which correspond to the primary applications and analyses, needed to construct and complete a full stock assessment for a metapopulation.

2.1 Model Construction

The first analysis layer of MAS produces a single metapopulation assessment model, denoted by M , which is created and iteratively refined and fitted in a chosen statistical framework; this is the **model construction layer** (Figure 3). The purpose of the model construction layer is to produce an object of the MAS model class, where m_j denotes the j^{th} model. This layer includes analysis functions to assess model convergence, to assess model goodness of fit, to iteratively reweight input data sources, and to produce model outputs for quantities of interest. Model construction is the basic or root layer upon which the other three analysis layers depend.

2.2 Ensemble Model Construction

The second layer is the **construction layer for ensemble models**. In general, several alternative models, perhaps on the order of dozens, will be developed and examined in the course of a particular stock assessment effort. The process of comparing, contrasting, and selecting the best model, or best set of credible models $\underline{M}=\left\{m_j\right\}$ comprises the second analysis layer (Figure 3). This layer includes analysis functions to compare model diagnostics and goodness of fit criteria, to compute model weights, to quantify uncertainty about quantities of interest, and to output results accounting for parametric and model selection uncertainty and associated statistics. The purpose of the model selection layer is to produce the set of information needed to select a best fitting model or best ensemble of models.

2.3 Model Forecasting

The third layer is the **model forecasting layer**. The purpose of the forecast layer is to produce the information needed to project the set of distributions of results from the best model or best set of models $\{f(M)\}$ into the future under alternative forecast scenarios (Figure 3). This layer includes model output information needed to calculate time series of catches or effort limits needed to produce selected probabilities of overfishing, to produce probabilities of achieving target management targets within selected periods, and distributions of quantities of interest.

2.4 Model Simulation

The fourth layer is the **model simulation or management strategy evaluation layer**, which implements simulation testing for model verification and has the capacity to conduct a management strategy evaluation of the robustness of metapopulation assessment models under management strategies (Figure 3). This layer includes analysis functions to generate simulated data sets from a set of operating models, produce assessments based on simulated data, and evaluate performance metrics for alternative operating models and management strategies. The purpose of the management strategy evaluation layer is to produce the target information set $\{I\}$ needed to assess the robustness and performance of the management strategies $\underline{S}$ conditioned on the operating models $\underline{M}_O$ and estimation models $\underline{M}_E$ under the relevant uncertainties. Each of the four analysis layers includes a generic algorithm that specifies the sequence of analytical options along with the model constraints, uncertainties and interfaces to data and functions in each layer.

2.5 Model Inputs and Outputs

Input and output objects are produced in each analysis layer to create and distribute the necessary fishery system information. Ideally, these I/O objects will be designed to provide ease of use and interpretability, flexible capacity for simulation testing and model verification, and allow for GUI-based model development in MAS. For example, the model selection layer will need to provide input and output information for comparing models and quantifying uncertainties. In this context, one wants to be able to implement structured model input and output objects that can be efficiently combined and disaggregated to provide compatibility for diverse types of input or output information, that is, for outputting quantities of interest in specific formats.

One approach used for MAS I/O is based on the JSON (JavaScript Object Notation) syntax to construct model configuration input and output storage objects for MAS because of its generality and simplicity. This notation provides a standard data-interchange format based on a subset of the JavaScript Programming Language, namely the Standard ECMA-262 3rd Edition - December 1999. JSON uses a text format that is language independent but also uses two structures, hash tables and arrays, which are basic information structures used in the C-family of languages and structured programming in general. Overall, JSON is a natural data-interchange language for defining array structure for input and output objects. The NetCDF (the Network Common Data Form) for data input and output processing may also needed to implement the inclusion of high-density environmental data sets in MAS. Here NetCDF consists of a set of software libraries and self-describing, machine-independent data formats that support the creation, access, and sharing of array-oriented scientific data. The use of NetCDF may facilitate the capacity of MAS to incorporate environmental data sets in the metapopulation analyses, including ocean and atmospheric data sets in binary format. NetCDF also has the advantages of providing efficient data storage and rapid data access, along with a standard set of applications to manipulate data objects. There is ongoing work to produce an R language interface for MAS and the current prototype is currently being developed on Github as part of the NOAA Fisheries Toolbox (https://github.com/nmfs-fish-tools/RMAS).

3. SYSTEM ARCHITECTURE

The model structure is represented in the class MAS that defines a model as an abstract object. The MAS class defines the structure of an individual metapopulation model and how it is comprised of data and modeling structures. The MAS class includes case structures for each of the analysis layers, noting that the single model construction layer is the minimal representation required for a MAS model, i.e., a single assessment model fit using a fixed input data set and fixed model structural assumptions.

3.1 Architectural Design

The model case structures are important because they specify the logical choice being made for each possible feature in a given model. For the single model construction layer (Figure 3), these choices specify the modeling information needed to represent: (1) the populations within the metapopulation (**Population**), (2) the set of observational data to be fit by the model (**Observation**), (3) the set of environmental information used to represent the effects of spatial and temporal variation on fishery and population dynamics within areas, if applicable (**Environment**), and (4) the set of structural choices made for the analyses of the set of selected input information (**Analysis**). The model case structures correspond to a list of lists with a specific set of logical possibilities for each array element. Here each array element represents a specific list or record structure to define a model feature. For example, an array element for the fishery selectivity of a fishing fleet would be a list that specifies the type of selectivity function being used to fit length observations, the number of selectivity parameters, information on the initial parameter values, prior distributions of these parameters, the estimation phase of each parameter, information to specify time- or space-varying effects on these parameters. There are model case structures for each of the four primary information components that comprise an instance of the **MAS Class** for a given metapopulation (Figure 4). These are:

(1) Population Component – this includes attributes and behaviors that describe the population numbers at age, its distribution among locations in the set of areas, and its movement attributes. In current assessments, one common approach is to model a single population that is completely mixed within in single stock area. In comparison, the treatment of multiple populations moving among multiple areas produces a much wider range of population configurations. Information on spatiotemporal variation is shared through the location and movement information in the Population Component.

(2) Observation Component – this includes observed data that describe the fish metapopulation and fishery system. Note that this includes information that humans could observe and that there are other types of data used in the MAS model. The observation component has subclass structures that match the possible types of available observations of fisheries data, survey data, research data from scientific studies that provide individual observations of size at age, maturity, or fecundity relationships or tag recapture data. Information on spatiotemporal variation is shared through the habitat and movement subclasses.

(3) Environment Component – this includes attributes and behaviors that describe the environmental characteristics encountered by the fish and fishing system among areas. The environment component contains information on habitat in areas and the unidirectional effects of spatial or temporal environmental forcing on population attributes and behaviors. Subclass structures can include biotic entities such as predator fields or abiotic factors such as sea surface temperature, with information on spatiotemporal variation being shared through the location and movement subclasses.

(4) Analysis Component – this includes the information on attributes and behaviors that specify the analytical components of the metapopulation assessment system. The analysis component contains subclasses for parameter input and output, creating simulated input data, likelihood components, model setup and domain parameters, model diagnostics, data weighting and iterative reweighting, model selection and multimodel inference, model averaging, constraints or priors and hyperpriors on model parameters, and uncertainty quantification methods including covariance estimation, bootstrapping, and Markov Chain Monte Carlo simulation and other approaches with information on spatiotemporal variation being shared through the location and movement subclasses.

Each of the four primary model components includes data objects and interface functions to transfer information among classes in order to model the dynamical structure of the populations, including their distribution in space-time and their movement rates between areas. Information is transmitted between classes via messages, or interface functions, as indicated by the arrows (Figure 4). In this context, the spatiotemporal distribution of a population is the set of areas it inhabits through time. That is, each population is associated with a particular set of areas through, which could range from one area to all of the areas incorporated in the model. Populations can migrate as groups of individuals, or propagules, through areas. As a result, abundances of populations within specific areas may be reduced through emigration or be increased through immigration.

For the model set selection layer, the model case structures are contingent on the single model construction layer specifications. This hierarchy allows for the stepwise development and comparison of alternative models from a template model that includes the full set of available data for the given type of metapopulation assessment model.

Similarly, for the model forecast layer, the model case structures are contingent on the model set selection layer specifications. This feature allows for the stepwise development of alternative sets of output data needed for forecasts based on a single model or an ensemble model.

For the management strategy evaluation layer, the model case structures do not necessarily have to come from the model set selection layer. This is to allow for the flexible development of management strategy evaluations, which may represent a range of unobservable states of nature. In addition to the model case structures, the management strategy evaluation layer will also include a set of alternative management strategy case structures that can be open loop, with no feedback from the simulated observations or closed loop, with feedback from the model observations through time.

In summary, the MAS Class holds the basic logical specifications needed to put a particular instance of a model object together using model case structures. In addition, the four primary components needed for constructing an instance of a MAS Class are: (1) the Population Component, this is where the population dynamics information is contained; (2) the Observation Component, this is where the observed data are stored; (3) the Environment Component, this is where the biotic and abiotic habitat and environmental information that affect population and fishery dynamics are stored; and (4) the Analysis Component, this is where the likelihood structure, model fitting, and data analysis information is stored.

3.1.1 Population Component

The structure of the population component in MAS includes multidimensional arrays for storing the numbers ($N^{(p)}$) of fish in each population (indexed by p) in particular space, age-size, and gender cells through time. The space dimension consists of S categories for spatial location. The convention of using S areas gives a total of $S-1$ full degrees of freedom for the empirical multinomial distribution in this dimension. Similarly, there are Y time categories for year and T time subcategories for seasons if a total of T seasonal time periods are included in the population dynamics, where the time dimension is indexed as a 2-tuple of year and season denoted as (y,t). In this general case, there are a total of $(Y-1)\text{x}(T-1)$ degrees of freedom. Last, we assume that there are a total of A age- or size-structured categories for population structure, and a total of G categories for gender structure with associated degrees of freedom of $A-1$, and $G-1$, respectively.

We will need to have a standard approach to indexing population information. The information on the population numbers in time and space (or distance) will be stored in multidimensional arrays with dimensions for year, season, spatial domain, age, and gender. The general convention for ordering the subscripts for these multidimensional population arrays is set to be $\left(\underline{Y}ear, \underline{T}ime, \underline{S}pace, \underline{A}ge, \underline{G}ender\right)$. This ordering focuses on temporal changes in the spatial distribution of populations within areas. It also provides the most efficient storage sequence for accessing computer memory within a time loop. In what follows, a reduced subscript set consisting of $\left(\underline{T}ime, \underline{S}pace, \underline{A}ge\right)$ will sometimes be ued, noting that if subscripts are omitted, then the index ordering convention remains the same. We also note that for some observations, such as catch biomass, we will need an additional subscript to indicate the fleet, or survey, which observed the quantity. In this case, we will augment the general convention for ordering the subscripts for these multidimensional arrays to include a fleet index as $\left(\underline{F}leet, \underline{Y}ear, \underline{T}ime, \underline{S}pace, \underline{A}ge, \underline{G}ender\right)$ or $\left(\underline{F}leet, \underline{T}ime, \underline{S}pace, \underline{A}ge\right)$.

The proportion of the p^{th} population in area s during season t in year y at age a is denoted by $P_{(y,t),s,a}^{(p)}$ and the corresponding population number of fish in area s at time t is $N_{(y,t),s}^{(p)} = \sum_a N_{(y,t),s,a}^{(p)} = \sum_a P_{(y,t),s,a}^{(p)} N_{(y,t),s}^{(p)}$. Similarly, the total number of fish in the p^{th} population during season t is $N_{(y,t)}^{(p)} = \sum_a \sum_s N_{(y,t),s,a}^{(p)} = \sum_a \sum_s P_{(y,t),s,a}^{(p)} N_{(y,t),s}^{(p)}$. Thus, the set of sufficient information needed to specify the p^{th} population numbers at any time includes the 3-dimensional population proportion array $\underline{\underline{\underline{P}}}^{(p)} = \left(P_{(y,t),s,a}^{(p)}\right)$ that contains the population proportions at age by area and the 2-dimensional population size array $\underline{\underline{N}}^{(p)} = \left(N_{(y,t),s}^{(p)}\right)$, which contains the total population numbers in each area by year and season.

Age composition data can be observed to characterize the age structure of the population in a given location and time. An age composition sample represents the age structure contained in a 1-dimensional subarray of the population array, as for example, the array slice $\underline{N}_{T,S}$ for the last season in the year which is shown by the red star and arrow (Figure 5), noting that the population superscript is omitted.

An important element of the population component is the set of areas the population can inhabit and have groups within the population move from area to area. In this case, we are focusing on box-transfer movement (i.e., Beverton and Holt 1957, Goethel et al. 2011) in this design document, noting that other movement models may need to be considered in future developments. This set of inhabitable areas is the habitat of the population. The set of habitable areas for a population can be represented as a directed graph in which the connected vertices (V_j) are the habitable areas and the edges (e_{jk}) are the directed movement paths between areas. Here is an example of the directed graph for a population inhabiting five areas and with one-step movement paths (Figure 6). The information on the nearness of the areas within a population's habitat is represented with an adjacency matrix $\underline{\underline{A}}$. If the directed habitat graph has S vertices or areas, numbered $V_1, V_2, ..., V_S$, then the adjacency matrix $\underline{\underline{A}} = \left(a_{i,j}\right)_{SxS}$ is SxS with entries $a_{i,j} = 1$ if there is an edge with initial vertex V_i and terminal vertex V_j in the directed graph and $a_{i,j} = 0$ if there is no edge. The adjacency matrix describes the set of possible one-step movements of the population within its habitat.

Here is the adjacency matrix $\underline{\underline{A}}$ for the example of a population with a habitat consisting of five areas (Figure 6).

(1) $$\underline{\underline{A}} = \begin{pmatrix} 0 & 0 & 1 & 1 & 0 \\ 1 & 0 & 0 & 0 & 0 \\ 1 & 1 & 0 & 0 & 0 \\ 1 & 1 & 1 & 0 & 1 \\ 0 & 1 & 0 & 0 & 0 \end{pmatrix}$$

In general, areas that are not part of the population habitat are represented as a row with zero entries. As a result, the adjacency matrices for each of the populations can be taken without loss of generality to have full dimension SxS. This provides a succinct representation of how populations can move through their habitat in one step or on a path of length one.

The adjacency matrix can also be used to determine the number of paths of any length between two areas. This follows from the fact that the entries of $\underline{\underline{A}}$ raised to the power $m \geq 0$ count the number of distinct paths of length m between two vertices. In particular, if $a^m_{i,j}$ denotes the $(i, j)^{th}$ entry in the matrix $\underline{\underline{A}}^m$, then $a^m_{i,j}$ is the number of paths of length m between the vertices V_i and V_j.

It is useful to note that the number of paths of length zero is given by $\underline{\underline{A}}^0 = \underline{\underline{I}}$, where $\underline{\underline{I}}$ is the identity matrix. This identity matrix corresponds to population groups that do no move between areas noting that a path of length zero connects an area to itself. Thus, the sum of the adjacency matrix and the identity matrix $\underline{\underline{A}}^0 + \underline{\underline{A}}$ defines the set of all possible connecting paths of edges between areas for the population movement probabilities.

The movement probabilities define the multiple flows, or transfers (*T*), of individuals in the population among areas and are associated with the edges in the population habitat graph. The probability that an individual fish of age a from population p in area s_i moves to area s_j during season t in year y is denoted by $T^{(p)}_{(y,t),(i,j),a}$, where these probabilities are all nonnegative and satisfy the constraint that they sum to unity for a given population (*p*), source area (*i*), age structure (*a*), and season (*t*) in year (*y*). That is,

(2) $$\sum_{j=1}^{S} T^{(p)}_{(y,t),(i,j),a} = 1$$

The movement probabilities can be represented as time-specific and age-specific matrices

$$\underline{\underline{T}}^{(p)}_{(y,t),a} \text{ where } \underline{\underline{T}}^{(p)}_{(y,t),a} = \begin{pmatrix} T^{(p)}_{(y,t),(1,1),a} & \cdots & T^{(p)}_{(y,t),(1,S),a} \\ \vdots & \ddots & \vdots \\ T^{(p)}_{(y,t),(S,1),a} & \cdots & T^{(p)}_{(y,t),(S,S),a} \end{pmatrix}_{S\,x\,S}$$

and $\underline{\underline{T}}^{(p)}_{(y,t),a}$ is the population movement matrix for size bin or age class a and season t in year y.

Each row of the population movement matrix $\underline{\underline{T}}^{(p)}_{(y,t),a}$ that is part of the population habitat has nonnegative entries that sum to unity as in equation (3). Rows of $\underline{\underline{T}}^{(p)}_{(y,t),a}$ that are not part of the population habitat have zero entries. The movement probability matrices can also be constant through time or constant across age structure or both, although the most general setting is for the probabilities to vary through time and by age structure.

Here is an example of a movement matrix $\underline{\underline{T}}$ corresponding to the five-area population habitat along with the associated habitat graph (Figure 6) where the movement probabilities are constant in time and by age structure

(3) $$\underline{\underline{T}} = \begin{pmatrix} T_{11} & 0 & T_{13} & T_{14} & 0 \\ T_{21} & T_{22} & 0 & 0 & 0 \\ T_{31} & T_{32} & T_{33} & 0 & 0 \\ T_{41} & T_{42} & T_{43} & T_{44} & T_{45} \\ 0 & T_{52} & 0 & 0 & T_{55} \end{pmatrix}$$

and satisfy the five probability constraints $T_{11}+T_{13}+T_{14}=1$, $T_{21}+T_{22}=1$, $T_{31}+T_{32}+T_{33}=1$, $T_{41}+T_{42}+T_{43}+T_{44}+T_{45}=1$, and $T_{52}+T_{55}=1$.

This shows the minimal architectural elements for the population component, a structured population distributed in space and time along with the associated movement probabilities. Recruitment processes for a population are modeled in a similar manner noting that only the spatial distribution of new recruits among areas is needed. The population component interfaces with the information component as well as the observation and environment components to describe the metapopulation dynamics through time.

3.1.2 Observation Component

The observation component is the set of observed data for the metapopulation and fishery system. This includes fisheries data, survey data, and life history parameter information from studies that provide estimates of growth, maturity, or fecundity curves or individual observations of tagging or size-at-age data. These observational data will be stored in multidimensional arrays. In the model construction layer, model parameters are fit to the observed data through functions that interface with the population, environment, and analysis components. For example, Methot and Wetzel (2013) describe a general approach to incorporating time-varying parameters in an integrated assessment model.

Overall, the observation component is comprised of the basic data, the objects used to store this information and interface with the population, environment, and information components, and these are described in the Data Design section.

3.1.3 Environment Component

The environment component characterizes the information on the metapopulation habitat distribution and other local spatial information for each area or set of areas where this information is available. The local spatial information for an individual area is mapped onto a location array. The location array can be a 2-dimensional grid for a habitat surface or a 3-dimensional grid for a habitat volume. The location array can be used to represent the effects of environmental forcing on population characteristics and observed data on a finer scale than an entire area. This component includes information on the abundances of biotic entities or magnitudes of abiotic factors in space and through time. As such, the environment component may require large storage if fine-scale information is incorporated into a MAS model. For example, satellite observations of ocean chlorophyll or sea surface temperatures mapped onto the model areas could represent the influence constant or time-varying survival and growth conditions dependent on the existing environmental conditions in each area. Overall, the environment component describes the exogenous conditions affecting the metapopulation dynamics by area and interfaces with the population, observation, and information components and its details are described in the Data Design section.

3.1.4 Analysis Component

The analysis component stores the information on the functions and algorithmic processes needed to fit the parameters of a general discrete-time metapopulation model structure that includes observation and process dynamics. This component includes information needed for parameter input, estimation, and output. The analysis component also includes algorithms for creating simulated input data, specifying likelihood components, model setup, and domain parameters, producing model diagnostics, applying data weighting or iterative reweighting, conducting model selection, multimodel inference, and model averaging, setting likelihood constraints or priors and hyperpriors on model parameters, and implementing uncertainty quantification methods including covariance estimation, bootstrapping, Markov Chain Monte Carlo simulation as well as approaches for single-model or model ensemble forcasting. In general, the model structure and information requirements depend on a first-order nonlinear difference equation formulation of the metapopulation dynamics, which can be formulated as a state-space model (i.e, Aoki 1990, Schnute 1994) as described below.

3.2 Subsystem Description

The form of the discrete-time state space model used in MAS depends on the relationships between the system state vector $\underline{\underline{X}}_T$, the observed data vector $\underline{\underline{D}}_T$, and the parameter vector to be determined $\underline{\Theta}$ that produces a potential model solution. Here we note without loss of generality that any set of vectors can be represented by as a single vector or structured as scalars, vectors, and subarrays in a list. The system state subvector $\underline{X}_t$ has dimension n_{X_t} and represents the set of unobserved population or other system state variables at time *t*. The data subvector for data observed during time period *t* is denoted as $\underline{D}_t \in \underline{\underline{D}}_T$ and has dimension n_{D_t}. This subvector represents the set of observed quantities at time *t*. If the set of control variables (i.e., catch or fishing effort) for the system are modeled as empirical observations, then these variables can also be considered as an empirical component of the observed data vector, in contrast to being included as a component of the parameter vector. The parameter subvector for time period *t* is denoted as $\underline{\Theta}_t \in \underline{\Theta}$ and has dimension n_{Θ_t}. This subvector represents the combined set of all parameters used to describe the process and observation dynamics as well as fitting of the state space model. This includes parameters for fishery system dynamics $\underline{\theta}_p$, parameters for prior or likelihood constraint distributions $\underline{\theta}_\pi$, parameters for hyperprior distributions $\underline{\theta}_\varphi$, parameters for process error distributions $\underline{\theta}_\sigma$, parameters for observation error distributions $\underline{\theta}_\tau$, parameters for numerical constraints and nuisance parameters $\underline{\theta}_\eta$, as needed, for example, to improve stability of the numerical computations. As a result, the overall parameter vector that determines the MAS model configuration is $\underline{\Theta} = \left(\underline{\theta}_p, \underline{\theta}_\pi, \underline{\theta}_\varphi, \underline{\theta}_\sigma, \underline{\theta}_\tau, \underline{\theta}_\eta\right)$ where the subvector $\underline{\Theta}_E$ of estimable parameters may include parameters for population dynamics, process errors and observations errors, that is $\underline{\Theta}_E = \left(\underline{\theta}_p, \underline{\theta}_\sigma, \underline{\theta}_\tau\right)$. Note that the estimable parameter vector $\underline{\Theta}_E$ contains the parameters that are freely estimated in the optimization of the objective function in contrast to fishery system dynamics or other parameters that are assumed to have fixed known values in the MAS state space model formulation. We would also note that there may be situations where it is reasonable given the information constraints to assume structural dependence of the observation process on the observed data, i.e., an empirical Bayes framework, and that this framework can be accommodated.

The state space model structure ensures that the time dimension can be represented as a memory-less process in which the next system state only depends on the current system state and where time-lagged variables are included in the state and parameter subvectors as needed. It also implies that the model structure is set up for Markov Chain Monte Carlo simulation which can be used to numerically integrate the posterior distribution of a given Bayesian model formulation (Gilks et al. 1996, Gelman et al. 2005) and also for conducting future forecasts which account for uncertainty in the estimate of system state (Brodziak et al. 1998, Patterson et al. 1999). Last, it is important to note that the state space modeling structure is general and can be applied to single- and multi-species models with spatial structuring through time. In what follows, the index "*t*" is used to denote a sequential time period and represents either seasons or years depending on whether the model includes seasonal dynamics.

3.2.1 MAS System Dynamics Model

The general framework for constructing a single MAS model includes a set of nonlinear first-order difference equations to describe system dynamics combined with a set of joint likelihood components to define observation errors and process errors. In general, a MAS model can be formulated as a state space model (e.g., Schnute et al. 1998) with mixed effects but this is not a requirement. That is, MAS models may exclude process error components a The joint likelihood of the observed data, the unobserved system state variables and the model parameters is comprised of three probability distributions: one for the initial system state, one for the system state dynamics, and one for the observed data dynamics.

3.2.1.1 Initial System State

The initial system state vector for time period t=1 is $\underline{X}_1$. This initial state is calculated based on an initial probability distribution $P_{Init}(\cdot)$ that produces the probability measure for the unknown initial system state conditioned on the initial system control vector $\underline{Z}_1$ and the model parameter vector $\underline{\Theta}$ as

$$P_{Initial}\left(\underline{X}_1 \mid \underline{Z}_1, \underline{\Theta}\right) \tag{4}$$

3.2.1.2 System State Dynamics

The system state variables for times $t \geq 2$ is denoted as $\underline{X}_t$. This unobserved state vector is calculated based on the system state probability distribution $P_{State}(\cdot)$ that produces the probability measure for the current system state conditioned on the previous system state vectors

$\underline{\underline{X}}_{t-1} = \left(\underline{X}_1, \underline{X}_2, \ldots, \underline{X}_{t-1}\right)$, the previous control vectors $\underline{\underline{Z}}_{t-1} = \left(\underline{Z}_1, \underline{Z}_2, \ldots, \underline{Z}_{t-1}\right)$, and the model parameter vector $\underline{\Theta}$. The system states are sequentially calculated for times $t \geq 2$ as

$$(5) \qquad P_{State}\left(\underline{X}_t \mid \underline{\underline{X}}_{t-1}, \underline{\underline{Z}}_{t-1}, \underline{\Theta}\right)$$

Where the system state probability distribution is a smooth function of the model parameters. Note that if there is no process error in the state dynamics then the value of the $P_{State}\left(\cdot\right)$ distribution is unity and the MAS model is in effect a nonlinear time series regression model.

3.2.1.3 Observed Data Dynamics

The observed data for the fishery system at time $t \geq 1$ are denoted by $\underline{D}_t$. The likelihood of the observed data at time t is calculated based on the observation probability distribution $P_{Observed}\left(\cdot\right)$. This distribution produces the probability measure of the data conditioned on the current and previous system state vectors $\underline{\underline{X}}_t = \left(\underline{X}_1, \underline{X}_2, \ldots, \underline{X}_t\right)$, the current and previous control vectors $\underline{\underline{Z}}_t = \left(\underline{Z}_1, \underline{Z}_2, \ldots, \underline{Z}_t\right)$, and the model parameter vector $\underline{\Theta}$. The observed data likelihood are sequentially calculated for times $t \geq 1$ as

$$(6) \qquad P_{Observed}\left(\underline{D}_t \mid \underline{\underline{X}}_t, \underline{\underline{Z}}_t, \underline{\Theta}\right)$$

Where the observed data likelihood is a smooth function of the model parameters.

There are two points about this general representation of the process and observation dynamics to keep in mind. First, the time dynamics are structured to occur in a discrete time step and, given this feature, if time-varying population attributes are included, then one needs to specify how these attributes change as fish move among spatial regions. Second, auxiliary spatiotemporal constraints may be needed to ensure that the state space model has identifiable parameters given the general nature of the initial state, system process and observation dynamics.

3.1.2.4 Joint Model Likelihood

The joint likelihood of the state variables, data and model parameters for a MAS model $L\left(\underline{\underline{X}}_T, \underline{\underline{D}}_T, \underline{\Theta}\right)$ is constructed from the product of the initial, state, and observation likelihoods through time as

$$(7) \quad L\left(\underline{\underline{X}}_T, \underline{\underline{D}}_T, \underline{\Theta}\right) = P_{Initial}\left(\underline{X}_1 \mid \underline{Z}_1, \underline{\Theta}\right) \cdot \prod_{t=2}^{T} P_{State}\left(\underline{X}_t \mid \underline{\underline{X}}_{t-1}, \underline{\underline{Z}}_{t-1}, \underline{\Theta}\right) \cdot \prod_{t=1}^{T} P_{Observed}\left(\underline{D}_t \mid \underline{\underline{X}}_t, \underline{\underline{Z}}_t, \underline{\Theta}\right)$$

noting that likelihoods that have no information have the value unity and do not affect the calculation of the joint likelihood value.

3.2.3 Model Objective Function

The objective function $\Psi_m\left(\underline{\Theta} \mid \underline{D}\right)$ for a single likelihood-based MAS model, indexed by *m*, is based on the joint likelihood and additional information for prior or hyperprior distributions or other constraints, as needed. The objective function can be optimized using a numerical optimization package that includes the capacity for automatic differentiation (Griewank 2008), such as ADMB (Fournier et al. 2012) or ATL (Supernaw, M., https://github.com/msupernaw/ATL/blob/master/docs/draft_developers_guide%20.pdf) to produce a model solution.

Three primary estimation frameworks are designed to be supported in MAS.

3.2.3.1 Frequentist Estimation

Under a frequentist estimation framework, the maximum likelihood estimate of the parameter vector $\underline{\Theta}_{MLE}$ is obtained by minimizing the objective function $\Psi_m\left(\underline{\Theta} \mid \underline{D}\right)$. The frequentist objective function is comprised of the negative joint loglikelihood of the initial, state, and observed data likelihoods and the sum of any additional penalty terms for numerical constraints or nuisance parameters $\Upsilon_\eta\left(\underline{\underline{X}}_T \mid \underline{\theta}_\eta\right)$. That is, the frequentist objective function can expressed as

(8)
$$\Psi_m\left(\underline{\Theta}_E \mid \underline{\underline{D}}\right) = -\log\left(L\left(\underline{\underline{D}}_T \mid \underline{\underline{X}}_T, \underline{\Theta}_E\right)\right) + \Upsilon_\eta\left(\underline{\underline{X}}_T \mid \underline{\theta}_\eta\right)$$

3.2.3.2 Bayesian Estimation

Under a Bayesian estimation approach, the posterior distribution of the model parameters is sampled through numerical simulation. For simple Bayes MAS models without hierarchical structure, the posterior distribution $P\left(\underline{\Theta}_E \mid \underline{\underline{D}}_T\right)$ is proportional to the product of the prior distributions $\pi_k\left(\underline{\theta}_\pi\right)$ and the joint likelihood of the observed data $L\left(\underline{\underline{D}}_T \mid \underline{\underline{X}}_T, \underline{\Theta}_E\right)$ expressed as $P\left(\underline{\Theta}_E \mid \underline{\underline{D}}_T\right) \propto \prod_k \pi_k\left(\underline{\theta}_\pi\right) \cdot L\left(\underline{\underline{D}}_T \mid \underline{\underline{X}}_T, \underline{\Theta}_E\right)$. Under the simple Bayesian estimation framework, the MAS objective function consists of the negative logarithm of the product of the priors and the joint likelihood along with the sum of any penalty terms. That is, the simple Bayes objective function can be expressed as

(9)
$$\Psi_m\left(\underline{\Theta}_E \mid \underline{\underline{D}}\right) = -\sum_k \log\left(\pi_k\left(\underline{\theta}_\pi\right)\right) - \log\left(L\left(\underline{\underline{D}}_T \mid \underline{\underline{X}}_T, \underline{\Theta}_E\right)\right) + \Upsilon_\eta\left(\underline{\underline{X}}_T \mid \underline{\theta}_\eta\right)$$

Under the hierarchical Bayes estimation framework, the posterior distribution will also include the prior parameter information contained in the hyperprior distribution $\varphi\left(\underline{\theta}_\varphi\right)$. In this case, the posterior distribution is proportional to the product of the hyperprior, prior and likelihood as

(10)
$$P\left(\underline{\Theta}_E \mid \underline{\underline{D}}_T\right) \propto \prod_j \varphi_j\left(\underline{\theta}_\varphi\right) \cdot \prod_k \pi_k\left(\underline{\theta}_\pi \mid \underline{\theta}_\varphi\right) \cdot L\left(\underline{\underline{D}}_T \mid \underline{\underline{X}}_T, \underline{\Theta}_E\right)$$

Under the hierarchical Bayes estimation framework, the MAS objective function consists of the negative logarithm of the hyperpriors, priors and the joint likelihood along with the sum of penalty terms. That is, the hierarchical Bayes MAS objective function is expressed as

(11)
$$\Psi_m\left(\underline{\Theta}_E \mid \underline{\underline{D}}\right) = -\sum_j \log\left(\varphi_j\left(\underline{\theta}_\varphi\right)\right) - \sum_k \log\left(\pi_k\left(\underline{\theta}_\pi \mid \underline{\theta}_\varphi\right)\right) - \log\left(L\left(\underline{\underline{D}}_T \mid \underline{\underline{X}}_T, \underline{\Theta}_E\right)\right) + \Upsilon_\eta\left(\underline{\underline{X}}_T \mid \underline{\theta}_\eta\right)$$

3.2.3.3 Mixed Model Estimation

In the mixed model estimation framework, MAS models that incorporate random effects can be expected to include random effects parameters for unobserved system state variables and fixed effects parameters for catch scaling, catchability, correlation and variance parameters in a state space modeling framework (e.g., Nielsen and Berg 2014). These parameters can be fitted through integrated nested Laplace approximation (Rue et al. 2009, Kristensen et al. 2016, Wood 2019) or restricted maximum likelihood-based estimation and other approaches (Demidenko 2004). Under the mixed-effects framework, parameter optimization is based on a hierarchical statistical model where all parameters are, in effect, estimated based on the observed data. This provides a more flexible treatment of hyperparameters, which are estimated from data in contrast to being assumed under a Bayesian framework.

Under either the frequentist or the Bayesian estimation frameworks, parametric uncertainty can characterized using standard techniques, e.g., estimating the asymptotic covariance matrix, parametric bootstrapping, or Markov Chain Monte Carlo simulation, given the parameter solution estimate $\hat{\underline{\Theta}}_E$ and the estimate of the parameter covariance matrix evaluated at the solution $\hat{\Sigma}=\Sigma\left(\hat{\underline{\Theta}}_E\right)$.

The capacity to conduct stock projections depends on the estimates of model parameters and their estimated covariance matrix. In practice, it is also important to have input and output structures that can efficiently support model verification through simulation testing as well as management strategy evaluation analyses. As noted previously, the use of JSON is being explored to produce the necessary input structures for MAS to handle binary input arrays.

3.2.4 Model Information Components

The MAS Class requires a model storage array, or list, for organizing the information on the definition of each parameter as part of the overall MAS model. An array representation of the set of model parameters has advantages and limitations including: physically contiguous storage in random access memory RAM, fixed length in RAM, elements are rapidly accessed by index, but insertion or removal of array elements is costly. Similarly, a linked list representation of the set of model parameters has advantages and limitations including: logically contiguous storage in RAM, changeable length, elements are accessed by traversing the list, and insertion and removal of list elements is efficient. The best or most computationally efficient representation of the model parameter information is dependent on the problem structure. Currently most assessment software systems typically use an array representation.

Regardless of how the model parameter information is to be stored and indexed, for any given estimation procedure, e.g., maximum likelihood (MLE), random effects (RE), Simple Bayes (SB), Hierarchical Bayes (HB) and so on, the information components needed to characterize each parameter include:

(1) **Parameter identifier**. Specifies the unique identifier for the parameter and the submodel(s) to which the parameter pertains.

(2) **Parameter type**. Specifies if the parameter is to be fixed (e.g., constant in space and time) or to be freely estimated in a statistical optimization procedure.

(3) **Estimation order**. Specifies the relative order in which the parameter or sets of parameters are to be estimated in the estimation procedure, relative to the set of other parameters. This allows for phased estimation of model parameters which can improve the efficiency of the search algorithm used to identify the best-fitting model parameters.

(4) **Derivative information**. Specifies whether first, second, or third order derivatives or other information about the objective function will be needed for optimization.

(5) **Parameter constraints**. Specify pointers to the prior and hyperprior distributions constraints to identify probable parameter values, as needed.

(6) **Environmental effects**. Specify linkages to time- or space-varying environmental variables that affect parameter value, as needed.

(7) **Other links**. Specify an extensible list of links to other information, as needed.

This flexible structure provides an extensible list for storing the MAS model parameter information.

Given the model parameter array, an overview of the set of subsystem data and component structure objects along with associated cases, or submodels, is provided below for each of the primary MAS model components.

3.2.4.1 Population Component

The population component information consists of the metapopulation data and structure. This information effectively defines the dynamics of the population and its associated processes of growth, movement, maturation, mortality, recruitment, and other processes as represented by specific cases or submodels. Algorithms to calculate the unfished equilibrium numbers at age, the fished equilibrium numbers at age, the dynamic fished numbers at age within the assessment time horizon, and the dynamic fished numbers at age within the forecast time horizon are provided in Appendices 1, 2, 3, and 4, respectively.

In general, the data for the Population Component includes:

- Population logic data – this is a list or case array storing the choices of submodels that have been selected for the population.
- Population numbers at age and structure data by location – this is a set of arrays storing population numbers by structuring variable, e.g., age or length, and associated derived quantities of interest.
- Population movement data by location – this is a set of arrays storing population movement parameters.
- Population dynamics parameter data by location – this is a set of arrays or lists storing the population dynamics parameters needed for the set of submodels represented by the logical case data.

In general, the population dynamics submodels for the Population Component include the structural subcomponents listed below.

3.2.4.1.1 Model domain

The model domain for each population will include a two-gender (g=2) or pooled-sex (g=1) population dynamics submodel analogous to the set of modeling options described in Methot and Wetzel (2013) with age classes ranging from a=0 (or a=1) to a=A years of age and annual (y) and seasonal time steps (t) jointly denoted as (y,t) with years ranging from y=1 to y=Y years and seasons ranging from t=1 to t=T seasons.

- Case 1. An annual cycle of Y years with T seasons and g=2 genders.
  This case represents a two-sex model with a fixed time frame.

- Case 2. An annual cycle of Y years with T seasons and g=1 genders.
  This case represents a pooled-sex model with a fixed time frame.

3.2.4.1.2 Seasonal structure

The seasonal structure of the fishery system includes the annual cycle of Y years and the seasonal, or within-year, component. The timing of the population processes is defined in the context of seasons, or time periods, indexed by t, within a year. There are a total of T seasons in each year, where the time period representing year y and season t is denoted as (y,t). For the case of a single season with T=1, the notation for the annual time steps is ($y,t=1$) with the single season label only included for consistency with the general case of multiple seasons. Each of the T seasons is defined in terms of its start and end time as a fraction of the year with the entire year comprising a unit interval. For example, season k has a start fraction of τ_{k-1} and end fraction τ_k

and is represented as the half-open interval $[\tau_{k-1,}\ \tau_k)$ for $k = 1, 2, ..., T$, where $\tau_0 \equiv 0$ and $\tau_T \equiv 1$. In particular, each year *y* is comprised of a sequence of *T* seasons which are represented by the unique set of *T* intervals, denoted by Ω_T , where $\Omega_T = \{[\tau_0,\tau_1),...,[\tau_{k-1},\tau_k),...,[\tau_{T-1},\tau_T)\}$, $0 = \tau_0 < \tau_1 < \tau_2 < ... < \tau_{T-1} < \tau_T = 1$, and $\underline{\tau}$ is the $T - 1$ dimensional vector $\underline{\tau} = (\tau_1, \tau_2, ..., \tau_{T-1})$ of the cutpoints between seasons. In addition, we denote the length of season *k* by $\Delta_k = \tau_k - \tau_{k-1}$ and note that the sum of the season lengths will always sum to unity, that is, $\sum_{k=1}^{T} \Delta_k = 1$.

- Case 1. An annual cycle of *Y* years with a single season (*T* =1).
  Population dynamics occur in an annual cycle and events within the year area represented as occurring with population numbers at age discounted for the amount of total instantaneous mortality experienced up to the time of the event.
- Case 2. An annual cycle of *Y* years with *T* >1 seasons.
  The discrete time box-transfer movement model where fishery catch occurs at the fraction ΔC_k of the length of season *k*, seasonal natural mortality proportional to season length, and fish movement occurs at the end of each season. A diagram of the seasonal sequence for an example with three seasons shows the timing of the fishery catch and of fish movement through the annual cycle (Figure 7).

3.2.4.1.3 Population numbers

The numbers of fish in the population by area (*s*), age (*a*) or size structure (*b*), and sex (*g*) at the start of time period (*y*,*t*), are denoted by $N^{(p)}_{(y,t),s,a,g}$. That is, $N^{(p)}_{(y,t),s,a,g}$ is the number of age-*a* and gender-*g* fish in area-*s* from population *p* at the start of season *t* in year *y*. The end point of the t^{th} season as a fraction of one year is denoted by τ_t. Given this notation, the season *t* consists of the time interval $[\tau_{t-1}, \tau_t)$. In general, specific points in time τ^* within the t^{th} season are denoted by $\tau^* = \tau_{t-1} + \Delta^*$ or as the sum of the starting point of the t^{th} season and the fraction of the season length Δ^* to time τ^* within season *t* where $0 \le \Delta^* < \Delta_t$.

- Case 1. Population numbers at age and gender by area for *Y* years and *T* seasons.
  Based on this, one can express the number of age-*a* and gender-*g* fish in area-*s* from population *p* at any time τ^* in season *t* of year *y* as

$$N^{(p)}_{(y,\tau^*),s,a,g} = N^{(p)}_{(y,\tau_{t-1}+\Delta^*),s,a,g} \tag{12}$$

3.2.4.1.4 Natural mortality processes

The natural mortality processes of fish in the population by area, age, and gender are represented by the instantaneous natural mortality rate during season *t* in year *y*, denoted by $M^{(p)}_{(y,t),s,a,g}$, where year and season both are indexed for the time dimension. For a population that is unfished and experiences no fishing mortality, the value of the instantaneous natural mortality rate during season *t* in year *y* determines the numbers at age and gender by area at any time τ^* during the season via

(13) $$N^{(p)}_{(y,\tau^*),s,a,g} = N^{(p)}_{(y,t),s,a,g} \cdot \exp\left(-\Delta^* \cdot M^{(p)}_{(y,t),s,a,g}\right)$$

- Case 1. Constant annual natural mortality by population as a function of maximum age. If the population annual natural mortality rate can be assumed to vary as a function of maximum age in the unfished population, denoted by $t_{\max}$, then Hoenig's (1983) linear regression model for fishes listed in equation (14) can be applied to predict the expected natural mortality rate, denoted by $M^{(p)}$, as

(14) $$M^{(p)} = \frac{4.31}{\left(t_{\max}\right)^{1.01}}$$

Two other recent approaches also characterized the relationship between maximum age and natural mortality rate using similar data sets to that used in Hoenig (1983). Then et al. (2015) updated the Hoenig estimator using a nonlinear least squares estimator and recommended using the following relationship to predict $M^{(p)}$ as

(15) $$M^{(p)} = \frac{4.899}{\left(t_{\max}\right)^{0.916}}$$

Hamel (2015) revisited the Hoenig estimator using a meta analytical approach and developed another maximum age-based predictive model for $M^{(p)}$ assuming a fixed exponent of 1 as

(16) $$M^{(p)} = \frac{4.374}{t_{\max}}$$

3.2.4.1.5 Total mortality processes

The total mortality processes of fish in the population by area, age, and gender are represented by the instantaneous total mortality rate during season *t* in year *y*, denoted by $Z^{(p)}_{(y,t),s,a,g}$, where year and season both are indexed for the time dimension. In general, the instantaneous total mortality rate will be the sum of the instantaneous natural and fishing mortality rates. That is, the population total mortality rate will be the sum of natural and fishing mortality by season, where population fishing mortality, natural mortality, and total mortality rates by area, age, and gender by season are denoted by $F^{(p)}_{(y,t),s,a,g}$, $M^{(p)}_{(y,t),s,a,g}$, and $Z^{(p)}_{(y,t),s,a,g}$, and the total instantaneous seasonal mortality rate is

$$Z^{(p)}_{(y,t),s,a,g} = M^{(p)}_{(y,t),s,a,g} + F^{(p)}_{(y,t),s,a,g} \tag{17}$$

Where the fishing mortality is calculated from the fleet-specific fishing mortality rates and the fleet-specific fishery selectivities as

$$F^{(p)}_{(y,t),s,a,g} = \sum_{v=1}^{V} S^{(p)}_{v,(y,t),s,a,g} F^{(p)}_{v,(y,t),s,a,g} \tag{18}$$

The total instantaneous seasonal mortality rate can be calculated from the population numbers at the beginning and end of the season as

$$Z^{(p)}_{(y,t),s,a,g} = \log\left(\frac{N^{(p)}_{(y,t),s,a,g}}{N^{(p)}_{(y,t+1),s,a,g}} \right) \tag{19}$$

Given the value of the instantaneous total mortality rate during season *t* in year *y*, denoted by $Z^{(p)}_{(y,t),s,a,g}$, the numbers at age and gender by area at any time τ^* during the season can be calculated as (Figure 8)

$$N^{(p)}_{(y,\tau^*),s,a,g} = N^{(p)}_{(y,t),s,a,g} \cdot \exp\left(-\Delta^* \cdot Z^{(p)}_{(y,t),s,a,g} \right) \tag{20}$$

- Case 1. Constant population annual natural mortality by season as a function of season length.
  If the population annual natural mortality rate varies by area, age, and gender but does not vary through time, denoted by $M^{(p)}_{s,a,g}$, and the seasonal natural mortality rate for season *t* is proportional to season length, then $M^{(p)}_{(y,t),s,a,g} = M^{(p)}_{s,a,g} \cdot \Delta_t$. In this case, the total instantaneous mortality rate for season *t* of year *y* is
  $Z^{(p)}_{(y,t),s,a,g} = M^{(p)}_{s,a,g} \cdot \Delta_t + F^{(p)}_{(y,t),s,a,g}$
  And the population size at any time τ^* in season t can be expressed as

$$N^{(p)}_{(y,\tau^*),s,a,g} = N^{(p)}_{(y,\tau_{t-1}+\Delta^*),s,a,g} = N^{(p)}_{(y,t),s,a,g} \cdot \exp\left(-\Delta^* \cdot \Delta_t \cdot M^{(p)}_{s,a,g} - F^{(p)}_{(y,t),s,a,g} \right) \tag{21}$$

3.2.4.1.6 Growth processes

The growth processes of fish in the population by area, age or size structure (*b*), and sex through time, are represented by mean weight $W^{(p)}_{(y,t),s,a,g}$ or mean length $L^{(p)}_{(y,t),s,a,g}$ in the population components with multiple case options. The mean weights or lengths can be based on empirical sample-based estimates or on growth functions fit outside or estimated within the assessment modeling process. Algorithms to calculate both the equilibrium and time-varying mean length of fish in the plus group are provided in Appendix 4.

- <u>Case 1. Empirical mean weights at age by area</u>.
  In the first case, the mean weights at age by area during season *t*, $W^{(p)}_{(y,t),s,a,g}$, are determined by sampling fish weights at age in the population. The weight data are input as an array with appropriate dimensioning to reflect sampling coverage and representativeness. For example, there may be a single weight at age array that is constant by area. Regardless, the empirical mean weights are assumed to represent the mean weight during the entire season (Figure 9).

- <u>Case 2. Empirical mean weights at age by area with seasonal timing</u>.
  In the second case, the mean weights at age by area at the fraction ΔW_t of the length of season *t*, $W^{(p)}_{(y,\tau^*),s,a,g}$, are also determined by sampling fish weights at age in the population. The weight data represent the expected value of fish weights at time $\tau^* = \tau_{t-1} + \Delta W_t$ within the season. Expected values for other points in time during the season are calculated by interpolation.
- <u>Case 3. Von Bertalanffy length-at-age model by area (*s*)</u>.
  Mean length at age *a* (measured in fractional years) in area *s* at the start of season *t* in year *y* is denoted by $L_{(y,t),s}(a)$ and follows a von Bertalanffy growth curve. That is, the mean length at age in area *s* is a function of three parameters: asymptotic length ($L_{\infty,s}$), Brody growth coefficient (k_s), and age at length 0 ($a_{0,s}$) via

(22)
$$L_{(y,t),s}(a) = L_{\infty,s}\left(1-\exp\left(-k_s\left(a-a_{0,s}\right)\right)\right)$$

In the third case, we use an alternative parameterization of the curve (Schnute and Fournier 1980, Ratkowsky 1983) that has better statistical properties than the original form of the von Bertalanffy curve. The expression for this modified von Bertalanffy curve is

(23)
$$L_{(y,t),s}(a) = L_{\min,s} + \left(L_{\max,s} - L_{\min,s}\right)\cdot\frac{1-\left(c_s\right)^{a-a_{\min}}}{1-\left(c_s\right)^{a_{\max}-a_{\min}}}$$

where $L_{\min,s}$ and $L_{\max,s}$ are the area-specific mean length parameters at the input ages $a_{\min}$ and $a_{\max}$, respectively, and c_s is the growth curvature parameter. In this case, the parameters of the two curves are directly related via the following expressions (Schnute and Fournier 1980) and dropping the area subscripts

$$(24)\qquad L_{\infty} = \frac{L_{\max} - L_{\min}\cdot c^{a_{\max}-1}}{1-c^{a_{\max}-1}} \quad k = -\log(c) \quad a_0 = a_{\min} - \frac{1}{\log(c)}\log\left(\frac{L_{\max} - L_{\min}}{L_{\max} - L_{\min}\cdot c^{a_{\max}-1}}\right)$$

Given the mean length at age curve, the mean weight at age *a* in area *s* at the start of season *t* in year *y* is calculated from the mean length and the expected weight-length relationship for area *s* as

$$(25)\qquad W_{(y,t),s}(a) = \alpha_s \cdot \left(L_{(y,t),s}(a)\right)^{\beta_s}$$

where α_s and β_s are length-weight parameters for area *s*.

- Case 4. Schnute's (1981) general 4-parameter growth model.
  In this case, mean length at age *a* at the start of season *t* in year *y* is

$$(26)\qquad L_{(y,t)}(a) = \left\{L_{\min}^{\beta} + \left(L_{\max}^{\beta} - L_{\min}^{\beta}\right)\cdot\frac{1-\exp\left(-\alpha\left(a-a_{\min}\right)\right)}{1-\exp\left(-\alpha\left(a_{\max}-a_{\min}\right)\right)}\right\}^{\beta^{-1}}$$

for parameters $\alpha, \beta, L_{\min}, L_{\max}$ where $L_{\min}$ is estimated size at the input minimum age $a_{\min}$ and $L_{\max}$ is estimated size at the input maximum age $a_{\max}$.

- Case 5. Schnute's (1981) first 3-parameter growth model.
  Mean length at age *a* at the start of season *t* in year *y* is

$$(27)\qquad L_{(y,t)}(a) = L_{\min}\cdot\exp\left(\log\left(\frac{L_{\max}}{L_{\min}}\right)\frac{1-\exp\left(-\alpha\left(a-a_{\min}\right)\right)}{1-\exp\left(-\alpha\left(a_{\max}-a_{\min}\right)\right)}\right)$$

for parameters $\alpha, L_{\min}, L_{\max}$.

- Case 6. Schnute's (1981) second 3-parameter growth model.
  Mean length at age *a* at the start of season *t* in year *y* is

$$(28)\qquad L_{(y,t)}(a) = \left\{L_{\min}^{\beta} + \left(L_{\max}^{\beta} - L_{\min}^{\beta}\right)\cdot\frac{a-a_{\min}}{a_{\max}-a_{\min}}\right\}^{\beta^{-1}}$$

for parameters $\beta, L_{\min}, L_{\max}$

- Case 7. Schnute's (1981) general 2-parameter growth model.

Mean length at age *a* at the start of season *t* in year *y* is

(29) $$L_{(y,t)}(a) = L_{\min} \cdot \exp\left(\log\left(\frac{L_{\max}}{L_{\min}}\right)\frac{a - a_{\min}}{a_{\max} - a_{\min}}\right)$$

for parameters $L_{\min}, L_{\max}$.

Mean length or weight at age can also be independent or dependent on environmental processes or population biomass by area or other factors.

- <u>Case 8. Density-dependence for the von Bertalanffy asymptotic weight value ($W^{(p)}_{\infty,(y,t),s}$) which depends on population biomass by spatial location (*s*) through time (*y,t*)</u>.

(30) $$W^{(p)}_{\infty,(y,t),s} = W_{\infty} - \gamma^{(p)} \cdot B^{(p)}_{(y,t),s}$$

for a metapopulation asymptotic length W_{∞} and population density-dependence parameter $\gamma^{(p)}$.

3.2.4.1.7 Weight-length processes

The weight-length processes of fish in the population by area and gender at the start of season *t* in year *y*, where weight is a function of length *f* and parameters θ

(31) $$W^{(p)}_{(y,t),s,g} = f\left(L^{(p)}_{(y,t),s,g}, \theta\right)$$

- <u>Case 1. Allometric model by spatial location (*s*)</u>.
  Mean weight at length *L* in area *s* at the start of season *t* in year *y* is denoted by $W^{(p)}_{(y,t),s}(L)$ and is given by

(32) $$W^{(p)}_{(y,t),s}(L) = \alpha^{(p)}_{s} \cdot L^{\beta^{(p)}_{s}}$$

where $\alpha^{(p)}_{s}$ and $\beta^{(p)}_{s}$ area area-specific length-weight parameters for the *p*th population.

3.2.4.1.8 Population biomass

The total biomass of fish in the population in area *s* at the start of season *t* in year *y* is the sum of the biomasses of all fish in the population, which is also the product of numbers by structure and their mean weights at the start of season *t*, and is denoted by $B^{(p)}_{(y,t),s}$.

- <u>Case 1. Two-sex population model</u>.

The total biomass in the population in area *s* at the start of season *t* is the sum of the biomasses of fish by age and gender via

(33) $$B^{(p)}_{(y,t),s} = \sum_a \sum_g B^{(p)}_{(y,t),s,a,g} = \sum_a \sum_g N^{(p)}_{(y,t),s,a,g} W^{(p)}_{(y,t),s,a,g}$$

While the total biomass at any time τ^* during season t is

(34) $$B^{(p)}_{(y,\tau^*),s} = \sum_a \sum_g B^{(p)}_{(y,\tau^*),s,a,g} = \sum_a \sum_g N^{(p)}_{(y,\tau^*),s,a,g} W^{(p)}_{(y,\tau^*),s,a,g}$$

- Case 2. Pooled-sex population model.
  The total biomass in the population in area *s* at the start of season *t* is the sum of the biomasses of fish by age as

(35) $$B^{(p)}_{(y,t),s} = \sum_a B^{(p)}_{(y,t),s,a} = \sum_a N^{(p)}_{(y,t),s,a} W^{(p)}_{(y,t),s,a}$$

While the total biomass at any time τ^* during season t is

(36) $$B^{(p)}_{(y,\tau^*),s} = \sum_a B^{(p)}_{(y,\tau^*),s,a} = \sum_a N^{(p)}_{(y,\tau^*),s,a} W^{(p)}_{(y,\tau^*),s,a}$$

3.2.4.1.9 Maturity processes

The maturity processes of fish in the population represent the probability that a fish is mature by area, age, and gender through time, where $P^{(p)}_{Mature,(y,t),s,a,g}$ is the probability that a given fish of age-*a* and gender *g* in area *s* is mature at the start of season *t* in year *y*.

- Case 1. Logistic maturity ogive by spatial location (*s*).
  The probability that an age-*a* fish of gender *g* in area *s* is mature is given by the logistic model

(37) $$P^{(p)}_{Mature,(y,t),s,a,g} = \frac{\exp\left(\dfrac{a-a^{(p)}_{50,s}}{\sigma^{(p)}_{Mature,s}}\right)}{1+\exp\left(\dfrac{a-a^{(p)}_{50,s}}{\sigma^{(p)}_{Mature,s}}\right)}$$

where $a^{(p)}_{50,s}$ is an area-specific age at 50% maturity and $\sigma^{(p)}_{Mature,s}$ is an area-specific slope parameter for the population. Here the maturity probabilities are assumed to represent the maturity state during the entire season.

- Case 2. Empirical maturity probabilities at age by area.

In the second case, the maturity at age probabilities by area during season *t*, $P^{(p)}_{Mature,(y,t),s,a,g}$, are input as an array with appropriate dimensioning to match the structure of the population model, similar to the empirical mean weights at age.

3.2.4.1.10 Spawning biomass

The spawning biomass of fish in the population in area *s* at the start of season *t* in year *y* is the sum of the biomasses of all adult fish in the population, which is also the product of numbers by structure and their mean weights at the start of season *t*, and is denoted by $SB^{(p)}_{(y,t),s}$.

- Case 1. Two-sex population model.

  The female biomass in the population in area *s* at time τ^* during season *t* is the sum of the biomasses of mature female fish by age and is

(38)
$$\begin{aligned} SB^{(p)}_{(y,\tau^*),s,g=female} &= \sum_a SB^{(p)}_{(y,\tau^*),s,a,g=female} \\ &= \sum_a N^{(p)}_{(y,\tau^*),s,a,g=female} W^{(p)}_{(y,\tau^*),s,a,g=female} P^{(p)}_{Mature,(y,\tau^*),s,a,g=female} \end{aligned}$$

  While the spawning biomass of all adult fish at any time τ^* during season t is

(39)
$$SB^{(p)}_{(y,\tau^*),s} = \sum_a \sum_g SB^{(p)}_{(y,\tau^*),s,a,g} = \sum_a \sum_g N^{(p)}_{(y,\tau^*),s,a,g} W^{(p)}_{(y,\tau^*),s,a,g} P^{(p)}_{Mature,(y,\tau^*),s,a,g}$$

- Case 2. Pooled-sex population model.

  The spawning biomass in the population in area *s* at time τ^* during season *t* is the sum of the biomasses of mature fish by age as

(40)
$$SB^{(p)}_{(y,\tau^*),s} = \sum_a SB^{(p)}_{(y,\tau^*),s,a} = \sum_a N^{(p)}_{(y,\tau^*),s,a} W^{(p)}_{(y,\tau^*),s,a} P^{(p)}_{Mature,(y,\tau^*),s,a}$$

3.2.4.1.11 Fecundity processes

The fecundity processes of fish in the population determine the production of eggs, or the output of early life history stage offspring, by area, and age or size through time, where $E^{(p)}_{(y,t),s,a}$ is the area-specific (*s*) number of eggs produced by an age-*a* spawner in season *t* of year *y* by the population.

- Case 1. Egg production is proportional to spawning biomass.

  In this case, total egg production in area *s* during season *t* of year *y* $E^{(p)}_{(y,t),s}$ is a linear function of the body mass of adult fish where

(41)
$$E^{(p)}_{(y,t),s} = \zeta \cdot SB^{(p)}_{(y,t),s}$$

and ζ is a positive constant.

- <u>Case 2. Egg production as a function of fish length by spatial location (*s*).</u>
  The expected egg production of a length-*L* female fish in area *s* is $E_s^{(p)}(L)$ and is given by

(42) $$E_s^{(p)}(L) = b_{0,s}^{(p)} + b_{1,s}^{(p)} \cdot L$$

where $b_{0,s}^{(p)}$ and $b_{1,s}^{(p)}$ are area-specific fecundity parameters for the population. The total egg production in area *s* during season *t* of year *y*, $E_{(y,t),s}^{(p)}$, is then the sum of the egg production at length over all females

(43) $$E_{(y,t),s}^{(p)} = \sum_L N_{(y,t),s,L,g=female}^{(p)} \cdot E_s^{(p)}(L)$$

3.2.4.1.12 Recruitment processes

The recruitment processes of fish in the population by area through time, $R_{(y,t),s}^{(p)}$, are indexed by season to allow for determinate spawning in a single season or indeterminate spawning occurring in seasons throughout the year. The recruitment processes for the subpopulation are modeled with four components. The first component is the set of seasons when spawning occurs during the year, denoted by Ω_S, and the second is the set of seasons when recruitment occurs during the year, Ω_R The first two components may typically be the same seasons but the separation allows for a time delay between spawning and the appearance of recruits in the population. The third component is the set of recruitment distribution matrices which contain the fraction of recruitment produced in area *i* during season *t* that occurs in area *s*, denoted by $Q_{(y,t),(i,s)}^{(p)}$. The fourth component is the expected relationship between spawning abundance and the production of recruits, which is typically modeled as age-0 or age-1 fish. The fifth component is the error distribution for the recruitment process, which could be a stationary or time-varying distribution. The sixth component is the environmental forcing distribution which characterizes the influence of one or more environmental variables on recruitment strength. In general, the spatial pattern of recruitment will depend on environmental processes and will also depend on maturation, spawning, and fecundity processes for the calculation of spawning biomass (see, for example, Subbey et al. 2014).

- <u>Case 1. Natal homing of genetically distinct populations with a population-specific Beverton-Holt stock-recruitment relationship to predict annual recruitment with lognormal variation.</u>

In this case, there is a single season for spawning and recruitment. The recruitment produced by population *p* occurs in the spawning season, denoted by $t_S^{(p)}$, and is denoted by $R^{(p)}_{(y)} \equiv R^{(p)}_{(y,t_S^{(p)})}$. Here the entire population migrates to its spawning area $S^{(p)}_{Spawn}$ in the season prior to the spawning season. The calculated value of recruitment using the steepness parameterization of the Beverton-Holt model is a function of population spawning biomass in the spawning season, denoted by $SB^{(p)}_{(y)} \equiv SB^{(p)}_{(y,t_S^{(p)})}$, and is

(44) $$R^{(p)}_{(y)} = \frac{4h^{(p)} \cdot R_0^{(p)} \cdot SB^{(p)}_{(y)}}{SB_0^{(p)}\left(1-h^{(p)}\right)+SB^{(p)}_{(y)}\left(5h^{(p)}-1\right)} \cdot e^{-0.5\sigma^2_{R^{(p)}}+\Lambda_{R^{(p)}_{(y)}}} \quad where\ \Lambda_{R^{(p)}_{(y)}} \sim N\left(0,\sigma^2_{R^{(p)}}\right)$$

where, $h^{(p)}$ is the stock-recruitment steepness parameter for the p^{th} population, $SB_0^{(p)}$ is the unfished spawning biomass or measure of spawning output, $R_0^{(p)}$ is the unfished recruitment parameter, $\Lambda_{R^{(p)}_{(y)}}$ is the log-scale recruitment deviation parameter in year *y*, and $\sigma^2_{R^{(p)}}$ is the log-scale variance parameter for the recruitment deviations. In this case, the process error distribution is a stationary lognormal distribution and there is no environmental forcing distribution. An alternative form of the Beverton-Holt curve uses the parameterization $\alpha^{(p)} = \frac{4h^{(p)} \cdot R_0^{(p)}}{5h^{(p)}-1}$ and $\beta^{(p)} = \frac{SB_0^{(p)}\left(1-h^{(p)}\right)}{5h^{(p)}-1}$.

Given the value of annual recruitment, the population recruitment in area *s*, denoted by $R^{(p)}_{(y),s} \equiv R^{(p)}_{(y,t_S^{(p)}),s}$, is the product of the annual recruitment times the probability that a recruit is transported to area *s* in season $t_S^{(p)}$, denoted by $Q^{(p)}_{(y),s} \equiv Q^{(p)}_{(y,t_S^{(p)}),s}$. That is, $R^{(p)}_{(y),s} = Q^{(p)}_{(y),s} \cdot R^{(p)}_{(y)}$.

- Case 2. Seasonal spawning of genetically distinct populations with a population-specific Ricker stock-recruitment relationship to predict seasonal recruitment with lognormal variation.
  In this case, spawning and recruitment occur in each season. The recruitment produced by population *p* occurs in each season *t* and is denoted by $R^{(p)}_{(y,t)}$. The expected value of recruitment is a function of population spawning biomass by season, denoted by $SB^{(p)}_{(y,t)}$, and is

(45) $$R^{(p)}_{(y,t)} = \alpha^{(p)} \cdot SB^{(p)}_{(y,t)} \cdot e^{-\beta^{(p)} \cdot SB^{(p)}_{(y,t)}} \cdot e^{-0.5\sigma^2_{R^{(p)}}+\Lambda_{R^{(p)}_{(y,t)}}} \quad where\ \Lambda_{R^{(p)}_{(y,t)}} \sim N\left(0,\sigma^2_{R^{(p)}}\right)$$

where, $\alpha^{(p)}$ is a stock-recruitment productivity parameter for the p^{th} population, $\beta^{(p)}$ is a density-dependence parameter, $\Lambda_{R^{(p)}_{(y,t)}}$ is the log-scale recruitment deviation parameter in season t of year y, and $\sigma^2_{R^{(p)}}$ is the log-scale variance parameter for the recruitment deviations.

Given the value of seasonal recruitment, the population recruitment in area s, denoted by $R^{(p)}_{(y,t),s}$, is the product of the seasonal recruitment times the probability that a recruit is transported to area s in season t, denoted by $Q^{(p)}_{(y,t),s}$. That is, $R^{(p)}_{(y,t),s} = Q^{(p)}_{(y,t),s} \cdot R^{(p)}_{(y,t)}$.

- Case 3. Annual spawning of a genetically distinct population with a population-specific Shepherd stock-recruitment relationship to predict annual recruitment with lognormal variation.
  In case 3, there is one season for spawning and recruitment. The recruitment produced by population p occurs in the spawning season and is $R^{(p)}_{(y)}$. The calculated value of recruitment using the Shepherd stock-recruitment model is a function of population spawning biomass in the spawning season, $SB^{(p)}_{(y)}$, and is

(46)
$$R^{(p)}_{(y)} = \frac{\alpha^{(p)} \cdot SB^{(p)}_{(y)}}{1+\left(\dfrac{SB^{(p)}_{(y)}}{\beta^{(p)}}\right)^{c^{(p)}}} \cdot e^{-0.5\sigma^2_{R^{(p)}}+\Lambda_{R^{(p)}_{(y)}}} \quad where\ \Lambda_{R^{(p)}_{(y)}} \sim N\left(0,\sigma^2_{R^{(p)}}\right)$$

- where $\left(\alpha^{(p)}, \beta^{(p)}, c^{(p)}\right)$ are the stock-recruitment parameters for the Shepherd curve, $\Lambda_{R^{(p)}_{(y)}}$ is the log-scale recruitment deviation parameter in year y, and $\sigma^2_{R^{(p)}}$ is the log-scale variance parameter for the recruitment deviations. In this case, the process error distribution is a stationary lognormal distribution and there is no environmental forcing distribution.
- Case 4. Natal homing of genetically distinct populations with population-specific mean recruitment values to predict annual recruitment with autocorrelated lognormal variation.
  As in Case 1, there is a single season for spawning and recruitment. The recruitment produced by population p occurs in the spawning season $t_S^{(p)}$ and is $R^{(p)}_{(y)}$. The expected value of recruitment in the p^{th} population is $\overline{R}^{(p)}$ and the annual recruitments are calculated using

(47)
$$R^{(p)}_{(y)} = \overline{R}^{(p)} \cdot e^{-0.5\sigma^2_{\varepsilon^{(p)}}+\varepsilon^{(p)}_{(y)}}$$
$$where\ \varepsilon^{(p)}_{(y)} = \phi^{(p)}\varepsilon^{(p)}_{(y-1)} + \Lambda_{R^{(p)}_{(y)}} \ \ and\ \ \Lambda_{R^{(p)}_{(y)}} \sim N\left(0,\sigma^2_{R^{(p)}}\right)$$

where $\phi^{(p)}$ is the autoregressive parameter for the p^{th} population, $\varepsilon_{(y)}^{(p)}$ is the autoregressive lognormal error, $\sigma^2_{\varepsilon^{(p)}}$ is the autoregressive error variance with $\sigma^2_{\varepsilon^{(p)}} = \sqrt{\sigma^2_{R^{(p)}}\left(1-\phi^2\right)}$, $\Lambda_{R^{(p)}_{(y)}}$ is the log-scale recruitment deviation parameter in year y, and $\sigma^2_{R^{(p)}}$ is the log-scale variance parameter for the recruitment deviations. In this case, the process error distribution is a time-varying distribution and there is no environmental forcing distribution. Based on the calculated value of annual recruitment, the population recruitment in area s is the product of the annual recruitment times the probability that a recruit is transported to area s, or $R^{(p)}_{(y),s} = Q^{(p)}_{(y),s} \cdot R^{(p)}_{(y)}$.

3.2.4.1.13 Movement probabilities

The movement probabilities of fish in the population from the initial area (source) to the destination area (sink) by age and gender through time are $T^{(p)}_{(y,t),(i,s),a,g}$, where year and season are both indexed in the time dimension. In general, the sums of movement probabilities from a specific source area to all sinks sum to unity during a given season and year, for the given population structure being modeled, e.g. an age-structured population model.

- <u>Case 1. Population movement is time-invariant, age-invariant, and gender-invariant</u>. Population p has a constant movement probability matrix and the probability of an individual fish moving from area i to area s is denoted by $T^{(p)}_{(i,s)}$.
- <u>Case 2. Population movement does not occur.</u> In this case, the individuals in the population are sessile after recruitment and the movement probability matrix is the identity matrix $T^{(p)}_{(i,s)} = \underline{\underline{I}}$. In particular, the probability of an individual fish moving from area i to area s is $T^{(p)}_{(i,s)} = 1$ if $i = s$ and otherwise $T^{(p)}_{(i,s)} = 0$.

3.2.4.1.14 Initial population numbers

The initial numbers of fish in the population by area, age, and gender, is the number of age-a and gender-g fish in area-s from population p at the start of the assessment time horizon during season t=1 in year y=1 is $N^{(p)}_{(y=1,t=1),s,a,g}$. The initial numbers at age in the population can be split into three categories: recruitment, true age classes, and the plus group or accumulator age group consisting of all fish age-A and older.

<u>Recruitment</u> is the number of age-*0* fish in the p^{th} population in area s of gender g during season t=1 in year y=1, denoted by $R^{(p)}_{(y,t),s,g}\left(\Theta,D\right) = N^{(p)}_{(y=1,t=1),s,0,g}$, where R is a function of model parameters and data. In practice, the initial recruitment size can be treated as a parameter

to be estimated. Given a constant female fraction of recruits r_g, that is, $N^{(p)}_{(y=1,t=1),s,0,g=female} = r_g \cdot N^{(p)}_{(y=1,t=1),s,0}$ for females and $N^{(p)}_{(y=1,t=1),s,0,g=male} = \left(1-r_g\right) \cdot N^{(p)}_{(y=1,t=1),s,0}$ for males.

<u>The true age classes</u> are the numbers of fish at ages a = age-1 to age-(A-1) fish in the population (p) that have survived to be in area s of gender g during season t=1 in year y=1, denoted by $N^{(p)}_{(y=1,t=1),s,a,g} = S^{(p)}_{s,a,g}\left(\Theta, D\right)$, where S is a function of model parameters and data.

<u>The plus-group</u> is the number of fish age a = age-A and older in the population (p) that have survived to be in area s of gender g during season t=1 in year y=1, denoted by $N^{(p)}_{(y=1,t=1),s,A,g} = S^{(p)}_{s,A,g}\left(\Theta, D\right)$, where S is a general function of model parameters and data.

- <u>Case 1. Pooled-sex model with constant age-specific movement probabilities and estimated total mortality rates based on a fishery system in equilibrium.</u>
  Consider the p^{th} population using a pooled-sex model with constant age- and area-specific movement probabilities from area i to area s ($T^{(p)}_{(i,s),a}$) and constant age-specific total mortality rates ($Z^{(p)}_{s,a}$). The initial number of fish in population p in area s of age a in season t=1 during year y=1 is $N^{(p)}_{(y=1,t=1),s,a}$. The initial numbers at age are in equilibrium with the total mortality rates at age and computed sequentially for ages a = 0, 1, …, A-1, A to account for the age-specific movement rates of fish between areas.

  <u>Recruitment (age a=0 or age a=1)</u>: Total recruitment to the population in area s is the sum over all source locations (i) of the number of recruits produced in each source location ($R^{(p)}_{(y=1,t=1),i}$) times the probability that a recruit is transported to area s ($Q^{(p)}_{(y=1,t=1),i,s}$). That is, the initial equilibrium recruitment in area s is

(48)
$$N^{(p)}_{s,0} \equiv N^{(p)}_{(y=1,t=1),s,0} = \sum_{i=1}^{S} R^{(p)}_{(1,1),i} \cdot Q^{(p)}_{(1,1),i,s}$$

  In practice, total recruitment can be apportioned to areas based on the amount of population spawning output in each area.

  <u>True age classes (ages a<A)</u>: Total population numbers at age in area s are calculated as the sum over all source locations (i) of the number of survivors in equilibrium, $N^{(p)}_{i,a-1} \cdot \exp\left(-Z^{(p)}_{i,a-1}\right)$, times the probability that an age-(a-1) survivor moves to area s, denoted by $T^{(p)}_{(i,s),a-1}$. That is, for a=1, 2, …, A-1, we have

(49) $$N^{(p)}_{(y=1,t=1),s,a} = \sum_{i=1}^{S} N^{(p)}_{i,a-1} \cdot \exp\left(-Z^{(p)}_{i,a-1}\right) \cdot T^{(p)}_{(i,s),a-1}$$

Here the total instantaneous mortality for age *a-1* in area *i* is the sum of the natural and fishing mortality rates for the equilibrium fishery.

Plus group (ages *a*=*A and older*): Total population numbers at age in area *s* in the plus group are calculated as the sum over all source locations (*i*) of the number of age-(*A*-1) survivors in equilibrium $\left(N^{(p)}_{i,A-1} \cdot \exp\left(-Z^{(p)}_{i,A-1}\right)\right)$ times the probability that a survivor moves to area *s* $\left(T^{(p)}_{(i,s),A-1}\right)$ times the plus group survival factor for ages *A* and older $\left(\dfrac{1}{1-\exp\left(-Z^{(p)}_{s,A}\right)}\right)$. That is,

(50) $$N^{(p)}_{(y=1,t=1),s,A} = \left(1-\exp\left(-Z^{(p)}_{s,A}\right)\right)^{-1} \cdot \sum_{i=1}^{S} N^{(p)}_{i,A-1} \cdot \exp\left(-Z^{(p)}_{i,A-1}\right) \cdot T^{(p)}_{(i,s),A-1}$$

3.2.4.1.15 Seasonal changes in population numbers

The seasonal changes in the number of fish in the population by area, age, and gender, in season *t* of year *y*, $N^{(p)}_{(y,t),s,a,g}$ with catch occurring at the fraction ΔC_t of the length of season *t* (Figure 10).

- Case 1. Two-sex model with age-specific movement probabilities
  Single true age class dynamics (*a*). the number of age-*a* and gender-*g* fish in area-*s* from population *p* at the start of season *t+1* in year *y*, $N^{(p)}_{(y,t+1),s,a,g}$, where the population annual natural mortality rate by area, age, and gender is $M^{(p)}_{s,a,g}$, depends on two components (Figure 11):
  (i) the previous number of age-(*a-1)* and gender-*g* fish in area *s* from population *p* at the start of season *t* in year *y* that stayed in area *s*, survived, and did not emigrate to another area not equal to *s*, noting that this movement probability is $T^{(p)}_{(y,t),(s,s),a-1,g}$
  (ii) the number of age-(*a-1)* and gender-*g* fish from population *p* that survive and immigrate into area *s* in season *t* during year *y* from another area *i* not equal to area *s*. For one area $i \neq s$, this movement probability is $T^{(p)}_{(y,t),(i,s),a-1,g}$, noting that this formulation of movement assumes that emigration and immigration occur at the end of season *t*. For a single age class *a*, the change in numbers at age in season $t+1<T$ during year *y* can be modeled as

(51)

$$N^{(p)}_{(y,t+1),s,a,g} = \left[N^{(p)}_{(y,t),s,a-1,g} \cdot \exp\left(-M^{(p)}_{s,a-1,g} \Delta_t \Delta C_t\right) - C^{(p)}_{(y,t),s,a-1,g} \right] \cdot \exp\left(-M^{(p)}_{s,a-1,g} \Delta_t \Delta C_t\right) \cdot T^{(p)}_{(y,t),(s,s),a-1,g}$$
$$+ \sum_{i \neq s} \left[N^{(p)}_{(y,t),i,a-1,g} \cdot \exp\left(-M^{(p)}_{i,a-1,g} \Delta_t \Delta C_t\right) - C^{(p)}_{(y,t),i,a-1,g} \right] \cdot \exp\left(-M^{(p)}_{i,a-1,g} \Delta_t \Delta C_t\right) \cdot T^{(p)}_{(y,t),(i,s),a-1,g}$$

While the change in numbers at age in the last season t=T during year y is

(52)

$$N^{(p)}_{(y+1,1),s,a,g} = \left[N^{(p)}_{(y,T),s,a-1,g} \cdot \exp\left(-M^{(p)}_{s,a-1,g} \Delta_T \Delta C_T\right) - C^{(p)}_{(y,T),s,a-1,g} \right] \cdot \exp\left(-M^{(p)}_{s,a-1,g} \Delta_T \Delta C_T\right) \cdot T^{(p)}_{(y,T),(s,s),a-1,g}$$
$$+ \sum_{i \neq s} \left[N^{(p)}_{(y,T),i,a-1,g} \cdot \exp\left(-M^{(p)}_{i,a-1,g} \Delta_T \Delta C_T\right) - C^{(p)}_{(y,T),i,a-1,g} \right] \cdot \exp\left(-M^{(p)}_{i,a-1,g} \Delta_T \Delta C_T\right) \cdot T^{(p)}_{(y,T),(i,s),a-1,g}$$

In the expressions for the changes in population numbers at age by season above, the observed catch numbers by population, area, age, gender, and season $C^{(p)}_{(y,t),s,a,g}$ is calculated as the product of the catch by area, age, gender, and season $C_{(y,t),s,a,g}$ and the proportion of population numbers by area, age, gender, and time $P^{(p)}_{t,s,a,g}$. That is,

(53) $$C^{(p)}_{(y,t),s,a,g} = C_{(y,t),s,a,g} \cdot P^{(p)}_{(y,t),s,a,g}$$

Typically, there may be little direct information on the proportion of population numbers that are caught by area, age, gender, and season. In the absence of observations on the catch composition, each population proportion of the catch will be calculated based on the assumption that the population proportion is equal to the population total numbers by area, age, gender, and season divided by the metapopulation total numbers by area, age, gender, and season. These population proportions are tracked in the assessment model and this leads to an approximation that the population proportion is

(54) $$P^{(p)}_{(y,t),s,a,g} = \frac{N^{(p)}_{(y,t),s,a,g}}{\sum_p N^{(p)}_{(y,t),s,a,g}}$$

This expression is a discrete approximation of movement through time because in general, the movement of individuals from populations across area boundaries will operate continuously during season t. In contrast, if there is direct information on the population proportions then these observations can be formulated as a likelihood component, noting that proportion information for one area affects the proportion information for all other areas.

For the plus-group or accumulator age *A*, the expression for $N^{(p)}_{(y,t+1),s,A,g}$ includes terms for age-(*A-1*) and age-*A* fish. Other than the additional factor of the age-*A* fish, the derivation of the changes in numbers is the same as for ages $a < A$.

- Plus group age class dynamics (*A*). Using a discrete time approximation with catch occurring at the midpoint of each season and seasonal natural mortality proportional to season length, the number of age-*A* and gender-*g* fish in area-*s* from population *p* at the start of season *t+1*, $N^{(p)}_{(y,t+1),s,A,g}$, depends on four components:
  - (i) the number of age-(*A-1)* and gender-*g* fish in area *s* from population *p* at the start of time period *t* that stayed in area *s* and did not emigrate to another area *i* not equal to *s*, noting that these fish are the new additions to the plus group and that this movement probability is $T^{(p)}_{(y,t),(s,s),A-1,g}$
  - (ii) the number of age-(*A-1)* and gender-*g* fish from population *p* that immigrate into area *s* in time period *t* from another area *i* not equal to area *s*. For one area $i \neq s$, this movement probability is $T^{(p)}_{(y,t),(i,s),A-1,g}$.
  - (iii) the number of age-*A* and gender-*g* fish in area *s* from population *p* at the start of time period *t* that stayed in area *s* and did not emigrate to another area not equal to *s*, noting that these are the existing already in the plus group at time *t* and that this movement probability is $T^{(p)}_{(y,t),(s,s),A,g}$
  - (iv) the number of age-*A* and gender-*g* fish from population *p* that immigrate into area *s* in time period *t* from another area *i* not equal to area *s*. For one area $i \neq s$, this movement probability $T^{(p)}_{(y,t),(i,s),A,g}$. For the plus group age group *A*, this can be modeled for season t+1<T as

(55)

$$\begin{aligned}
N^{(p)}_{(y,t+1),s,A,g} &= \left[N^{(p)}_{(y,t),s,A-1,g}\cdot\exp\left(-M^{(p)}_{s,A-1,g}\Delta_t\Delta C_t\right)-C^{(p)}_{(y,t),s,A-1,g}\right]\cdot\exp\left(-M^{(p)}_{s,A-1,g}\Delta_t\Delta C_t\right)T^{(p)}_{(y,t),(s,s),A-1,g}\\
&+\sum_{i\neq s}\left[N^{(p)}_{(y,t),i,A-1,g}\cdot\exp\left(-M^{(p)}_{i,A-1,g}\Delta_t\Delta C_t\right)-C^{(p)}_{(y,t),i,A-1,g}\right]\cdot\exp\left(-M^{(p)}_{i,A-1,g}\Delta_t\Delta C_t\right)\cdot T^{(p)}_{(y,t),(i,s),A-1,g}\\
&+\left[N^{(p)}_{(y,t),s,A,g}\cdot\exp\left(-M^{(p)}_{s,A,g}\Delta_t\Delta C_t\right)-C^{(p)}_{(y,t),s,A,g}\right]\cdot\exp\left(-M^{(p)}_{s,A,g}\Delta_t\Delta C_t\right)\cdot T^{(p)}_{(y,t),(s,s),A,g}\\
&+\sum_{i\neq s}\left[N^{(p)}_{(y,t),i,A,g}\cdot\exp\left(-M^{(p)}_{i,A,g}\Delta_t\Delta C_t\right)-C^{(p)}_{(y,t),i,A,g}\right]\cdot\exp\left(-M^{(p)}_{i,A,g}\Delta_t\Delta C_t\right)\cdot T^{(p)}_{(y,t),(i,s),A,g}
\end{aligned}$$

And for the last season t=T as

(56)

$$
\begin{aligned}
N^{(p)}_{(y+1,1),s,A,g} \; = \; & \left[N^{(p)}_{(y,T),s,A-1,g} \cdot \exp\left(-M^{(p)}_{s,A-1,g} \Delta_T \Delta C_T\right) - C^{(p)}_{(y,T),s,A-1,g} \right] \cdot \exp\left(-M^{(p)}_{s,A-1,g} \Delta_T \Delta C_T\right) T^{(p)}_{(y,T),(s,s),A-1,g} \\
+ & \sum_{i \neq s} \left[N^{(p)}_{(y,T),i,A-1,g} \cdot \exp\left(-M^{(p)}_{i,A-1,g} \Delta_T \Delta C_T\right) - C^{(p)}_{(y,T),i,A-1,g} \right] \cdot \exp\left(-M^{(p)}_{i,A-1,g} \Delta_T \Delta C_T\right) \cdot T^{(p)}_{(y,T),(i,s),A-1,g} \\
+ & \left[N^{(p)}_{(y,T),s,A,g} \cdot \exp\left(-M^{(p)}_{s,A,g} \Delta_T \Delta C_T\right) - C^{(p)}_{(y,T),s,A,g} \right] \cdot \exp\left(-M^{(p)}_{s,A,g} \Delta_T \Delta C_T\right) \cdot T^{(p)}_{(y,T),(s,s),A,g} \\
+ & \sum_{i \neq s} \left[N^{(p)}_{(y,T),i,A,g} \cdot \exp\left(-M^{(p)}_{i,A,g} \Delta_T \Delta C_T\right) - C^{(p)}_{(y,T),i,A,g} \right] \cdot \exp\left(-M^{(p)}_{i,A,g} \Delta_T \Delta C_T\right) \cdot T^{(p)}_{(y,T),(i,s),A,g}
\end{aligned}
$$

For age-*0* fish, the expression for seasonal recruitment by area and gender, denoted as $N^{(p)}_{(y,t+1),s,0,g}$, depends on the choice of a recruitment model described above as $N^{(p)}_{(y,t+1),s,0,g} \; = \; R^{(p)}_s\left(\Theta, D\right)$.

3.2.4.1.16 Tag-recovery dynamics

The tag-recovery dynamics of tagged groups of fish consist of population tag recoveries by tag group (*G*), season *t* in year *y*, tagging area (*i*), tag recovery area (*j*), and age $U^{(p)}_{G,(y,t),(i,j),a}$.

3.2.4.2 Observation Component

- Observed Data
    - Observed data logical inclusion array
    - Data weighting

      Francis (2011) and Punt (2016) provide some alternative viewpoints on weighting observational data including relative abundance indices and size compositions.
    - Fisheries data
        - Catch amount by area and fleet.
            - Catch biomass by area and fleet.
            - Catch numbers by area and fleet
        - Catch per unit effort by area and fleet.
            - CPUE as a relative abundance index
        - Selectivity by area and fleet.
        - Age composition by area and fleet.
        - Size composition by area and fleet.
        - Sex composition by area and fleet.
        - Mean size by area and fleet.
        - Tag recovery information by area and fleet.
    - Research survey data
        - Catch biomass by area and survey.

        - Catch numbers by area and survey.
        - Catch per unit effort by area and survey.
        - Selectivity by area and survey.
        - Age composition by area and survey.
        - Size composition by area and survey.
        - Sex composition by area and survey.
        - Mean size by area and survey.
    - Tag recovery data
        - Conventional tag-recovery data.
        - Close-kin mark-recapture data.
    - Research study data
        - Size-at-age data by area and study.
        - Maturity-at-age or –size data by area and study.
        - Fecundity-at-age or –size data by area and study.
        - Length-weight data by area and study.

3.2.4.3 Environment Component

- Environment Data
    - Environmental data logical inclusion array
    - Environmental forcing data
        - Biotic processes
            - Prey abundance
            - Predator abundance
        - Abiotic processes
            - Recruitment impacts
            - Distributional impacts
            - Growth impacts
                - Length at age impacts
                - Weight at length impacts
            - Maturity impacts
                - Maturation impacts
                - Fecundity impacts
                - Spawning frequency impacts
            - Natural mortality impacts
                - Age-specific impacts
                - Size-specific impacs
- Environmental Information Structure
    - Population component linkages
        - Recruitment
        - Growth

    - Natural mortality
    - Reproduction
    - Spatial distribution
    - Movement
- Observation component linkages
    - Fishery observations by area.
    - Survey observations by area.
    - Tag-recovery observations by area.
    - Research study observations by area.
- Analysis component linkages
    - Biotic process impacts on likelihood components.
    - Abiotic process impacts on likelihood components.

3.2.4.4 Analysis Component

3.2.4.4.1 Analytical data

- Analytical data logical inclusion array
- Analytical input and output objects
    - Model object.
    - Population object.
    - Observed data object.
    - Environment object.
    - Analysis object
        - Model construction object.
        - Ensemble model construction object.
        - Model forecasting output data object.
        - Model simulation testing object.

3.2.4.4.2 Analytical predictions

- Predicted fishery catch biomass by fleet (v), season (t) in year y, and area (s), denoted by $\widehat{C}_{B,v,(y,t),s}$.

(57)
$$\widehat{C}_{B,v,(y,t),s} = \sum_p \sum_a \sum_g N^{(p)}_{(y,t),s,a,g} W^{(p)}_{(y,t),s,a,g} \frac{F^{(p)}_{v,(y,t),s} S^{(p)}_{v,(y,t),s,a,g}}{\left(F^{(p)}_{v,(y,t),s} S^{(p)}_{v,(y,t),s,a,g} + M^{(p)}_{(y,t),s,a,g}\right)} \cdot \left(1 - \exp\left[-\left(F^{(p)}_{v,(y,t),s} S^{(p)}_{v,(y,t),s,a,g} + M^{(p)}_{(y,t),s,a,g}\right)\right]\right)$$

for fleet v in area s in season t, where $N^{(p)}_{(y,t),s,a,g}$, $W^{(p)}_{(y,t),s,a,g}$, and $M^{(p)}_{(y,t),s,a,g}$ are numbers-at-age, mean weight-at-age, and natural mortality-at-age, respectively, for population p, area s, age a, gender g, in year y and season t; $F^{(p)}_{v,(y,t),s}$ is the fully-selected fishing mortality for fleet v, population p, area s, in year y and season t; and $S^{(p)}_{v,(y,t),s,a,g}$ is selectivity-at-age for fleet v, population p, area s, age a, gender g, in year y and season t.

- Predicted fishery catch numbers by fleet (v), by year (y) and season (t), area (s) and age (a), denoted by $\widehat{C}_{v,(y,t),s,a}$.

(58)

$$\widehat{C}_{v,(y,t),s,a} = \sum_{p}\sum_{g} N^{(p)}_{(y,t),s,a,g} \frac{F^{(p)}_{v,(y,t),s} S^{(p)}_{v,(y,t),s,a,g}}{\left(F^{(p)}_{v,(y,t),s} S^{(p)}_{v,(y,t),s,a,g} + M^{(p)}_{(y,t),s,a,g}\right)} \left\{1-\exp\left[-\left(F^{(p)}_{v,(y,t),s} S^{(p)}_{v,(y,t),s,a,g} + M^{(p)}_{(y,t),s,a,g}\right)\right]\right\}$$

for fleet v in area s in year y and season t, where $N^{(p)}_{(y,t),s,a,g}$ and $M^{(p)}_{(y,t),s,a,g}$ are numbers-at-age and natural mortality-at-age, respectively, for population p, area s, age a, gender g, in season t; $F^{(p)}_{v,(y,t),s}$ is the fully-selected fishing mortality for fleet v, population p, area s, in year y and season t; and $S^{(p)}_{v,(y,t),s,a,g}$ is selectivity-at-age for fleet v, population p, area s, age a, gender g, in year y and season t.

- Catch per unit effort by area and fleet.
- Fishery selectivity by fleet or area.
  - Logistic fishery selectivity at age ($S_{v,s,a}$) by fleet (indexed by v) or area (indexed by s) with age at 50% selection ($a_{v,s,50}$) and slope ($\sigma_{v,s}$) parameters.

(59)

$$S_{v,s,a} = \frac{1}{1+e^{\frac{-\left(a-a_{v,s,50}\right)}{\sigma_{v,s}}}}$$

  - Thompson fishery selectivity at age ($S_{v,s,a}$) by fleet or area with age at 50% selection ($a_{v,s,50}$), slope ($\sigma_{v,s}$), and shape ($\gamma_{v,s}$) parameters.

(60)

$$S_{v,s,a} = \frac{1}{1-\gamma_{v,s}} \cdot \left(\frac{1-\gamma_{v,s}}{\gamma_{v,s}}\right)^{\gamma_{v,s}} \cdot \frac{e^{\frac{-\gamma_{v,s}\left(a-a_{v,s,50}\right)}{\sigma_{v,s}}}}{1+e^{\frac{-\left(a-a_{v,s,50}\right)}{\sigma_{v,s}}}}$$

    - Double-logistic fishery selectivity at age ($S_{v,s,a}$) by fleet or area with parameters for the ascending age at 50% selection ($a_{v,s,50,ASC}$) and slope ($\sigma_{v,s,ASC}$) and for the descending age at 50% selection ($a_{v,s,50,DESC}$) and slope ($\sigma_{v,s,DESC}$).

$$S_{v,s,a} = \frac{1}{1+e^{\frac{-\left(a-a_{v,s,50,ASC}\right)}{\sigma_{v,s,ASC}}}} \cdot \left(1-\frac{1}{1+e^{\frac{-\left(a-a_{v,s,50,DESC}\right)}{\sigma_{v,s,DESC}}}}\right) \tag{61}$$

  - Age composition by area and fleet.
  - Size composition by area and fleet.
  - Sex composition by area and fleet.
  - Mean size by area and fleet.
  - Tag recovery information by area and fleet.
- Predicted research survey data
  - Survey catch biomass by area and survey.
  - Survey catch numbers by area and survey.
  - Survey selectivity by survey and area.
    - Logistic survey selectivity at age ($S_{I,s,a}$) by survey (indexed by *I*) or area (indexed by *s*) with age at 50% selection ($a_{I,s,50}$) and slope ($\sigma_{I,s}$) parameters – see fishery selectivity.
    - Thompson survey selectivity at age ($S_{I,s,a}$) by fleet or area with age at 50% selection ($a_{I,s,50}$), slope ($\sigma_{I,s}$), and shape ($\gamma_{I,s}$) parameters – see fishery selectivity.
    - Double-logistic survey selectivity ($S_{I,s,a}$) by fleet or area with parameters for the ascending age at 50% selection ($a_{I,s,50,ASC}$) and slope ($\sigma_{I,s,ASC}$) and for the descending age at 50% selection ($a_{I,s,50,DESC}$) and slope ($\sigma_{I,s,DESC}$) – see fishery selectivity.
  - Age composition by area and survey.
  - Size composition by area and survey.
  - Sex composition by area and survey.
  - Mean size by area and survey.

        - Tag recovery information by area and survey.
- Predicted Study Data
    - Size-at-age data by area and study.
    - Maturity-at-age or –size data by area and study.
    - Fecundity-at-age or –size data by area and study.
    - Length-weight data by area and study.

3.2.4.4.3 MAS objective function

The MAS objective function for the m^{th} model, $\Psi_m\left(\underline{\Theta}_E \mid \underline{\underline{D}}_T\right)$, with a focus on negative loglikelihood components for abundance indices and age or size compositions

(62) $$\Psi_m\left(\underline{\Theta}_E \mid \underline{\underline{D}}_T\right) = -\sum_i \log L_i\left(\underline{O}_i \mid \underline{\Theta}_E\right) - \sum_j \log L_j\left(\underline{\underline{O}}_j \mid \underline{\Theta}_E\right) + Other\ terms$$

<u>3.2.4.4.3.1 Likelihood component for fishery catch</u>

The likelihood component for fishery catch is denoted by $L_{\underline{C}}\left(\underline{C} \mid \underline{\Theta}_E\right)$ and is comprised of the product of the individual likelihood components for catch time series by fleet (*v*) and area (*s*), $L_{\underline{C}_{v,s}}\left(\underline{C}_{v,s} \mid \underline{\Theta}_E\right)$. That is,

$$L_{\underline{C}}\left(\underline{C} \mid \underline{\Theta}_E\right) = \prod_v \prod_s L_{\underline{C}_{v,s}}\left(\underline{C}_{v,s} \mid \underline{\Theta}_E\right)$$

The likelihood component for fleets that report catch time series in units of catch biomass is $L_{\underline{C}_{v,s}}\left(\underline{CB}_{v,s} \mid \underline{\Theta}_E\right)$. Here it is assumed that catch biomass is observed with lognormal observation error and a fleet- and area-specific constant coefficient of variation, $CV_{CB_{v,s}}$. In this case, the negative loglikelihood for the observed catch biomass values from the y^{th} year by fleet and area $\left(CB_{v,s,y}\right)$ relative to predicted catch biomass value $\left(\widehat{CB}_{v,s,y}\right)$ based on a multiplicative lognormal error distribution with a constant coefficient of variation $CV_{CB_{v,s}} = \sqrt{\exp\left(\sigma^2_{CB_{v,s}}\right) - 1}$ and a bias correction is

(63) $$-\log L_{\underline{C}_{v,s}}\left(\underline{CB}_{v,s} \mid \underline{\Theta}_E\right) = \sum_y \log\left(\sigma_{CB_{v,s}}\right) + 0.5 \sum_y \left(\frac{\log\left(\dfrac{CB_{v,s,y}}{\widehat{CB}_{v,s,y}}\right)}{\sigma_{CB_{v,s}}} + 0.5\sigma_{CB_{v,s}} \right)^2$$

For fleets that report catch time series in units of catch numbers, the likelihood component is $L_{\underline{C}_{v,s}}\left(\underline{CN}_{v,s} \mid \underline{\Theta}_E\right)$. Given a lognormal observation error and a fleet- and area-specific constant coefficient of variation, $CV_{CN_{v,s}} = \sqrt{\exp\left(\sigma^2_{CN_{v,s}}\right)-1}$, the negative loglikelihood for the observed catch number values from the y^{th} year by fleet and area $\left(CN_{v,s,y}\right)$ relative to predicted catch biomass value $\left(\widehat{CN}_{v,s,y}\right)$ with a bias correction is

(64) $$-\log L_{\underline{C}_{v,s}}\left(\underline{CN}_{v,s} \mid \underline{\Theta}_E\right) = \sum_y \log\left(\sigma_{CN_{v,s}}\right) + 0.5\sum_y \left(\frac{\log\left(\frac{CN_{v,s,y}}{\widehat{CN}_{v,s,y}}\right)}{\sigma_{CN_{v,s}}} + 0.5\sigma_{CN_{v,s}} \right)^2$$

3.2.4.4.3.2 Likelihood component for initial population deviations

The likelihood component for a total of J initial population deviations is $L_{\underline{N}(1)^{(p)}}\left(\underline{\Lambda}^{(p)}_{\underline{N}(1)} \mid \underline{\Theta}_E\right)$. Initial population deviations from an equilibrium recruitment value have a lognormally distributed observation error with a constant coefficient of variation. In this case, the negative loglikelihood of the deviation for the j^{th} initial cohort $\left(\Lambda^{(p)}_j\right)$ based on a multiplicative lognormal error distribution with constant coefficient of variation $CV_{\Lambda^{(p)}_{\underline{N}(1)}} = \sqrt{\exp\left(\sigma^2_{\Lambda^{(p)}_{\underline{N}(1)}}\right)-1}$ with bias correction is

(65) $$-\log L_{\underline{N}(1)^{(p)}}\left(\underline{\Lambda}^{(p)}_{\underline{N}(1)} \mid \underline{\Theta}_E\right) = \sum_{j=1}^{J} \log\left(\sigma_{\Lambda^{(p)}_{\underline{N}(1)}}\right) + 0.5\sum_{j=1}^{J} \left(\frac{\Lambda^{(p)}_j}{\sigma_{\Lambda^{(p)}_{\underline{N}(1)}}} + 0.5\sigma_{\Lambda^{(p)}_{\underline{N}(1)}} \right)^2$$

3.2.4.4.3.3 Likelihood component for population recruitment deviations

The likelihood component for recruitment deviations is $L_{R^{(p)}}\left(\underline{\Lambda}^{(p)} \mid \underline{\Theta}_E\right)$. Recruitment deviations from stock-recruitment curve have a lognormally distributed observation error with a constant coefficient of variation. In this case, the negative loglikelihood for the recruitment deviation from the y^{th} year $\left(\Lambda^{(p)}_y\right)$ based on a multiplicative lognormal error distribution with constant coefficient of variation $CV_{\Lambda^{(p)}} = \sqrt{\exp\left(\sigma^2_{\Lambda^{(p)}}\right)-1}$ with bias correction is

$$(66)\qquad -\log L_{R^{(p)}}\left(\underline{\Lambda}^{(p)} \mid \underline{\Theta}_E\right) = \sum_{y=1}^{Y}\log\left(\sigma_{\Lambda^{(p)}}\right) + 0.5\sum_{y=1}^{Y}\left(\frac{\Lambda_y^{(p)}}{\sigma_{\Lambda^{(p)}}} + 0.5\sigma_{\Lambda^{(p)}}\right)^2$$

3.2.4.4.3.4 Likelihood components for relative abundance indices

The likelihood components for relative abundance indices are $L_i\left(\underline{O}_i \mid \underline{\Theta}_E\right)$.

- Survey relative abundance index with normal observation error and annual coefficients of variation. In this case, the negative loglikelihood $\left(-\log L_i\left(\underline{O}_i \mid \underline{\Theta}_E\right)\right)$ for the observed survey abundance index values from the i^{th} survey by year $\left(O_{i,(y,t)}\right)$, indexed by *y* in season *t* as (*y,t*), relative to predicted or expected index values for the i^{th} survey by year $\left(E_{i,(y,t)}\right)$ based on an additive normal error distribution with annual coefficients of variation $CV_{i,(y,t)}$ is

$$(67)\qquad -\log L_i\left(\underline{O}_i \mid \underline{\Theta}_E\right) = \sum_{y=1}^{Y}\log\left(CV_{i,(y,t)}E_{i,(y,t)}\right) + 0.5\sum_{y=1}^{Y}\left(\frac{O_{i,(y,t)} - E_{i,(y,t)}}{CV_{i,(y,t)}E_{i,(y,t)}}\right)^2$$

- Survey relative abundance index with normal observation error and annual standard deviations. In this case, the negative loglikelihood for the observed survey abundance index values from the i^{th} survey by year and season $\left(O_{i,(y,t)}\right)$ relative to predicted index values $\left(E_{i,(y,t)}\right)$ based on an additive normal error distribution with annual standard deviations $\sigma_{i,(y,t)}$ is

$$(68)\qquad -\log L_i\left(\underline{O}_i \mid \underline{\Theta}_E\right) = \sum_{y=1}^{Y}\log\left(\sigma_{i,(y,t)}\right) + 0.5\sum_{y=1}^{Y}\left(\frac{O_{i,(y,t)} - E_{i,(y,t)}}{\sigma_{i,(y,t)}}\right)^2$$

- Survey relative abundance index with lognormal observation error and annual coefficients of variation. In this case, the negative loglikelihood for the observed survey abundance index values from the i^{th} survey by year and season $\left(O_{i,(y,t)}\right)$ relative to predicted index values $\left(E_{i,(y,t)}\right)$ based on a multiplicative lognormal error distribution with annual coefficients of variation $CV_{i,(y,t)} = \sqrt{\exp\left(\sigma_{i,(y,t)}^2\right) - 1}$ and a bias correction for $E\left[O_{i,(y,t)}\right] = E_{i,(y,t)}$ is

(69) $$-\log L_i\left(\underline{O}_i \mid \underline{\Theta}_E\right) = \sum_{y=1}^{Y}\log\left(\sigma_{i,(y,t)}\right)+0.5\sum_{y=1}^{Y}\left(\frac{\log\left(\frac{O_{i,(y,t)}}{E_{i,(y,t)}}\right)}{\sigma_{i,(y,t)}}+0.5\sigma_{i,(y,t)}\right)^2$$

- <u>Survey relative abundance index with lognormal observation error and annual coefficients of variation</u>. In this case, the negative loglikelihood for the observed survey abundance index values from the *i*th survey by year and season $\left(O_{i,(y,t)}\right)$ relative to predicted index values $\left(E_{i,(y,t)}\right)$ based on a multiplicative lognormal error distribution with annual coefficients of variation $CV_{i,(y,t)} = \sqrt{\exp\left(\sigma^2_{i,(y,t)}\right)-1}$ and $E\left[\log O_{i,(y,t)}\right] = \log E_{i,(y,t)}$ is

(70) $$-\log L_i\left(\underline{O}_i \mid \underline{\Theta}_E\right) = \sum_{y=1}^{Y}\log\left(\sigma_{i,(y,t)}\right)+0.5\sum_{y=1}^{Y}\left(\frac{\log\left(\frac{O_{i,(y,t)}}{E_{i,(y,t)}}\right)}{\sigma_{i,(y,t)}}\right)^2$$

<u>3.2.4.4.3.5 Likelihood components for age or size composition data</u>

The likelihood components for age or size composition data are $L_j\left(\underline{\underline{O}}_j \mid \underline{\Theta}_E\right)$.

- <u>Age or size composition data with multinomial error distribution and annual effective sample sizes</u>. In this case, the negative loglikelihood $\left(-\log L_j\left(\underline{\underline{O}}_j \mid \underline{\Theta}_E\right)\right)$ for the observed bin values, indexed by *b*, for the *j*th composition data set with $n_{bin,j}$ bins by year and season $\left(O_{j,b,(y,t)}\right)$ relative to predicted bin values $\left(E_{j,b,(y,t)}\right)$ based on a multinomial error distribution with seasonal effective sample sizes $n_{eff,j,(y,t)}$ is

(71) $$-\log L_j\left(\underline{\underline{O}}_j \mid \underline{\Theta}_E\right) = -\sum_{y=1}^{Y}\sum_{t=1}^{T} n_{eff,j,(y,t)}\sum_{b=1}^{n_{bin,j}} O_{j,b,(y,t)}\log E_{j,b,(y,t)}$$

- <u>Age or size composition data with a robust multivariate normal error distribution and annual effective sample sizes</u>. In this case, the negative loglikelihood for the observed bin values, indexed by *b* from the *j*th

composition data set with $n_{bin,j}$ bins by year and season $\left(O_{j,b,(y,t)}\right)$ relative to predicted bin values $\left(E_{j,b,(y,t)}\right)$ based on a robust multivariate normal error distribution (Fournier et al. 1990, Starr et al. 1999) with seasonal effective sample sizes $n_{eff,j,(y,t)}$ is

$$\begin{aligned} -\log L_j\left(\underline{\underline{O}}_j \mid \underline{\Theta}_E\right) &= 0.5\sum_{y=1}^{Y}\sum_{t=1}^{T}\sum_{b=1}^{n_{bin,j}}\log\left(\left(1-O_{j,b,(y,t)}\right)O_{j,b,(y,t)}+0.1/n_{bin,j}\right) \\ &- \sum_{y=1}^{Y}\sum_{t=1}^{T}\sum_{b=1}^{n_{bin,j}}\log\left(\exp\left[\frac{-\left(O_{j,b,(y,t)}-E_{j,b,(y,t)}\right)^2}{2\left(\left(1-O_{j,b,(y,t)}\right)O_{j,b,(y,t)}+0.1/n_{bin,j}\right)/n_{eff,j,(y,t)}}\right]+0.01\right) \end{aligned} \tag{72}$$

- Age or size composition data with a Dirichlet multinomial distribution (Appendix 5).

3.2.4.4.3.6 Likelihood components for mean size data

- Gedamke and Hoenig (2006) and Methot and Wetzel (2013)

3.2.4.4.3.7 Likelihood components for tag recovery data

- Hilborn (1990) and Goethel et al. (2014)

3.2.4.4.3.8 Likelihood components for close kin mark recapture data

- Bravington et al. (2016)

3.2.4.4.3.9 Other objective function components

- Univariate parameter prior distributions, $\pi_k\left(\theta_\pi\right)$ or $\pi_k\left(\theta_\pi \mid \theta_\varphi\right)$
- Multivariate parameter prior distributions, $\underline{\pi}_k\left(\underline{\theta}_\pi\right)$ or $\underline{\pi}_k\left(\underline{\theta}_\pi \mid \underline{\theta}_\varphi\right)$, e.g., for example, McAllister and Kirkwood (1999)
- Hyperprior parameter distributions, $\varphi_j\left(\theta_\varphi\right)$
- Multivariate hyperprior parameter distributions, $\underline{\varphi}_j\left(\underline{\theta}_\varphi\right)$
- Numerical constraints or nuisance parameters, $\Upsilon_\eta\left(\underline{\underline{X}}_T \mid \underline{\theta}_\eta\right)$

3.2.4.4.3.10 Data weighting factors

- Catch biomass
- Initial population deviations
- Recruitment deviations
- Relative abundance data

- Age or size composition data
- Mean size data
- Tag recovery data
- Close kin mark recapture data

3.2.4.4.4 Model diagnostics

3.2.4.4.4.1 Convergence criteria

- Gradient analysis for objective function parameters
- Eigenvalue analysis of Hessian matrix to evaluate positive definiteness and condition number
- Convergence diagnostics for Markov Chain Monte Carlo simulation
  - Geweke convergence diagnostic (Geweke et al., 1992)
  - Gelman and Rubin diagnostic (Gelman and Rubin, 1992; Brooks et al., 1998)
  - Heidelberger and Welch stationarity and half-width diagnostics (Heidelberger and Welch, 1992)
  - Markov Chain Monte Carlo standard errors
- Randomized initial parameter analysis

3.2.4.4.4.2 Residual analyses

- Catch biomass
- Initial population abundance
- Recruitment
- Relative abundance data
- Age or size composition data
- Mean size data
- Tag recovery data
- Close kin mark recapture data

3.2.4.4.4.3 Likelihood profiling

- Catch biomass
- Initial population abundance
- Recruitment
- Relative abundance data
- Age or size composition data
- Mean size data
- Tag recovery data
- Close kin mark recapture data

3.2.4.4.4.4 Goodness-of-fit criteria

- Parameter correlations
- Root mean-squared errors
- Chi-square tests
- Empirical distribution function statistics
- Age-structured production model analyses
- Outlier detection
- Bayesian P-value analysis (Gelman et al. 2004)
- Retrospective analysis
- Cross validation

3.2.4.4.4.5 Information theoretic criteria

- Akaike information criterion
- Bayesian information criterion
- Deviance information criterion
- Widely applicable information criterion
- Healthy Akaike information criterion
- Other information criteria

3.2.4.4.5 Model results

- Harvest rate time series
  - Metapopulation harvest rate
  - Population harvest rate
  - Area-based harvest rate
  - Fleet-based harvest rate
- Biomass time series
  - Population biomass
  - Exploitable biomass
  - Spawning biomass
  - Catch biomass
- Population numbers time series
  - Population numbers at age
  - Exploitable numbers at age
  - Spawning numbers at age
  - Recruitment
  - Catch numbers at age
  - Survey numbers at age
- Yield per recruit for a single-area, pooled-sex population

  Yield per recruit for a given population in a single area model with a pooled-sex gender in equilibrium provides a measure of the sum of the expected yield at age over a cohort's life span as a function of a constant annual fishing mortality rate. We denote the yield per recruit as $YPR\left(F\right)$, where subscripts for indexing population, area and gender are fixed and omitted without loss of generality. Here the so-called *ICES* approach for $YPR\left(F\right)$ of Thompson and Bell (1934) is used with the first modeled age in the population denoted as a_R . Given this, the probability-based expression for yield per recruit with mean catch weight at age-a $\left(\widetilde{W}_{C,a}\right)$ in equilibrium is

$$\begin{aligned} YPR\left(F\right) = {} & \sum_{a=a_R}^{A-1} \widetilde{W}_{C,a} \cdot \Pr(Captured\ at\ age\ a) \cdot \Pr(Survive\ to\ age\ a) \\ & + \widetilde{W}_{C,A,F_A} \cdot \Pr(Captured\ at\ age\ A\ or\ older) \cdot \Pr(Survive\ to\ age\ A) \end{aligned} \tag{73}$$

And the corresponding computational formula for $YPR\left(F\right)$ is

$$\begin{aligned} YPR\left(F\right) = {} & \sum_{a=a_R}^{A-1} \left\{ \frac{\widetilde{W}_{C,a} \cdot F \cdot \widetilde{S}_a}{F \cdot \widetilde{S}_a + M_a} \left(1 - \exp\left(-F \cdot \widetilde{S}_a - M_a\right)\right) \cdot \exp\left(-\sum_{k=1}^{a-1}\left(F \cdot \widetilde{S}_k + M_k\right)\right)\right\} \\ & + \frac{\widetilde{W}_{C,A,F_A} \cdot F \cdot \widetilde{S}_A}{F \cdot \widetilde{S}_A + M_A} \exp\left(-\sum_{k=1}^{A-1}\left(F \cdot \widetilde{S}_k + M_k\right)\right) \end{aligned} \tag{74}$$

Also note that the equilibrium fishery yield Y_{Eq} in units of catch biomass for a fixed recruitment *R* at a constant fishing mortality *F* is given by

$$Y_{Eq} = R \cdot YPR\left(F\right) \tag{75}$$

- Spawning biomass per recruit for a single-area, pooled-sex population
  Spawning biomass per recruit for a given population by area and gender in equilibrium provides a measure of the sum of the expected spawning biomass at age over a cohort's life span as a function of a constant annual fishing mortality rate. We denote the spawning biomass per recruit as $SBPR\left(F\right)$, where subscripts for indexing population, area and gender are fixed and omitted without loss of generality and also noting that spawning biomasses of both females and males may both be needed for protogynous stock reference points. Here the approach of Gabriel et al. (1989) is used. Given this, the probability-based expression for spawning biomass per recruit with mean spawning weight at age-a $\left(\widetilde{W}_{S,a}\right)$ in equilibrium is

$$SBPR(F) = \sum_{a=a_R}^{T} \widetilde{P}_{Mature,a} \cdot \widetilde{W}_{S,\,a} \cdot \Pr(Spawn\ at\ age\ a) + \widetilde{P}_{Mature,A} \cdot \widetilde{W}_{S,\,A,F_A} \cdot \Pr(Spawn\ at\ age\ A) \cdot E\left[Spawnings\ at\ age\ A\ \ and\ \ older\right] \tag{76}$$

And the corresponding computational formula for $SBPR(F)$ is

$$SBPR(F) = \sum_{a=a_R}^{A-1} \left\{ \widetilde{P}_{Mature,a} \cdot \widetilde{W}_{S,\,a} \cdot \exp\left(-C_F F \cdot \widetilde{S}_a - C_M M_a - \sum_{k=1}^{a-1} \left(F \cdot \widetilde{S}_k + M_k \right) \right) \right\} + \widetilde{P}_{Mature,A} \cdot \widetilde{W}_{S,\,A,F_A} \cdot \frac{\exp\left(-C_F F \cdot \widetilde{S}_A - C_M M_A - \sum_{k=1}^{A-1} \left(F \cdot \widetilde{S}_k + M_k \right) \right)}{1 - \exp(-\left(F \cdot \widetilde{S}_A + M_A \right))} \tag{77}$$

where C_F and C_M are the fraction of annual *F* and *M* that occurs before spawning.

The fished and unfished spawning biomass per recruit values are also sometimes denoted as $SBPR(F) = \Phi_F$ and $SBPR(0) = \Phi_0$.

Also note that the equilibrium spawning biomass SB_{Eq} for a fixed recruitment *R* at a constant fishing mortality *F* is given by

$$SB_{Eq} = R \cdot SBPR(F) \tag{78}$$

- Spawning potential ratio for a single-area, pooled-sex population
  The spawning potential ratio for a given population by area and gender in equilibrium provides a measure of relative spawning potential as a function of a constant annual fishing mortality rate. We denote the spawning potential ratio as $SPR(F)$, where subscripts for indexing population, area and gender are fixed. The spawning potential ratio for a given *F* is calculated as

$$SPR(F) = \frac{SBPR(F)}{SBPR(0)} \tag{79}$$

- Fishing mortality rate (F) and spawning biomass (SB) reference points (e.g., Shertzer et al. 2014) for a single-area, pooled-sex population

F that produces the maximum sustainable yield (e.g., Brodziak and Legault 2005), F_{MSY}

Here maximum sustainable yield (MSY) is defined as

"Th*e largest average catch that can be continuously taken from a stock under existing environmental conditions* (Ricker 1975)."

To calculate the value of MSY in a single-population, single-area, single-gender MAS model, we note that the stock-recruitment relationship at equilibrium for a constant *F* can be expressed as $R_{Eq} = f\left(SB_{Eq}\right)$. As a result, the equilibrium spawning biomass at a constant *F* can be expressed as $SB_{Eq}\left(F\right) = SBPR\left(F\right)\cdot f\left(SB_{Eq}\right)$.

For the Beverton-Holt stock-recruitment curve (3.2.4.1.12, case 1), the equilibrium spawning biomass is given by

$$SB_{Eq} = \frac{4h\cdot R_0\cdot SBPR\left(F\right) - SB_0\left(1-h\right)}{5h-1} = \alpha\cdot SBPR\left(F\right) - \beta \tag{80}$$

For the Ricker stock-recruitment curve (3.2.4.1.12, case 2), the equilibrium spawning biomass is given by

$$SB_{Eq} = \frac{\log\left(\alpha\cdot SBPR\left(F\right)\right)}{\beta} \tag{81}$$

For the Shepherd stock-recruitment curve (3.2.4.1.12, case 3), the equilibrium spawning biomass is given by

$$SB_{Eq} = \beta\cdot\left(\alpha\cdot SBPR\left(F\right) - 1\right)^{\frac{1}{c}} \tag{82}$$

F_{MSY} Algorithm

Given the formula for equilibrium spawning biomass at a constant *F*, one can use the following numerical search algorithm to calculate F_{MSY}, B_{MSY} and MSY.

1. Construct a uniform grid of fishing mortality rates $\underline{F}$ with mesh size δ where $\underline{F} = \left(F_1, F_2, \ldots, F_{Upper}\right)$ and $F_j = \left(j-1\right)\cdot\delta$ and F_{Upper} is a maximal value of fishing mortality, say for example, $F_{Upper} = 3.00$ with $\delta = 0.01$.
2. For each $F_j \in \underline{F}$, calculate the spawning biomass and yield per recruit, $SBPR\left(F_j\right)$ and $YPR\left(F_j\right)$.
3. For each $F_j \in \underline{F}$, calculate the equilibrium spawning biomass $SB_{Eq}\left(F_j\right)$ given the value of $SBPR\left(F_j\right)$.

4. For each $F_j \in \underline{F}$, calculate the equilibrium recruitment R_{Eq} from the equilibrium spawning biomass as $R_{Eq}\left(F_j\right) = f\left(SB_{Eq}\left(F_j\right)\right)$.
5. For each $F_j \in \underline{F}$, calculate the equilibrium fishery yield Y_{Eq} from the equilibrium recruitment and yield per recruit as $Y_{Eq}\left(F_j\right) = R_{Eq}\left(F_j\right) \cdot YPR\left(F_j\right)$
6. Find the index $k \in \{1, 2, \ldots, Upper\}$ that produces the maximum equilibrium yield such that $Y_{Eq}\left(F_k\right) \geq Y_{Eq}\left(F_j\right) \; for \; all \; j \in \{1, 2, \ldots, Upper\}$
7. Set $F_{MSY} = F_k$, $SB_{MSY} = SB_{Eq}\left(F_k\right)$, and $MSY = Y_{Eq}\left(F_k\right)$

F that produces the maximum yield per recruit, F_{MAX}

F_{MAX} Algorithm

Given the yield per recruit as a function of *F*, one calculates F_{MAX} as

1. Construct a uniform grid of fishing mortality rates $\underline{F}$ with mesh size δ where $\underline{F} = \left(F_1, F_2, \ldots, F_{Upper}\right)$ and $F_j = \left(j-1\right) \cdot \delta$ and F_{Upper} is a maximal value of fishing mortality and for each $F_j \in \underline{F}$, calculate the yield per recruit, $YPR\left(F_j\right)$.
2. Find the index $k \in \{1, 2, \ldots, Upper\}$ that produces the maximum equilibrium yield per recruit such that $YPR\left(F_k\right) \geq YPR\left(F_j\right) \; for \; all \; j \in \{1, 2, \ldots, Upper\}$
3. Set $F_{MAX} = F_k$ and $SB_{MAX} = SB\left(F_k\right)$.

F that produces X% of unfished spawning biomass, $F_{X\%}$

The fishing mortality that produces a fixed percentage $X\%$ of the unfished spawning biomass is $F_{X\%}$. To calculate $F_{X\%}$, one first needs to start with an estimate of the equilibrium spawning biomass as a function of *F*.

$F_{X\%}$ Algorithm

Given the spawning biomass per recruit as a function of *F*, one calculates $F_{X\%}$ as

1. For each $F_j \in \underline{F}$, calculate the spawning biomass and yield per recruit, $SBPR\left(F_j\right)$ and $YPR\left(F_j\right)$.
2. For each $F_j \in \underline{F}$, calculate the equilibrium spawning biomass $SB_{Eq}\left(F_j\right)$ given the value of $SBPR\left(F_j\right)$.

3. For each $F_j \in \underline{F}$, calculate the equilibrium recruitment R_{Eq} from the equilibrium spawning biomass as $R_{Eq}\left(F_j\right) = f\left(SB_{Eq}\left(F_j\right)\right)$.
4. For each $F_j \in \underline{F}$, calculate the equilibrium fishery yield Y_{Eq} from the equilibrium recruitment and yield per recruit as $Y_{Eq}\left(F_j\right) = R_{Eq}\left(F_j\right) \cdot YPR\left(F_j\right)$
5. For each $F_j \in \underline{F}$, calculate the ratio $R_j = \frac{SB_{Eq}\left(F_j\right)}{SB_{Eq}\left(0\right)}$ and the difference $\Delta_j = \left|R_j - X_{\%}\right|$
6. Find the index $k \in \{1,2,...,Upper\}$ that produces the smallest difference $\Delta_k \le \Delta_j \text{ for all } j \in \{1,2,...,Upper\}$.
7. Set the fishing mortality, spawning biomass and fishery yield at $F_{X\%}$ as $F_{X\%} = F_k$ and $SB_{X\%} = SB_{Eq}\left(F_k\right)$ and $Y_{X\%} = Y_{Eq}\left(F_k\right)$.

F where the slope of the *YPR* curve is 10% that at the origin, $F_{0.1}$

The reference point $F_{0.1}$ was developed by Gulland and Boerema (1973) as a reference point that was based on maintaining marginal fishery yield at 10% of the initial fishery CPUE in order to support an economically efficient fishery. This reference point is calculated from the yield per recruit curve and is the value of *F* that produces 10% of the slope of the yield per recruit curve at the origin.

$F_{0.1}$ Algorithm

Given the spawning biomass per recruit as a function of *F*, one calculates $F_{0.1}$ as

1. Construct a uniform grid of fishing mortality rates $\underline{F}$ with mesh size δ where $\underline{F} = \left(F_1, F_2, ..., F_{Upper}\right)$ and $F_j = \left(j-1\right) \cdot \delta$ and F_{Upper} is a maximal value of fishing mortality.
2. Calculate the derivative of the yield per recruit curve as a function of fishing mortality *F* as $\frac{\partial YPR\left(F\right)}{\partial F}$ and calculate 10% of the slope at the origin as $0.1\frac{\partial YPR\left(0\right)}{\partial F}$.
3. For each $F_j \in \underline{F}$, calculate the derivative of the yield per recruit function at F_j as $\frac{\partial YPR\left(F_j\right)}{\partial F}$ and the difference $\Delta_j = \left|\frac{\partial YPR\left(F_j\right)}{\partial F} - 0.1\frac{\partial YPR\left(0\right)}{\partial F}\right|$
4. Find the index $k \in \{1,2,...,Upper\}$ that produces the smallest difference $\Delta_k \le \Delta_j \text{ for all } j \in \{1,2,...,Upper\}$ and set $F_{0.1} = F_k$.

F that produces 50% of year classes with stock replacement, F_{Med}

The reference point F_{Med} is the fishing mortality rate that produces the value of spawning biomass per recruit equal to the inverse of the median of the observed survival ratios for a stock. This is an empirically-derived reference point that depends on the observed time series of recruitment values and the spawning biomasses that produced them. Let $\underline{R} = \left(R_1,\ldots,R_T\right)$ and $\underline{SB} = \left(SB_1,\ldots,SB_T\right)$ be the observed recruitment and spawning biomass time series.

F_{Med} Algorithm

Given the observed recruitment and spawning biomass time series, one calculates F_{Med} as

1. Construct a uniform grid of fishing mortality rates $\underline{F}$ with mesh size δ where $\underline{F} = \left(F_1, F_2,\ldots,F_{Upper}\right)$ and $F_j = \left(j-1\right)\cdot\delta$ and F_{Upper} is a maximal value of fishing mortality.
2. Calculate the distribution of observed survival ratios $\underline{RS}$ as $\underline{RS} = \left(\frac{R_1}{S_1},\ldots,\frac{R_T}{S_T}\right)$, the median of this distribution $Median\left(\underline{RS}\right)$ and its inverse $\frac{1}{Median\left(\underline{RS}\right)}$.
3. For each $F_j \in \underline{F}$, calculate the spawning biomass per recruit, $SBPR\left(F_j\right)$ and then calculate the difference $\Delta_j = \left|SBPR\left(F_j\right) - \frac{1}{Median\left(\underline{RS}\right)}\right|$
4. Find the index $k \in \{1,2,\ldots,Upper\}$ that produces the smallest difference $\Delta_k \le \Delta_j \; for \; all \; j \in \{1,2,\ldots,Upper\}$ and set $F_{Med} = F_k$.
5. Calculate the equilibrium spawning biomass at F_{Med} as $SB_{Med} = SB_{Eq}\left(F_{Med}\right)$ given the value of $SBPR\left(F_{Med}\right)$.

Dynamic *F* that produces X% of time-varying unfished spawning biomass, $F_{X\%,T}$

The dynamic fishing mortality that produces a fixed percentage $X\%$ of the time-varying calculated unfished spawning biomass is $F_{X\%,T}$. To calculate $F_{X\%}$, one needs to start with a time interval $T = \left[T_1, T_2\right]$ and an estimate of the calculated unfished spawning biomass that would have occurred during *T* in the absence of fishing. Here the time interval *T* is chosen to reflect a period of expected stability in recruitment or life history parameters from the recent past to the present, i.e., an appropriate time window for a stable fishery productivity regime within a dynamic fishery system (e.g., Berger et al. 2013).

$F_{X\%}$ Algorithm

Given the time interval $T = [T_1, T_2]$, one calculates $F_{X\%,T}$ as

1. For each $F_j \in \underline{F}$, calculate the expected spawning biomass and yield per recruit during the time interval *T*, $SBPR_T(F_j)$ and $YPR_T(F_j)$.
2. Calculate the time-varying unfished spawning biomass during the time interval *T* from the average value of observed recruitment times the expected unfished spawning biomass per recruit as $SB_{Eq,T}(0) = SBPR_T(0) \cdot \frac{\sum_{t=T_1}^{T_2} R_t}{T_2 - T_1 + 1}$
3. For each $F_j \in \underline{F}$, calculate the ratio $\rho_j = \frac{SBPR_T(F_j)}{SBPR_T(0)}$ and the difference $\Delta_j = |\rho_j - X_{\%}|$
4. Find the index $k \in \{1, 2, ..., Upper\}$ that produces the smallest difference $\Delta_k \le \Delta_j \ for\ all\ j \in \{1, 2, ..., Upper\}$.
5. Set the dynamic fishing mortality, spawning biomass and fishery yield reference points at $\underline{F_{X\%,T}}$ as $F_{X\%,T} = F_k$ and $SB_{X\%,T} = SBPR_T(F_k) \cdot \frac{\sum_{t=T_1}^{T_2} R_t}{T_2 - T_1 + 1}$ and $Y_{X\%,T} = YPR_T(F_k) \cdot \frac{\sum_{t=T_1}^{T_2} R_t}{T_2 - T_1 + 1}$.

<u>Relative fishing mortality rate and relative spawning biomass time series</u>

Given fishing mortality and spawning biomass reference points, namely F_{RP} and SB_{RP}, the relative fishing mortality rate and spawning biomass time series for a given time series of fishing mortality rates $\underline{F} = (F_1, ..., F_T)$ and spawning biomasses $\underline{SB} = (SB_1, ..., SB_T)$ are the time series of ratios $rel\underline{F} = \left(\frac{F_1}{F_{RP}}, ..., \frac{F_T}{F_{RP}} \right)$ and $rel\underline{SB} = \left(\frac{SB_1}{SB_{RP}}, ..., \frac{SB_T}{SB_{RP}} \right)$.

In general, the multi-area calculations of reference points and relative status for a 2-gender population listed below can by numerically approximated using simulation to achieve equilibrium values.

- Yield per recruit for a multi-area, 2-gender population
- Spawning biomass per recruit for a multi-area, 2-gender population
- Spawning potential ratio for a multi-area, 2-gender population
- Yield per recruit for a multi-area, 2-gender population
- Fishing mortality rate and spawning biomass reference points a multi-area, 2-gender population

- Uncertainty quantification
    - Standard deviations for estimated parameters
    - Percentiles for estimated parameters
    - Confidence or credibility regions for estimated parameters
    - Standard deviations for derived parameters
    - Percentiles for derived parameters
    - Confidence or credibility regions for derived parameters
    - Covariance matrix for estimated parameters
    - Correlation matrix for estimated parameters
    - Bootstrap replicates of estimated parameters
    - Bootstrap estimates of quantities of interest
    - Joint posterior distribution
    - Marginal distributions
    - Markov Chain Monte Carlo simulation replicates
    - Jackknifed estimates of quantities of interest
    - Cross validation estimates of quantities of interest
    - Model averaged quantities of interest
    - Covariances of model-averaged quantities of interest
    - Other measures of uncertainty
        - Ouija board
        - Tarot cards
        - Oracle of Delphi
        - I Ching

3.2.4.4.6 Assessment model output information for forecasting

- Deterministic or stochastic forecasts
- Single model or ensemble model forecasts of quantities of interest
- Catch-based or effort-based harvest control
- Harvest control rule based catches or fishing mortality rates
- Implementation error-based forecasts
- Probability of exceeding overfishing level as a function of catch quota
- Probability of breaching limit reference point

    - Biomass limit
    - Harvest rate limit
- Probability of being within neighborhood of target
    - Biomass target
    - Harvest rate target
- Other forecast quantities of interest

3.2.4.4.7 Model simulation testing

- Simulated data generation
    - Single operating model
    - Ensemble of operating models
- Management strategy evaluation
    - Quantification of objectives
    - Specification of uncertainty distributions
    - Set of operating models
    - Setting true parameter values
    - Set of parameter estimation models
    - Simulated parameter attributes
        - Bias
        - Covariance
        - Skewness
        - Kurtosis
    - Performance measures
    - Harvest control rules
    - Management strategies

3.3 Design Rationale

The MAS component structures were conceived to be flexible enough to produce what we now want or imagine we may want in the future from a spatially explicit assessment system. The design choice of beginning with the end in mind is an important part of this approach, noting that we have grouped potential features into related categories to facilitate structured system development. Overall, we note that the suggested categorizations of features were intended to facilitate, but not rigidly define, possible model structures and capacities for understanding and prediction.

One goal that we want to achieve with the MAS is the implementation of a well-documented, high quality, reliable, and easily extensible programming system. We chose to implement MAS in C++ to emphasize an object-oriented programming style. This choice will facilitate the maintenance, extensibility, and reusability of code and model structure, and most importantly will facilitate rapid model prototyping and testing. Another key structural component for efficient and reliable coding is the use of input and output structures, where these I/O objects can be tailored to specific needs of specific stock assessment applications using JSON. Overall, the programming design of MAS is integrated with a living design document that includes necessary and sufficient information to define and reconstruct MAS and also to extend it with new modules through stepwise quality assurance and quality control procedures.

The MAS model structure is designed to reflect metapopulation dynamics. Multiple population habitats and areas are part of the system and can be used to represent spatial dynamics for ocean zoning and fisheries management. The MAS includes the capacity for frequentist and Bayesian population dynamics processes for model fitting to provide adequate generality and flexibility. In general, it is preferable to employ Bayesian approaches to address parameter uncertainty in a direct manner but it is very important to have the option to avoid subjective prior assumptions in a frequentist context. The structural issue of the mode of inference is also linked to the choice of error structure. Error terms can be broadly dichotomized as being additive and normally distributed or as being multiplicative and lognormally distributed. Alternative distributional forms for additive errors are the T-distribution and Cauchy distribution and alternative distributional forms for the multiplicative are the gamma and exponential distributions. It is also expected that the MAS needs to provide the capacity to fit both near-symmetric and skewed error structures to be a flexible platform for assessment modeling. Following on this point, there needs to be clear output information for model diagnostics and selection among competing alternative models. MAS also includes options for data weighting, to emphasize or deemphasize information, as well easy to implement data inclusion or exclusion in alternative models. Last, the MAS also needs to provide standard assessment quantities of interest for fishery management, including biological reference points, status determination information, and forecasts.

4. DATA DESIGN

4.1 Data Description

The data and model structures needed to define a particular analytical model are stored in the model object file, which records the logical relations between the population, observation, environment, and analysis information specific to each constructed model. The input data for the model are also included in the model object file. An overview of the input data types for the MAS is provided for the population component (section 3.2.1), the observation component (section 3.2.2) the environment component (section 3.2.3), and the analysis component (section 3.2.4). Data structure information needed to access the entire set of available input data is included in the model object file. This facilitates developing analyses using subsets of the entire available data set for alternative model configurations. Each of the input data objects has a unique identifier and associated lookup code that points to relevant portion of the model object file. That is, this code can be used to address the file locations where each input data object starts and ends. By convention, instances of input data objects are contiguous and are listed sequentially through time.

4.1.1 Population Component Data

This section describes data structures and variable naming conventions for the population component data. The population logic data consists of the case arrays and associated lists of population information. The population numbers at age data represents the information on age-structured abundance by location through time. The population movement data represents the information on age-structured movement by location through time. The population dynamics data described the population dynamics information by location through time.

4.1.2 Observation Component Data

This section describes data structures and variable naming conventions for the observation component data. The observation logic data consists of the case arrays and associated lists of observed information. The fisheries observations represent the information on fishing fleet or fishery collected by location through time. The research survey observations represent the information collected on the metapopulation dynamics by location through time. The research study observations represent the individual fish data collected to describe metapopulation dynamics parameters by location through time.

4.1.3 Environment Component Data

This section describes data structures and variable naming conventions for the environment component data. The environment logic data consists of the case arrays and associated lists of environmental information. The biotic environmental observations represent the information on other species impacts on the metapopulation collected by location through time. Similarly, the abiotic environmental observations represent the information on physical oceanographic and climate impacts on metapopulation dynamics collected by location through time.

4.1.4 Analysis Component Data

This section describes data structures and variable naming conventions for the analysis component data. The analysis logic data consists of the case arrays and associated lists of analysis information. The fisheries analysis data represents the information on model analyses and predictions of fishing fleet or fishery data by location through time. The research survey analysis data represents the information on model analyses and predictions for the surveyed metapopulation dynamics by location through time. The research study analysis data represents the model analyses and predictions of individual fish data collected to describe metapopulation dynamics parameters by location through time.

4.2 Model Metadata

Each model object file contains sufficient metadata about the structure of itself to reconstruct itself. This metadata includes the unique acronym and location of each data type in the model object file. Most importantly, the metadata describes the entire set of available input data that are available to be applied in the given model.

4.2.1 Population Component Metadata

This section describes the metadata needed to specify the population component for each of the four model analysis layers: (i) model construction; (ii) model set selection; (iii) model forecasts; (iv) model simulation.

4.2.2 Observation Component Metadata

This section describes the metadata needed to specify the observation component for each of the three model analysis layers: (i) model construction; (ii) model set selection; (iii) model forecasts; (iv) model simulation.

4.2.3 Environment Component Metadata

This section describes the metadata needed to specify the environment component for each of the three model analysis layers: (i) model construction; (ii) model set selection; (iii) model forecasts; (iv) model simulation.

4.2.4 Analysis Component Metadata

This section describes the metadata needed to specify the analysis component for each of the three model analysis layers: (i) model construction; (ii) model set selection; (iii) model forecasts; (iv) model simulation.

5. MODEL ANALYSES

The integrated assessment model is the fundamental unit in the metapopulation assessment system. We describe the general components of each layer in the MAS fitting approach in what follows including model construction, model selection, model forecasts, and management strategy evaluation.

5.1 Model Construction

The construction of a single metapopulation model consists of a unique sequence of lists, or case structures, that specify the components and relationships of population, observation, environment, and analysis components. These model logical inclusion arrays, or case structures, are defined for the MAS Class, as well as the interrelationships between the Population, Observation, Environment, and Analysis Components used in a given MAS model.

5.1.1 Input Data

Input data file constructed with a graphical user interface or user-constructed file comprised of a model construction header and input data. The model construction header specifies where data to fill out each model construct are found in the subsequent input data section. The input data section reflects the structure specified in the data design.

5.1.2 Model Structure

The model structure specifies the components and timing of the processes that change or sample biomass in an area during a time step. The time step could be a year or it could be a season within a year. In this context, processes that increase biomass are somatic growth, recruitment, and immigration and processes that decrease biomass are natural deaths, fishery yields, and emigration. Spawning is another process needed to calculate the reproductive output of the population while tagging is a process that may provide information on movement and harvest intensity.

5.1.3 Model Parameters

The set of MAS model parameters to be freely estimated $\underline{\Theta}_E$ is mapped to the likelihood components specified in the analysis components and encapsulated in the MAS model case structure list. The set of model parameters to be fixed (and not estimated) is the set difference $\underline{\Theta} - \underline{\Theta}_E$ and these are mapped to the appropriate MAS submodels and fitting algorithms.

5.1.4 Parameter Estimation

Parameter estimation is based on maximum likelihood-based, simple Bayes, hierarchical Bayes, random effects, and may be extended to other estimation approaches, e.g. maximum entropy estimation (Jaynes 2003). The maximum likelihood-based estimation approach requires specification of the likelihood components of a given model m and maximization of the objective function Ψ_m which includes the joint likelihoods and other fitting components. The simple Bayes approach requires a similar specification of the likelihood components and the additional specification of parameter priors for the numerical sampling of the posterior distribution. The hierarchical Bayes approach requires specification of the likelihood components, the parameter priors, and hyperpriors for the model and numerical sampling of the posterior distribution. The random effects approach requires the specification of the marginal likelihood and its maximization, which for some models may be efficiently calculated using integrated nested Laplace approximations (i.e., Rue and Martino 2009).

Parameter optimization for the objective function $\Psi_m\left(\underline{\Theta}_E\right)$ is achieved through application of a function minimizer or through numerical integration of the posterior distribution. The maximum or modal value of the estimable parameter vector is $\widehat{\underline{\Theta}}_E$ and a second order Taylor series expansion of $\Psi_m\left(\underline{\Theta}_E\right) = \Psi_m\left(\underline{\Theta}_E \mid \underline{\Theta} - \underline{\Theta}_E\right)$ about $\widehat{\underline{\Theta}}_E$ leads to the relationship

(83)
$$\Psi_m\left(\underline{\Theta}_E\right) = \Psi_m\left(\widehat{\underline{\Theta}}_E\right) - 0.5\left(\underline{\Theta}_E - \widehat{\underline{\Theta}}_E\right)^T H\left(\widehat{\underline{\Theta}}_E\right)\left(\underline{\Theta}_E - \widehat{\underline{\Theta}}_E\right) + h.o.t.$$

Where $H\left(\underline{\widehat{\Theta}}_E\right)$ is the Hessian matrix of second partial derivatives of the objective function $\Psi_m\left(\underline{\widehat{\Theta}}_E\right)$ evaluated at the maximum likelihood estimate or highest posterior density estimate (HPD), noting that this is a p-dimensional vector if there are a total of p freely estimated parameters in the model. This leads to the asymptotic normal approximation for the solution to the problem of minimizing the objective function whose exact solution vector $\underline{\Theta}_E^{True}$ has a multivariate normal distribution with mean equal to the MLE or HPD vector $\underline{\widehat{\Theta}}_E$ and the estimated covariance matrix equal to the inverse of the Hessian matrix $\hat{\Sigma} = H\left(\underline{\widehat{\Theta}}_E\right)^{-1}$. That is,

(84) $$\underline{\Theta}_E^{True} \sim MVN\left(\underline{\widehat{\Theta}}_E, H\left(\underline{\widehat{\Theta}}_E\right)^{-1}\right)$$

Convergence of the model parameter estimates is checked using the gradient of the objective function evaluated at the solution vector $\underline{\widehat{\Theta}}_E$. In particular the first order condition required for $\underline{\widehat{\Theta}}_E$ to be a solution in a frequentist estimation context is that the gradient of the objective function evaluated at the solution is the zero vector, or

5.1.5 Model Outputs

MAS model outputs include information on model convergence and fits to the data, model diagnostics, parameter estimates as well as estimates of quantities of interest (QOIs). The quantities of interest will typically include point estimates of population size, spawning potential, stock status, fishery productivity information, and associated estimates of parametric uncertainty. In addition, bootstrap or Markov Chain Monte Carlo replicates of the estimator uncertainty evaluated at the MLE or HPD will generally be needed for conducting future stock projections or model forecasts.

To calculate measures of parametric uncertainty for QOIs, we note that the information on parametric uncertainty for the freely estimated model parameters is contained in the estimated covariance matrix $\hat{\Sigma} = H\left(\underline{\widehat{\Theta}}_E\right)^{-1}$. In particular, the approximate $1-\alpha$ probability confidence interval for the j^{th} parameter $\theta_{E,j}$ is $\left[\hat{\theta}_{E,j} - z_{\frac{\alpha}{2}} \cdot \hat{\sigma}_j, \hat{\theta}_{E,j} + z_{\frac{\alpha}{2}} \cdot \hat{\sigma}_j\right]$ given the z-score $z_{\frac{\alpha}{2}}$.

Similarly, the $1-\alpha$ confidence ellipsoid for the parameter vector $\underline{\Theta}_E$ is

(85) $$\left(\underline{\Theta}_E - \underline{\widehat{\Theta}}_E\right)^T \hat{\Sigma}^{-1}\left(\underline{\Theta}_E - \underline{\widehat{\Theta}}_E\right) \le X_p^2(\alpha)$$

where $\mathrm{X}_p^2(\alpha)$ is the $(100\alpha)^{th}$ upper percentile of a chi square distribution with p degrees of freedom.

For QOIs, or derived parameters, the information needed to characterize parametric uncertainty can be calculated using the generalized delta method. This method provides a first order approximation of the variance for a derived quantity of interest, like the estimated spawning biomass of a given population in a particular year and area.

5.1.5.1 Generalized Delta Method

Here is a description of the first order approximation used in the generalized delta method. Let $\underline{\Theta}_E$ denote the vector of freely estimable parameters for the MAS model and assume that there are a total of p freely estimated parameters. Then each element of the estimable parameter vector $\theta_j \in \underline{\Theta}_E$ has a variance estimate $Var\left[\theta_j\right]$ and each pair of elements of the parameter vector $\left(\theta_j, \theta_k\right)$ have a covariance estimate $Cov\left[\theta_j, \theta_k\right]$ based on the asymptotic multivariate normal approximation for the distribution of the MLE (or HPD) solution to the minimization of the model objective function. Let $\Sigma = H\left(\underline{\Theta}_E\right)^{-1}$ denote the covariance matrix evaluated at a point $\underline{\Theta}_E$ in a neighborhood of the solution vector $\widehat{\underline{\Theta}}_E$. Now let $Z = g\left(\underline{\Theta}_E\right)$ be any twice differentiable, scalar-valued function of the freely estimated parameters. Here the variable Z represents a quantity of interest derived from the freely estimated parameters and other fixed model parameters, like the spawning biomass of a given population in a particular year and area. We want to estimate the variance of Z evaluated at the solution vector. To do this, we Taylor expand $g\left(\underline{\Theta}_E\right)$ around the point $\underline{\Theta}_E^{True}$, apply the variance operator and substitute $\underline{\Theta}_E^{True} = \widehat{\underline{\Theta}}_E$ to calculate the approximate variance of Z as

$$(86) \qquad Var[Z] = Var\left[g\left(\widehat{\underline{\Theta}}_E\right)\right] \approx \nabla g\left(\widehat{\underline{\Theta}}_E\right)^T \Sigma\left(\widehat{\underline{\Theta}}_E\right) \nabla g\left(\widehat{\underline{\Theta}}_E\right)$$

Here is an example to illustrate the delta method for a derived quantity of interest. Suppose we want to calculate the variance of the estimated spawning biomass in year y for single population-single area MAS model with one fishery and one survey index starting at an unfished equilibrium state. In this case, the estimated spawning biomass SB_y depends on estimable parameters for unfished recruitment R_0, the time series of deviations from a Beverton-Holt stock-recruitment curve $\underline{\theta}_\Lambda = \left(\Lambda_1, \ldots, \Lambda_y\right)$, the time series of fishing mortalities $\underline{\theta}_F = \left(F_1, \ldots, F_y\right)$, the fishery selectivity parameters $\underline{\theta}_V$ and the survey selectivity parameters $\underline{\theta}_S$. That is, $SB_y = g\left(R_0, \underline{\theta}_\Lambda, \underline{\theta}_F, \underline{\theta}_V, \underline{\theta}_S\right)$. Given the point estimate and covariance matrix of $\underline{\Theta}_E$ at the solution, one can approximate the variance of the spawning biomass estimate in year y, SB_y, as

(87) $$Var\left[SB_y\right] \approx \nabla g\left(\hat{\underline{\Theta}}_E\right)^T \Sigma\left(\hat{\underline{\Theta}}_E\right) \nabla g\left(\hat{\underline{\Theta}}_E\right) = \begin{pmatrix} \frac{\partial g}{\partial R_0}\left(\hat{\underline{\Theta}}_E\right) \\ \nabla g_{\underline{\theta}_\Lambda}\left(\hat{\underline{\Theta}}_E\right) \\ \nabla g_{\underline{\theta}_F}\left(\hat{\underline{\Theta}}_E\right) \\ \nabla g_{\underline{\theta}_V}\left(\hat{\underline{\Theta}}_E\right) \\ \nabla g_{\underline{\theta}_S}\left(\hat{\underline{\Theta}}_E\right) \end{pmatrix}^T \Sigma\left(\hat{\underline{\Theta}}_E\right) \begin{pmatrix} \frac{\partial g}{\partial R_0}\left(\hat{\underline{\Theta}}_E\right) \\ \nabla g_{\underline{\theta}_\Lambda}\left(\hat{\underline{\Theta}}_E\right) \\ \nabla g_{\underline{\theta}_F}\left(\hat{\underline{\Theta}}_E\right) \\ \nabla g_{\underline{\theta}_V}\left(\hat{\underline{\Theta}}_E\right) \\ \nabla g_{\underline{\theta}_S}\left(\hat{\underline{\Theta}}_E\right) \end{pmatrix}$$

Note that this variance calculation requires calculation of the gradient of the function defining the quantity of interest and evaluating this gradient at the estimated solution vector.

5.1.5.2 Conditional Parametric Bootstrap

Parametric estimation uncertainty for either the MLE or HPD solution and associated quantities of interest can also be generated by resampling the distribution of the estimator of the MAS model parameters using the estimated solution vector and associated covariance matrix. Here we briefly describe the application of the conditional, parametric bootstrap, a frequentist approach conditioned on the assessment model formulation. Note that Bayesian MCMC calculations for sampling the joint posterior distribution using the approximate covariance matrix as the jumping distribution are conceptually analogous but are not detailed in this draft.

To generate a total of *B* parametric bootstrap replicates for a vector of quantities of interest $\underline{Q} = \underline{Q}\left(\underline{\Theta}_E\right)$ that depend on the estimable parameters, we first generate a set of *B* samples from the asymptotic normal approximation of the solution vector for the MAS model $\left\{\underline{\Theta}_E^{(b)}\right\}_{b=1,\ldots,B}$ and compute the vector of quantities of interest for each bootstrap replicate of the solution vector, $\left\{\underline{Q}^{(b)}\right\}_{b=1,\ldots,B}$. To generate the parametric bootstrap samples of the QOIs, we note that the following multivariate normal distribution approximation holds asymptotically for the distribution of each bootstrapped solution replicate $\underline{\Theta}_E^{(b)}$

(88) $$\underline{\Theta}_E^{(b)} \sim MVN_p\left(\hat{\underline{\Theta}}_E, \Sigma\left(\hat{\underline{\Theta}}_E\right)\right)$$

Now one can apply the following steps to calculate the boostrap replicates $\underline{\Theta}_E^{(b)}$ and $\underline{Q}^{(b)}$ for *b*=1,…,*B*. First calculate the Choleski decomposition matrix *A* of the positive definite *p*x*p* covariance matrix $\Sigma\left(\hat{\underline{\Theta}}\right)$ as $AA^T = \Sigma\left(\hat{\underline{\Theta}}\right)$.

Next, for each *b*=1,…,*B*, do the following:

(i) Generate a random sample of p iid standard normal variates $z_j \sim N(0,1)$.

(ii) Form the p-dimensional vector $\underline{z} = (z_1,...,z_p)$.

(iii) Calculate the parametric bootstrap replicate of the solution vector $\underline{\Theta}_E^{(b)} = A\underline{z} + \widehat{\underline{\Theta}}_E$.

(iv) Calculate the bootstrap replicate of the QOI vector $\underline{Q}^{(b)} = \underline{Q}\left(\underline{\Theta}_E^{(b)}\right)$.

5.1.5.3 Unconditional Parametric Bootstrap

The unconditional nonparametric boostrap assigns probability distributions to parameter estimates from observed data, such as abundance indices. These probability distributions are then sampled in a Monte Carlo simulation to form new observed data sets that can then be fitted to produce the set of bootstrap replicates of freely estimated parameters and derived quantities of interest.

5.1.5.4 Conditional Nonparametric Bootstrap

The conditional nonparametric bootstrap operates on the residuals of the fitted stock assessment model. The residuals from the base model fit are randomly resampled with replacement add added to the appropriate subset of the observed data for each observed data point. Here the residuals of the fitted abundance indices from the base model fit would be randomly sampled and added to the observed abundance index values to form new subsets of abundance indices. Similarly, size composition and other model residuals are resampled to create new observed data subsets for refitting the base model. This process is repeated to produce the set of bootstrap replicates for making inferences about estimated parameters and derived quantities of interest.

5.1.5.4 Unconditional Nonparametric Bootstrap

The unconditional nonparametric bootstrap operates directly on the observed data, which are resampled with replacement to generate new observed data sets. The set of observed data sets are then fit with the base model structure to produce the set of bootstrap replicates for inference. This is the original empirically based bootstrap approach due to Efron (1981, 1982).

5.1.5.4 Markov Chain Monte Carlo Sampling

5.1.5.4.1 Metropolis-Hastings Sampling

- Metropolis-Hastings sampling (Gelman et al. 2004)

5.1.5.4.2 Gibbs Sampling

- Gibbs sampling (Gelman et al. 2004)

5.1.5.4.3 No-U-Turn Sampling

- No-U-Turn sampling (Hoffman et al. 2014, Monnahan et al. 2017)

5.1.6 Model Performance

Evaluating the performance of alternative models is important for understanding their robustness and reliability, noting that such evaluations will be ongoing process. Standard model diagnostics provide evidence of poor model performance but do not prove that a given model represents the best representation of the fishery system dynamics. Model performance measures are subject to non-random factors and structural assumptions that may limit their application and interpretation in cases where data are heterogeneous with varying sampling frames. To evaluate model robustness and reliability, we want to build models that can readily be tested in a simulation framework. In the ideal situation, quality assurance and quality control for metapopulation models would be achieved through an iterative process of model verification, validation, and uncertainty quantification (Figure 13). This stepwise approach to quality assurance is important for confirming the reliability of complex models (NRC 2012).

The model produces predictions (P) of observed data points (O). Let O_i be the ith observation and P_i denote the corresponding ith prediction, where there are a total of n observations. Let $E[O] = \frac{1}{n}\sum_{i=1}^{n} O_i$ and $E[P] = \frac{1}{n}\sum_{i=1}^{n} P_i$ be the expected values of the observations and predictions. Here are some standard measures of model performance in terms of predictive accuracy and precision.

5.1.6.1 Standardized Residuals

Standardized residuals are a multivariate performance measure of the nearness of observed and predicted values in a set of system observations. The residual for the ith prediction is denoted as $\varepsilon_i = O_i - P_i$ and represents the difference between the observed and predicted values. For a given set of system observation indexed by S, the root-mean squared error of the S^{th} observation set is the square root of the sum of the squared residual values for the set of a total of n_S observations and is denoted as $RMSE_S = \sqrt{\frac{1}{n_S}\sum_{i=1}^{n_S} \varepsilon_i^2}$. Given the root-mean squared error for a model fit to the observations, the standardized residual for the ith prediction is denoted as z_i, where

(89)
$$z_i = \frac{\varepsilon_i}{RMSE_S}$$

The standardized residuals provide a measure of the goodness of fit of the model to the individual observations and may be expected to conform to a set of independent random samples from a standardized normal distribution if sample size is sufficient.

5.1.6.2 Correlation

Correlation is a performance measure (ρ) that can measure the linear association between observations and predictions. In particular, correlation indicates whether observed trends are matched by model predictions where the Pearson correlation coefficient is

(90) $$\rho = \frac{\sum_{i=1}^{n}\left(O_i - E[O]\right)\left(P_i - E[P]\right)}{\sqrt{\sum_{i=1}^{n}\left(O_i - E[O]\right)^2 \sum_{i=1}^{n}\left(P_i - E[P]\right)^2}}$$

Positive correlation indicates the relative match of predicted trends with values of ρ closer to 1 indicating better predictions of the observations. A model with a higher positive correlation exhibits a closer agreement in trend than a model with a lower positive correlation. Negative correlations generally indicate that model predictions and observations have opposite trends through part of the data set. Values of correlation near zero indicate that there was no association between the observed and predicted trend.

Correlation can also be used to gauge the identifiability of pairs of estimated parameters θ_i and θ_j where $CORR\left(\theta_i, \theta_j\right) = \frac{COVAR\left(\theta_i, \theta_j\right)}{VAR\left(\theta_i\right) \cdot VAR\left(\theta_i\right)}$ with estimates of covariances being derived from the inverse Hessian matrix of the fitted MAS model.

5.1.6.3 Root Mean Square Error

The root mean square error ($RMSE$) measures model prediction accuracy and identifies biases where root mean square error is

(91) $$RMSE = \sqrt{\frac{1}{n}\sum_{i=1}^{n}\left(O_i - P_i\right)^2}$$

The $RMSE$ performance measure is always positive. In general, a model with a smaller $RMSE$ provide a more accurate set of predictions than a model with a higher $RMSE$.

5.1.6.4 Modeling Efficiency

Modeling efficiency (MEF) measures how well the model makes predictions in comparison to the mean of the observations where modeling efficiency is

(92) $$MEF = \frac{\sum_{i=1}^{n}\left(O_i - E[O]\right)^2 - \sum_{i=1}^{n}\left(P_i - E[O]\right)^2}{\sum_{i=1}^{n}\left(O_i - E[O]\right)^2}$$

Smaller absolute values of modeling efficiency indicate a poorer fit to the observed mean. One characterization due to Allen et al. (2007. Quantifying uncertainty in high-resolution coupled hydrodynamic-ecosystem models. J. Mar. Syst. 64:3-14) suggested some reference values for MEF . These were: MEF <0.2, poor efficiency; 0.2< MEF <0.5, good efficiency; 0.5< MEF <0.65, very good efficiency; MEF >0.65, excellent efficiency.

5.1.6.5 Durbin-Watson Test

- Durbin and Watson (1971)

5.1.6.6 Runs Test

- E.g. Kennedy and Gentle (1980)

5.1.6.7 Chi-Square Test

- E.g. Kennedy and Gentle (1980)

5.1.6.8 Age-Structured Production Model Diagnostic

- Maunder and Piner (2015)

5.1.6.9 Retrospective Analysis

- Mohn (1999) and Hurtado et al. (2014)

5.1.6.10 Simulation-Based Approaches

Some simulation-based approaches for evaluating model performance include: (1) clearly defining the quantities of interest for model verification; (2) identifying the algorithmic structures to be tested; and (3) using code-to-alternative-code comparison and testing. Ideally, solution verification is best done using an analytic solution for a well-posed problem. The quantities of interest for model performance must also be identified before starting the validation process. That is, identify the important quantities to be well estimated a priori. It is also recommended to use a broad range of possible inputs to quantify and bound the error from a model application. In this context, the use of cross validation and other predictive accuracy checks are also recommended for characterizing model validity and predictive performance. If possible, use physical observations to constrain uncertainties in model inputs. Document assumptions about the sources of variation used to characterize uncertainty in the quantities of interest and use replication to estimate variability and measurement uncertainty.

5.1.7 Numbers at Age Algorithms

Algorithms to calculate dynamics changes in numbers at age in a MAS model are listed in the following Appendices:

(i) Initial Unfished Equilibrium Numbers at Age Calculation (Appendix 1)
(ii) Initial Fished Equilibrium Numbers at Age Calculation (Appendix 2)
(iii) Dynamic Fished Numbers at Age Calculation (Appendix 3)

5.2 Ensemble Models

Ensemble models are sets of models that can be jointly used for estimating stock status or predicting fishery outcomes under future conditions for a metapopulation. The set of models in the model ensemble comprise the candidate descriptions or hypotheses about the true state of nature, each of which makes a distinct claim about system dynamics and process outcomes. The estimated quantities of interest and forecasts for individual candidate models are going to differ by some amount because the models are distinct and provide a unique description of system dynamics, e.g. Scott et al. (2016). In general, the candidate models in the ensemble will need to be sufficiently different so as not to be redundant.

5.2.1 Ensemble Model Construction

The approach we use for ensemble model construction and multimodel inference is conceptually based on ideas expressed and popularized for ecological modeling by Burnham and Anderson (2002). The multimodel inference approach starts with a set of candidate models M_j, denoted by $\underline{M} = \left\{ M_j \right\}$, that represent the set of plausible hypotheses about metapopulation dynamics. Here the emphasis is on applying the method of multiple working hypotheses (Chamberlain 1965) and constructing candidate models that have an empirical basis and are grounded in scientific plausibility (e.g., Hilborn and Mangel 1997). In this context, there should be an emphasis on both keeping an open mind about the set of plausible hypotheses and not seeking to derive a dichotomous null versus alternative hypothesis in order to simplify the model selection process. Burnham and Anderson (2002) advocate limiting the set of candidate models for parsimony and this is an important point to reduce the possibility of chance results due to sampling variability. That is, when more models are included in the set of candidate models with a fixed sample size, then the power to detect important differences between models decreases as the relative sample size per model decreases. Further, it is also important to avoid including subsets of models that are highly collinear or functionally redundant.

The multimodel inference approach is designed to address the important issue of model selection uncertainty. A key feature of the multimodel inference approach is to avoid the risk of making decisions based on overconfidence and overinterpretation of modeling results due to the underestimation of uncertainty and the a priori acceptance of a single best hypothesis without critical examination. Because our understanding of complex fishery systems is and will always be incomplete, there needs to be an ongoing emphasis on confronting our alternative hypotheses about ecosystem dynamics with observed data (Hilborn and Mangel 1997). In this context, we emphasize a tiered approach to the evaluation of each candidate model as being judged to be a credible model that is appropriate for inference in fishery management application. First and foremost, candidate models have to satisfy convergence requirements and statistical optimization criteria, this is a minimal requirement. Second, standard model goodness-of-fit diagnostics need to provide evidence that each candidate model conforms to assumptions. Last, the selected credible models among the set of candidate models should have quantitative support based on information theoretic criteria that provide an estimate of model distance from the unknowable true state of nature (Burnham and Anderson 2002). In the case of one selected, best-fitting credible metapopulation model, inference and scientific information for management will be based on that single model.

5.2.2 Ensemble Model Selection

The model selection process depends on both the choice of the input data for the metapopulation assessment model and the goodness of fit of model predictions of the chosen data. Here it will be assumed that the model construction layer has produced more than one potentially useful candidate model. Otherwise, if only one model has been judged to be the best model with associated point estimates and uncertainty estimates, such as confidence intervals, then there is no need for model set selection. Selecting a single best-fitting model paradigm has the advantage of parsimony and simplicity but the model-based uncertainties may not provide an accurate representation of the actual uncertainty in predicted outcomes. Given this, we will assume that there is a set of candidate models from which a set of credible models will be selected for use in managing the fishery system.

Each individual model in the set of candidate models has a specific set of input data for parameter estimation. For any pair of candidate models, there are four possible cases for comparing the input data sets. First, the sets of input data for the two candidate models are identical. Second, the set of input data for one model is a subset of the input data for the other model. Third, the sets of input data for the two models intersect but, for both models, some of the input data are unique to that model. Last, the sets of input data for the two candidate models do not intersect and are independent. These four categories can also be applied to any set of models without loss of generality. In what follows, we will directly treat the case of identical input data sets for all candidate models and then discuss general approaches to deal with the cases of unequal input data sets across candidate models.

For many fisheries assessment applications, the set of candidate models in the ensemble model will use identical input data sets. In the case of identical input data sets for all candidate models, one can apply a multimodel inference approach (e.g., Burnham and Anderson 2002) for judging the credibility of alternative models. Structural uncertainty in approximating models used for inference about metapopulations is an important feature of the incomplete knowledge of complex marine system dynamics. Structural uncertainty, when combined with natural variability and observational error, makes it challenging to provide the understanding and predictive information needed to manage human impacts (Peterman 2004, Link et al. 2012). The multimodel inference approach in MAS uses a state space modeling formulation (e.g., Aoki 1990, Schnute 1994) to represent alternative hypotheses with Markov process dynamics. A frequentist (Burnham and Anderson 2002) or Bayesian estimation framework (Punt and Hilborn 1997, Ellison 2004) can be used to assess the evidence for alternative models, which are formulated as either simple or hierarchically structured models (Clark 2005) with time as a hierarchical dimension. Information theoretic model selection criteria are used to weight the probability that each candidate model provides the best approximation and predictive information about the system state, given the observed fixed data. Model averaging can be used when the weight of evidence to support a single operating model is ambiguous (Hoeting et el. 1999, Burnham and Anderson 2002), else the results of a single best operating model are identified and directly applied. This approach can account for the probable range of uncertainty in model structure while both incorporating relevant prior information and providing probabilistic interpretations of results for risk assessment.

5.2.3 Ensemble Model Weights

Model ensembles are sets of models that can be jointly used for predicting outcomes of some process of interest, like a stock assessment model. The set of models in the model ensemble comprise the candidate descriptions of the state of nature, each of which makes a distinct claim about system dynamics and process outcomes. The predictions of each candidate model are expected to differ by some amount because the models are distinct and provide a unique description of system dynamics. Given various predictions of a total of *M* candidate models, we want to be able to meld or combine the candidate model predictions to produce a model averaged result. To do this we need to determine the vector of model weights, $\underline{w} = \left(w_1, w_2, ..., w_M\right)$, that satisfy $w_m \geq 0 \; and \; \sum_{m=1}^{M} w_m = 1$. The model weights are applied to the predictions of the candidate models $\widehat{Y_1}, \widehat{Y_2}, ..., \widehat{Y_M}$ produce the model-averaged prediction $\widetilde{Y} = \sum_{m=1}^{M} w_m \widehat{Y_m}$. The set of feasible model weights is a proportion simplex with $\left(M-1\right)$ dimensions. For example, the proportion simplex for a model ensemble with three candidate models is a 2-dimensional linear surface (see below) and the model-averaging question is what vector of weights $\underline{w}^*$ should we use to achieve the best predictive accuracy for a given problem? Here we follow the characterization of approaches to estimating model weights for averaging by Dormann et al (2018), who identify four general approaches: (i) equal weights, (ii) information-theoretic weights, (iii) tactical weight and (iv) Bayesian weights, noting that (iv) is not fully treated in this version 1.0 of the MAS software design document.

5.2.3.1 Equal Weights

In some cases, there may be limited information to measure the relative quality or credibility of individual model estimates or predictions of quantities of interest. In this case, the application of equal model weights may provide a means to account for the inherent structural model uncertainty in the ensemble model without a priori preference for any particular model-based hypothesis. Under the equal model weights approach, the chosen set of models weights is $\underline{w}^* = \left(w_1^*, w_2^*, ..., w_M^*\right)$, where $w_j^* = \frac{1}{M}$ for each model. This equal weighting approach does not account for potential differences in each model's estimation or prediction accuracies but can provide a simple approach to dealing with sets of credible hypotheses that are difficult to compare or judge.

5.2.3.2 Information-Theoretic Weights

In what follows, the multimodel inference approach and the development of a set of candidate models is discussed, including the calculation of model likelihoods and weights, the multimodel inference process, and model averaging when appropriate. Alternative hypotheses can be formulated as either frequentist, or random effects, or simple Bayes, or hierarchical Bayes models for estimation purposes and these model-based hypotheses can then be fit to the observed input data. Model selection and multimodel inference is used to judge the adequacy of the models, including formulating model-averaged results.

Alternatively, when more than one credible metapopulation model exists, model averaging can be applied to account for model selection uncertainty. In what follows, we describe the use of the Deviance Information Criterion (*DIC*, Spiegelhalter et al. 2002) as a plug-in measure of the information-theoretic goodness of fit of the alternative candidate models where *DIC* values are empirically calculated based on the information generated by the convergent Markov Chain Monte Carlo (*MCMC*) simulations conducted for each model.. We also note that alternative information theoretic criteria are available, for example, Akaike information criterion (*AIC*, Akaike 1973), Bayesian information criterion (*BIC*, Schwarz 1978), or Watanabe-Akaike and widely-applicable Bayesian information criterion (*WAIC* and *WBIC*, Watanabe 2009, 2010, 2013). In some cases, these alternative information-theoretic criteria (*AIC*, *BIC*, *WAIC* or *WBIC*) may provide better approximations of the relative goodness of fit among alternative models than *DIC*, especially when the estimate of the covariance matrix is not approximately multivariate normal. Furthermore, we note that each of these criteria can be treated as a plug-in likelihood to calculate approximate model weights (e.g., equation (101)).

To provide some background on the logical basis for *DIC* as a measure of goodness of fit or conversely the amount of discrepancy between the candidate model and the data (Burnham and Anderson 2002, Gelman et al. 2004), observe that the model deviance $Dev\left(\underline{\underline{D}}_T, \underline{\widehat{\Theta}}_E\right)$ is typically defined as -2 times the log-likelihood of the observed data $\underline{\underline{D}}_T$ conditioned on the estimated parameters $\underline{\widehat{\Theta}}_E$ where

$$Dev\left(\underline{D}, \underline{\widehat{\Theta}}_E\right) = -2 \cdot \log\left(L\left(\underline{D} \mid \underline{\widehat{\Theta}}_E\right)\right) \tag{93}$$

The expected deviance, which is calculated by averaging $Dev\left(\underline{\underline{D}}_T, \underline{\widehat{\Theta}}_E\right)$ over the true but unknown sampling distribution, is equal to 2 times the Kullback-Leibler information value up to a constant that does not depend on the estimated parameters $\underline{\widehat{\Theta}}_E$. This relation to the Kullback-Leibler information implies that the parameters that produce the lowest expected deviance will produce the maximum information and have the highest posterior probability. However, the true sampling distribution is not known and therefore one needs an accurate way to estimate the expected deviance. To this end, note that the discrepancy between the model and the data depends on both data $\underline{\underline{D}}_T$ and the set of parameters being estimated in the bootstrapping or *MCMC* simulation process $\hat{\underline{\Theta}}_E$. To get a deviance measure that depends only on the data, one can approximate the model deviance value $\overline{Dev}\left(\underline{\underline{D}}_T\right)$ conditioned on a mean point estimate of $\underline{\Theta}_E$

(94) $$\overline{Dev}\left(\underline{\underline{D}}_T\right) = \overline{Dev}\left(\underline{\underline{D}}_T, \hat{\underline{\Theta}}\left(\underline{\underline{D}}_T\right)\right)$$

where the point estimate $\hat{\underline{\Theta}}_E$ was calculated as the mean of the posterior *MCMC* simulations for $\underline{\Theta}_E$. That is,

(95) $$\hat{\underline{\Theta}}_E\left(\underline{\underline{D}}_T\right) = E\left[\underline{\Theta}_E \mid \underline{\underline{D}}_T\right] = \frac{1}{J}\sum_{j=1}^{J}\underline{\Theta}_E^{(j)}$$

where $\underline{\Theta}_E^{(j)}$ is the jth iterate of $\underline{\Theta}_E$ in a total of J posterior simulations. This is one estimate of the expected deviance for a fixed point estimate of $\underline{\Theta}_E$ calculated from the posterior simulations.

Another natural approach to estimating the expected deviance would be to use the expected value of $\widehat{Dev}$, the estimate of model discrepancy, calculated over the posterior distribution as our estimate of the model deviance

(96) $$\widehat{Dev}\left(\underline{\underline{D}}_T\right) = E\left[Dev\left(\underline{\underline{D}}_T, \underline{\Theta}_E\right) \mid \underline{\underline{D}}_T\right]$$

Of course, one does not have complete knowledge or information about the true posterior distribution and so an analytic calculation of the integral for the expected value is not generally possible except for simple problems. However one can use the natural plug-in estimate of the expected deviance by taking the average of $Dev\left(\underline{\underline{D}}_T, \underline{\Theta}_E\right)$ over the posterior simulations to be the estimated model deviance $\widehat{Dev}$, where

(97) $$\widehat{Dev}\left(\underline{\underline{D}}_T\right) = \frac{1}{J}\sum_{j=1}^{J}Dev\left(\underline{\underline{D}}_T, \underline{\Theta}_E^{(j)}\right)$$

Given this, we observe that the difference between the posterior mean of the deviance ($\widehat{Dev}$) minus the deviance evaluated at the posterior mean of the stochastic parameters being estimated

($\overline{Dev}$) provides a measure of the effect of model fitting and can be used as a measure of the effective degrees of freedom in the model (ρ_D) as shown by Spiegelhalter et al. (2002) under the assumption that the posterior distribution is asymptotically a multivariate normal distribution as

(98) $$\rho_D = \widehat{Dev} - \overline{Dev}$$

The value of *DIC* was then calculated as twice the posterior mean of the deviance minus the deviance evaluated at the posterior mean of the stochastic nodes

(99) $$DIC = 2\widehat{Dev} - \overline{Dev} = \widehat{Dev} + \rho_D = \overline{Dev} + 2\rho_D$$

The alternative candidate models, indexed by j (M_j), can then be ranked by their DIC values (DIC_j). The best fitting model (M^*) with the minimum value of *DIC* (DIC_{Min}) produced the best fit to the observed data. For each model, the difference in the model's value of *DIC* from the minimum was calculated (Δ_j) as

(100) $$\Delta_j = DIC_j - DIC_{Min}$$

For judging model fits, one typically considers models with values of Δ_j less than 2 likelihood units to have similar support to the minimum *DIC* model and can be included in the set of credible candidate models that have similar goodness of fit to the observed data. In contrast, models with Δ_k greater than 3 differ from the best-fitting model and have limited support (Spiegelhalter et al. 2002). In this context, evidence indicated that the credible models also provided adequate fits to the observed data and should be considered as viable alternative states of nature in comparison to the best fitting model. The results from the set of credible models, denoted by $\underline{M}$, were model-averaged based on the likelihood $L_j\left(\underline{\underline{D}}_T \,|\, \underline{\Theta}_E\right)$ of each model $M_j \in \underline{M}$. In this context, the model likelihood was proportional to the exponential of the Δ_j value through the expression

(101) $$L_j\left(\underline{\underline{D}}_T \,|\, \underline{\Theta}_E\right) \propto \mathrm{e}^{-0.5\Delta_j}$$

One can apply model averaging to the set of credible models using the *DIC*-based approximation of the candidate model likelihood. This produced a model-averaged set of results, which were used for probabilistic inference about stock status determination through time and were also available for as a distribution for future population projections under alternative harvest patterns and states of nature.

To apply model averaging, prior model probabilities (π_k) are needed to express the relative belief that each of the credible models represents the true state of nature. One can adopt an objective approach for setting the prior model probabilities in the absence of any information for preferring one credible model over another (Berger 2006). In this case, the prior model probabilities are equal based on the principle of indifference, where for a total of $N_M \le M$ credible models

$$\pi_j = \pi_k = \frac{1}{N_M} \; and \; \sum_{j=1}^{N_M} \pi_j = 1 \tag{102}$$

Given the integrated likelihoods of the credible models and the prior model probabilities, one can calculate the posterior model probabilities or Bayesian model weights (w_j) over the set of credible models as

$$w_j = \frac{\pi_j \cdot \mathrm{e}^{-0.5\Delta_j}}{\sum_{i=1}^{N_M} \pi_i \cdot \mathrm{e}^{-0.5\Delta_i}} \tag{103}$$

Here the posterior model probabilities quantify the relative support for each model contained in the observed data given the assumed prior model probabilities. If one does not have any evidence to assume one model was a priori more likely than another was, then the posterior model probabilities are effectively based on the observed data. In this case, the calculation of the model weights can be viewed as being analogous to an objective Bayesian estimation approach (Berger 2006).

5.2.2.3 Tactical Weights

Here we describe a generic cross validation algorithm to estimate model weights for an assessment model ensemble using a common testing or validation data set. The algorithm requires that there exists a common model testing data subset for measuring the predictive accuracy of each model across the set of credible models. However, from a practical engineering point of view, there is no necessity that each model uses the same data set for model training or parameter fitting.

The set of credible models is $\underline{M} = \{M_1, ..., M_{N_M}\}$ where M_j is the jth model in the set. Each candidate model requires data for fitting and parameter estimation. D_j is the data required for the jth model. The data subset that is common to all of the D_j is $\underline{y} = \{y_1, ..., y_n\}$ where $\underline{y} \subset D_j$ for all j.

The set of time periods that is common to all of the models is $\underline{T} = \{1, 2, ..., T\}$. For a given assessment model, each data point is observed in a unique time period. As a result, the data for each model D_j can be partitioned into subsets by time period where $D_{j,t}$ is the data for model *j* from time period *t* and $D_j = \left\{D_{j,1}, D_{j,2}, ..., D_{j,T}\right\}$. The common or target data subset $\underline{y}$ can also be partitioned into subsets by time period where $\underline{y}_t$ is the subset of $\underline{y}$ that occurs in time period *t,* $\underline{y} = \left\{\underline{y}_1, \underline{y}_2, ..., \underline{y}_T\right\}$ and n_t is the number of target data points in time period *t.*

The model-weighting algorithm is based on cross validation over time. The cross validation analysis can be conducted in a number of ways depending on how one constructs the training and testing data sets. To keep it simple, we first describe the cross validation based on a leave one out approach by time period. To do this, we partition the data by time period for each candidate model into two parts: the subset of target data $\underline{y}_t$ and the subset of non-target $\underline{d}_{j,t} \not\subset \underline{y}_t$. This gives $D_{j,t} = \left\{\underline{y}_t, \underline{d}_{j,t}\right\}$. To compute the predictive accuracy of each model by time period, the subset of target data is excluded from the data by time period for each model to form the reduced subset $D_{j\setminus t,t} = \left\{\underline{d}_{j,t}\right\}$. This reduced data subset along with the remaining data are the leave one out data set for time period *t* which is denoted by $D_{j\setminus t} = \left\{D_{j,1}, D_{j,2}, ..., d_{j,t}, ..., D_{j,T}\right\}$. The leave one out data sets are then used to fit each model, predict the value of the missing datum $\underline{y}_t$ and calculate the cross validation score for each model in time period *t.*

The prediction of a target data point y_i in time period *t* by a given model in a given time period is based on a true unknown function $f_{j,i}$ where $y_i = f_{j,i}\left(D_j\right) + \varepsilon_{j,i}$ where the random shocks $\varepsilon_{j,i}$ are iid normally distributed with zero mean and constant variance $\varepsilon_{j,i} \sim N\left(0, \sigma_j^2\right)$. The model-based prediction of $f_{j,i}$ is then denoted as $\hat{f}_{j,i}$. Given this, the predicted value of the *i*th target data point using the full data set is $\hat{f}_{j,i}\left(D_j\right)$ while the predicted value of the *i*th target data point using the leave one out data set is $\hat{f}_{j\setminus t,i}\left(D_{j\setminus t}\right)$.

The ordinary cross validation score for a given model in a given time period is denoted as $V_{j,t}$ where the score is the sum of the squared differences between the value of the excluded or missing data and its predicted value. That is, the cross validation score for a given model in a given time period is

$$V_{j,t} = \frac{1}{n_t}\sum_{i \in \underline{y}_t}\left(\hat{f}_{j\setminus t,i} - y_i\right)^2 \tag{104}$$

The score in equation (104) provides an estimate of the expected squared error in predicting a new instance of an element of $\underline{y}_t$. That is, if the mean-square error for a given model in a given time period is denoted as $MSE_{j,t}$, where $MSE_{j,t} = \frac{1}{n_t}\sum_{i \in \underline{y}_t}\left(\widehat{f}_{j,i} - f_{j,i}\right)^2$, then the expected square error for a new prediction is $E\left[MSE_{j,t}\right] + \sigma_j^2$. Substituting $y_i = f_{j,i}\left(D_j\right) + \varepsilon_{j,i}$ into equation (104) gives

$$V_{j,t} = \frac{1}{n_t}\sum_{i \in \underline{y}_t}\left(\widehat{f}_{j\backslash t,i} - f_{j,i} - \varepsilon_{j,i}\right)^2 = \frac{1}{n_t}\sum_{i \in \underline{y}_t}\left[\left(\widehat{f}_{j\backslash t,i} - f_{j,i}\right)^2 - 2\left(\widehat{f}_{j\backslash t,i} - f_{j,i}\right)\varepsilon_{j,i} + \varepsilon_{j,i}^2\right] \tag{105}$$

As a result, the expected value of the cross validation score for a given model in a given time period noting that the random shocks have zero mean and are iid with constant variance is

$$E\left[V_{j,t}\right] = \frac{1}{n_t}E\left[\sum_{i \in \underline{y}_t}\left(\widehat{f}_{j\backslash t,i} - f_{j,i}\right)^2\right] + \sigma_j^2 \tag{106}$$

Now the asymptotic argument can be invoked that as n_t becomes large enough, the leave one out data prediction is approximately equal to the full data prediction, or $\widehat{f}_{j\backslash t,i}\left(D_{j\backslash t}\right) \approx \widehat{f}_{j,i}\left(D_j\right)$, then one can see that equation (106) implies that the expected squared error or prediction inaccuracy for a new instance of $\underline{y}_t$ is

$$E\left[V_{j,t}\right] \approx \frac{1}{n_t}E\left[MSE_{j,t}\right] + \sigma_j^2 \tag{107}$$

Thus, the cross validation scores provide estimates of the inverse of the predictive accuracy for a given model in a given time period. The inverse cross validation scores can, in turn, be used to estimate model weights based on relative model skill or predictive accuracy as

$$w_{j,t} = \frac{V_{j,t}^{-1}}{\sum_{k=1}^{N_M} V_{j,t}^{-1}} \tag{108}$$

where *j* indexes model and *t* indexes time period with $0 < w_{j,t} < 1$ and $\sum_{j=1}^{N_M} w_{j,t} = 1$.

5.2.2.4 Bayesian Weights

The Bayesian approach to setting weights for individual models M_i is based on calculating the marginal likelihoods of the models, $P\left(\underline{\underline{D}}_T | M_i\right)$, given the data $\underline{\underline{D}}_T$ (Gelman et al. 2004). The marginal likelihoods are then combined with the prior model weights, $P\left(M_i\right)$, to compute the posterior model weights, $w_i = P\left(M_i \mid \underline{\underline{D}}_T\right)$, using Bayes' theorem, where $w_i = \dfrac{P\left(\underline{\underline{D}}_T \mid M_i\right) P\left(M_i\right)}{\sum_{j=1}^{N_M} P\left(\underline{\underline{D}}_T \mid M_j\right) P\left(M_j\right)}$.

Given the posterior model probabilities of each model, a Bayesian ensemble prediction of a QOI can be calculated from the weighted average of the individual model predictions times the posterior model probabilities. Bayesian approaches are easy to implement in a variety of software platforms, however the specification of model priors requires subjective decisions. While a null hypothesis of equal prior model weights is an obvious option in the absence of auxiliary information, it is recommended that the sensitivity of the ensemble results to alternative priors be tested.

5.2.3 Ensemble Model Results

The derived or assumed model weights for the ensemble model provide the essential information for model averaging of the conditional model distributions for any resulting individual state space model parameter or for any derived model output or quantity of interest, denoted by Y. The model-averaged estimate of the quantity of interest Y is denoted as $\tilde{Y}$ and its distribution depends on the expected estimates $\widehat{Y}_j$ from each candidate model, indexed by j. The expected value of the model-averaged estimate of Y averaged over the set of credible models is

(109) $$\tilde{Y} = E\left[\widehat{Y}\right] = \sum_j w_j \widehat{Y}_j$$

(e.g., Buckland et al. 1997, Burnham and Anderson 2002) and the variance of the model-averaged estimate is

(110) $$VAR\left[\widehat{Y}\right] = \left[\sum_j w_j \sqrt{VAR\left[\widehat{Y}_j\right] + \left(\widehat{Y}_j - E\left[\widehat{Y}\right]\right)^2}\,\right]^2$$

The variance of the model-averaged estimation result includes two components, the first is the variance of the individual model estimates and the second is an expression for the variance contribution of model uncertainty in the point estimate of the result $\tilde{Y}$. Given these two fundamental quantities for ensemble model inference, one can use the mean and the unconditional variance estimate of the model-averaged result for risk analyses. Alternatively, other measures of model goodness of fit may be applied to subsets of the assessment data when there are differences among the input data sets used within the alternative models.

5.3 Model Forecasting

Future forecasts in MAS can be conducted for a single metapopulation model or for an ensemble of multiple credible models wherein each credible model has an associated set of future forecasting models.

5.3.1 Model Forecast Components

One can understand the genealogy of combining forecasts as it has developed in the modern context by noting that humans have been making forecasts about the future for a long time. Besides the genealogy of forecasting it will also be useful to describe what forecasting is and also what it is not.

To begin, we consider the historical and influential paper on combining forecasts by Bates and Granger (1969). The basic forecasting problem is that we are very interested in calculating the expected value of an event at a future time t and we have two or more forecasts for this event. Which forecast is better, and which one should we use? One simple solution would be to use the "better" forecast for a given measure of forecast performance or quality. This is not necessarily a wise procedure if the goal is to produce as accurate a forecast as is possible because if we choose a single forecast as the best, then the discarded forecast, or forecasts, nearly always contains some useful independent information. This independent information can be of at least two kinds, and a discarded forecast may have both kinds of information. In particular, these two kinds of information are:

(i) The discarded forecast is based on some variable or information that is not used in the best forecast.

(ii) The discarded forecast makes different assumptions about the form of the relationship between the predictive variables used to produce a good forecast.

Note that for case (i), it can be shown that there is a combined forecast that improves the forecast precision whereas for case (ii), it is not necessarily true that a combined forecast will have a lower forecast precision. Note that in this context, we take better to mean having lower predictive error or having the smallest mean squared forecast error.

Next, we want to use some notation, which is consistent of the Bates and Granger (1969) exposition. Let y_t be the observed event we want to forecast at time t noting that this event could represent as a univariate value or an array of values. Let $F_{i,t}$ be the value of the forecast produced by forecast method i at time t. Let $e_{i,t}$ be the forecast error produced by forecast method i at time t. By definition, the forecast error is the difference between the observed and the predicted value of the event. That is,

$e_{i,t} = y_t - F_{i,t}$. In addition, we assume that the individual forecasts, indexed by i, are unbiased and we also assume that the individual forecast processes have constant variance. That is, the individual forecasts are stationary zero-mean processes, which can be expressed in operator notation as the expected value of the forecast errors has zero mean $E\left[e_{i,t}\right] = 0 \;\; for \;\; \forall i,t$ and as the variance of the forecast error has a constant within-forecast precision with $Var\left[e_{i,t}\right] = \sigma_i^2 \;\; for \;\; \forall t$.

In what follows, we will need to be able to express forecasts that are specific to a particular model and in this case, the model will be indexed by "j" and the notation for the model-specific event, the forecast, the forecast error, and the variance of the forecast error will be $y_{i,j,t}$, $F_{i,j,t}$, $e_{i,j,t}$, and $\sigma^2_{i,j}$.

Given this setup, one natural question to ask is why assume that the forecast methods are unbiased? Without loss of generality, we can assume that we have two forecasts, which is the situation described in Bates and Granger (1969) in their example of an equally weighted combination $F_{C,t} = F_{1,t} + F_{2,t}$ of two forecasts ($F_{1,t}$, an exponential smoothing and $F_{2,t}$, an adaptive errors ARIMA) that improved the forecast of monthly airline passengers during 1951-1960 substantially (i.e., p. 452 in Bates and Granger). The logic is that if one forecast is unbiased and the other is biased, then any combination of the two, other than the trivial 100% to 0% weighting, will have some bias. This is not a desirable property and as such, we will assume that if there is known bias, then that bias has been corrected for, a priori, or at least an estimate of an appropriate bias correction has been applied. Therefore, it should be emphasized that a first step developing forecasts is to check for biased predictions of the event y_t for each individual forecast, noting that if bias is detected then it needs to be corrected or the forecast method needs to be discarded.

Equal forecast weights may be adequate to produce an improvement by using a combined forecast, but can one do better in the choice of a method for determining forecast weight ? The answer is yes, at least in theory, but equal forecasting has performed surprisingly well in empirical studies and this has led to what has become known as the "forecast combination puzzle", which is discussed in some further detail below. For now, let us go over some of the theory of optimal combinations of two or more forecasts as developed by Bates and Granger (1969).

The first thing we need to add notation for is the weight of a forecast, denoted as w_i, which represents the weight assigned to the i^{th} forecast model. In general, we might expect that the weights of individual forecasts will be nonnegative with $w_i \in [0,1]$ and that they could be interpreted in a probabilistic sense, although this is not a necessity when the goal is to minimize the mean squared error of the combined forecast. Regardless, it is typical to constrain the forecast weights to sum to unity over the set of forecasts. That is, $\sum_i w_i = 1$. For the case of two forecasts, the combined forecast $F_{C,t}$ is a weighted average of the individual forecasts, where the weight of the first forecast $F_{1,t}$ is w and the combined forecast is $F_{C,t} = wF_{1,t} + (1-w)F_{2,t}$. The combined forecast variance is denoted as σ_C^2 and this variance is a weighted combination of the individual forecast variances along with an adjustment for the correlation ρ between the forecast errors. That is, $\rho = Corr[\underline{e}_1, \underline{e}_2]$, the error covariance is $\sigma_{12} = \rho\sigma_1\sigma_2$ and σ_C^2 is

$$(111)\quad \sigma_C^2 = w^2\sigma_1^2 + (1-w)^2\sigma_2^2 + 2\rho w\sigma_1(1-w)\sigma_2 = w^2\sigma_1^2 + (1-w)^2\sigma_2^2 + 2w(1-w)\sigma_{12}$$

It is notable that the value of the combined forecast variance is never greater than either of the individual forecast variances (Bates and Granger 1969). That is, $\sigma_C^2 \le \min(\sigma_1^2, \sigma_2^2)$ and that the minimum, or optimal value of the combined forecast variance w^* is exactly (Bates and Granger 1969)

$$(112)\qquad w^* = \frac{\sigma_2^2 - \rho\sigma_1\sigma_2}{\sigma_1^2 + \sigma_2^2 - 2\rho\sigma_1\sigma_2} = \frac{\sigma_2^2 - \sigma_{12}}{\sigma_1^2 + \sigma_2^2 - 2\sigma_{12}}$$

Now, if the error covariance is large relative to the individual error variances then it is possible to obtain a negative weight, e.g., if $\sigma_{12} > \sigma_2^2$. It is also notable that if the error covariance is zero, then the optimal weight for the two-forecast case reduces to

$$(113)\qquad w^* = \frac{\sigma_2^2}{\sigma_1^2 + \sigma_2^2} = \frac{\dfrac{1}{\sigma_1^2}}{\dfrac{1}{\sigma_1^2} + \dfrac{1}{\sigma_2^2}}$$

which is exactly inverse variance weighting of the individual forecasts. In this context, it is useful to observe that a greater weight will be assigned to the forecast that is more precise. It is also true that in practice, we do not know the true error variances and only have estimates of the forecast error variances and these are of course used for numerical calculation of the weights based on the plug-in principle.

Now we can briefly describe the extension of Bates and Granger (1969) to a set of N_F forecast models, details of which can be found in Elliott (2011. Averaging and the optimal combination of forecasts. UC San Diego Working Paper, available at: www.econweb.ucsd.edu/~grelliott/AverageingOptimal.pdf). To do this we will use some vector notation. Let $\underline{e}_t$ be the forecast prediction error vector and $\underline{w}$ be the weight vector for the N_F forecasts at time t. Then the mean squared prediction error (MSE) is

$$(114) \qquad MSE \;=\; E\left[\underline{w}^T \underline{e}_t\right]^2 \;=\; \underline{w}^T E\left[\underline{e}_t \underline{e}_t^{\,T}\right]\underline{w} \;=\; \underline{w}^T \Sigma_e \underline{w}$$

where Σ_e is the variance-covariance matrix of the forecast errors. Again, in practice we will use the sample estimate of Σ_e for numerical calculations. We also have the constraint that the weights sum to unity which one can write as $\underline{I}^T\,\underline{w} = 1$ where $\underline{I}$ is the all-ones vector in N_F dimensions. Given this setup, the minimizing weight vector $\underline{w}^*$ is given by

$$(115) \qquad \underline{w}^* \;=\; \left(\underline{I}^T \Sigma_e^{-1} \underline{I}\right)^{-1} \Sigma_e^{-1} \underline{I}$$

in addition, the minimum mean squared error is

$$(116) \qquad MSE\left(\underline{w}^*\right) \;=\; \left(\underline{I}^T \Sigma_e^{-1} \underline{I}\right)^{-1}$$

If one assumes that the error covariance matrix is sparse and primarily a diagonal matrix, i.e., the forecast covariances are small in relation to the individual forecast variances, then one obtains what we will call inverse variance forecast weighting. That is,

$$(117) \qquad w_i^* \;=\; \frac{\left(MSE_i^*\right)^{-1}}{\sum_{k=1}^{N_F}\left(MSE_k^*\right)^{-1}} \;\approx\; \frac{\dfrac{1}{\sigma_i^2}}{\sum_{k=1}^{N_F}\dfrac{1}{\sigma_k^2}}$$

This was the “recommended” approach among the five weighting methods examined by Bates and Granger (1969), noting that the weighting can be made time-dependent by updating the MSE values as more information accumulates through time. Bates and Granger also state, “*The choice of the method to use is somewhat arbitrary. We have made our choice on the grounds of simplicity*.”

Given this background, let us turn to the issue of the combination of multiple unbiased forecasts, noting that the above methods for minimizing the MSE of the combined forecast serve as a first cut solution to the problem. That is, minimizing the combined forecast MSE with covariance assumed nonnegligible, which will be denoted as MSE_C, and minimizing the combined forecast MSE with negligible covariance, which will be denoted as MSE_C. We begin with a return to the very simple approach of assigning an equal weight to each independent forecast, which we will denote as the E_W approach.

The equal weighting approach has a unique role in the combination of multiple forecasts. The EW approach can be shown to be equivalent to the MSE_C approach when two conditions are true. First, the individual forecasts have identical forecast error variances σ^2 and second, the individual forecasts have identical pair-wise correlations ρ. When are these two conditions likely to be nearly satisfied ? Well, if the individual forecast models all use the same data and produce about the same amount of forecast accuracy, then one can expect that the E_W approach is a reasonable approximation of the optimal MSE_C approach. In particular, the technical conditions for the optimality of E_W for minimizing combined forecast MSE are provided in Elliott (2011) and can be paraphrased as, if the maximal eigenvalue of the forecast combination covariance matrix is bounded, then the expected MSE loss from applying both E_W and MSE_C approaches is approximately equal as the number of forecasts included in the combination becomes large enough. Therefore, the current bottom line on the MSE minimizing approach to combining forecasts is that, if we have enough forecasts that use the same information and produce roughly similar MSE values in practice, we might as well use the simpler E_W approach. This is, in effect, provides an approximate answer to the forecast combination puzzle as suggested in a number of recent studies (e.g., Claeskens et al. 2014). Two reasons for the good empirical performance of E_W appear to be (i) estimation errors are substantial and large for quantities needed to calculate forecast optimal weights, under a variety of schemes, and (ii) the improvements achieved from setting forecast weights equal to their calculated values are small in comparison to using equal weights. Thus, the overall situation at present is that there is no consensus on an optimal forecast weighting procedure.

Before moving into the diverse set of forecast combination methods that have fruitfully developed since the consideration of the general problem by Bates and Granger, let us consider two additional simple statistical approaches to forecast combination that can be easily applied in practice. First, one can set the combined forecast to be the median of the distribution of the forecast event across the individual forecasts. That is, the combined forecast F_C is set to be the median of the distribution of the individual forecasts, where

$$F_C^{median} = Median\{F_i\}_{i=1\ldots N_F} \tag{118}$$

This approach is simple and uses a robust measure of central tendency for the forecast distribution of the predicted event. The second approach is to set the forecast combination equal to a trimmed mean of the distribution of the forecast event across the individual forecasts. In this case, one needs to choose a trimming percentage, denoted by δ, which we will assume is equal for upper and lower trimming. To do this we need to order the individual forecasts according to their calculated value for the event where the ordered rank of the i^{th} forecast F_i in the set of the ordered individual forecasts is $r \equiv rank(i)$ and is denoted as $F_{(r)}$. The combined forecast based on the trimmed mean is then

$$F_C^{trimmed} = \frac{1}{N_F\left(1-2\delta\right)} \sum_{r=\lfloor \delta N_F+1 \rfloor}^{\lfloor (1-\delta)N_F \rfloor} F_{(r)} \tag{119}$$

This is another simple numerical approach to provide a robust measure of central tendency for the forecast distribution of the predicted event. In both of these cases, the quality of the combined forecast depends on the distribution of the selected individual forecasts, and if this forecast set is well-formed, then one may expect a reasonable combined forecast result.

5.4.2 Information Requirements for Forecasts

Given this historic background, we note that the components of a single forecast model or of an ensemble forecast model will generally include:

- Forecast Domain Parameters
    - Time Frame
    - Best or Most Credible Model for Single Model Forecast
    - Set of Credible Models for Ensemble Model Forecasts
    - Credible Model Attributes
        - Population Dynamics
            - Initial Conditions
            - Deterministic Components
            - Stochastic Components
        - Fishery Dynamics
            - Initial Conditions
            - Deterministic Components
            - Stochastic Components
        - Management Procedure
            - Initial Conditions
            - Deterministic Components
            - Stochastic Components
- Forecast Models for Credible Models
    - Distributions of Quantities of Interest (QOI)
        - Based on Individual Forecast Models
        - Based on a Combination of Individual Forecast Models
    - Measures of Central Tendency of QOI
        - Mean
            - Arithmetic
            - Trimmed

            - Harmonic
            - Geometric
        - Median
    - Measures of Dispersion of QOI
        - Variance, Standard Deviation, CV
        - Interquartile or Other Percentile Ranges
        - Confidence or Credible Intervals
    - Measures of Bias of QOI
        - Retrospective Patterns
        - Bootstrap Bias Estimation (Efron 1982)
        - Mohn's Rho (Mohn 1999)
- Forecast Components of Key Quantities of Interest
    - Calculate FMSY based on future stochastic simulation results
    - Calculate FREBUILD, the constant F to rebuild a population, based on future stochastic simulation results
    - Calculate Probability of Overfishing as a Function of the Annual Catch Limit (ACL) based on future stochastic simulation results
    - Calculate Probability of Depletion as a Function of ACL based on future stochastic simulation results
    - Calculate Probability of Achieving Target Fishing Mortality Rate as a Function of ACL based on future stochastic simulation results
    - Calculate Probability of Achieving Target Biomass as a Function of ACL based on future stochastic simulation results
    - Calculations for Multiyear ACLs based on future stochastic simulation results

The combination and interpretation of an ensemble of forecasts is a relatively new analytical topic for fisheries stock assessment and has some of its modern origins in econometric forecasting. As such, there is limited information on the best approaches for doing ensemble model forecasts, noting that the best procedures are likely situation dependent. Regardless, here are some analytical approaches that may be useful for producing ensemble model forecasts.

- There are essentially three steps to construct an ensemble model forecast:
    - (1) Construct a set of credible forecast models for each model in the ensemble
    - (2) Combine forecast estimates within each model in the ensemble
    - (3) Combine the within-model forecasts across all models in the ensemble
- Some algorithmic approaches that could be applied to construct and evaluate a set of models in an ensemble forecast are:
    - Cross validation (e.g., Efron 1982)
    - Generalized cross validation (e.g., Wood 2006)
    - Bayesian model averaging (e.g. Hoeting et al. 1999)
    - Bootstrap aggregating (i.e., bagging, Breiman 1996a)

    - Stacking (Wolpert 1992)
    - Random forest (Ho 1995)
    - AdaBoost (Freund and Shapire 1997)
    - Boosted regression trees (e.g., Elith et al. 2008)
    - ARCing (Breiman 1996b)
    - Gradient boosting (Friedman 2001)
    - Neural networks and associated algorithmic approaches, e.g., Kaastra and Boyd (1996)
    - Subjective weighting based on expert opinion, e.g. Morgan and Henrion (1990)
- Regularization of forecast estimates within credible models in the ensemble can:
    - Help to balance simplicity and accuracy of models ensemble used for inference
    - Reduce the flexibility of the model fitting process by augmenting the loss (objective) function to include penalties for model complexity
    - Some regularization techniques include:
        - Lasso (Tibshirani 1996)
        - Garrotte (Breiman 1993)
        - LARS (Efron et al. 2004)

Given the individual predictions of the *M* individual models in the ensemble, the goal is to be able to set weights for these individual predictions to produce a model ensemble prediction (Figure 12). In general, achieving this goal can be approached in several ways. For example, Dormann et al. (2018) describe several approaches to estimating model weights to compute the model ensemble prediction, where this prediction represents the central tendency or best point estimate conditioned on the available information.

Regardless of the approach used, a vector of model weights, $\underline{w} = \left(w_1, w_2, ..., w_M\right)$ that satisfy $\sum_{m=1}^{M} w_m = 1$ will generally be needed to combine the model predictions. These model weights $\underline{w}$ are applied to the individual predictions of the models $\widehat{Y_1}, \widehat{Y_2}, ..., \widehat{Y_M}$ to produce the model-averaged prediction $\widetilde{Y}$ where

$$\widetilde{Y} = \sum_{m=1}^{M} w_m \widehat{Y_m}$$

This model ensemble prediction has variance $Var\left(\widetilde{Y}\right)$ based on the variances of the individual model predictions and associated covariances between the individual model predictions (Dormann et al. 2018) where

$$Var\left(\widetilde{Y}\right) = \sum_{m=1}^{M} w_m^2 \cdot Var\left(\widehat{Y_m}\right) + \sum_{m=1}^{M} \sum_{n \neq m} w_m w_n \cdot Cov\left(\widehat{Y_m}, \widehat{Y_n}\right)$$

The variance of the model-averaged prediction can also be expressed in terms of the correlations between model predictions $\rho_{m,n}$ and standard deviations of predictions $\sigma\left(\widehat{Y_m}\right)$ and $\sigma\left(\widehat{Y_n}\right)$ as

$$Var\left(\widetilde{Y}\right) = \sum_{m=1}^{M}\sum_{n=1}^{M} w_m w_n \, \rho_{m,n} \, \sigma\left(\widehat{Y_m}\right)\sigma\left(\widehat{Y_n}\right)$$

As noted above, there are many ways to quantify model weights ranging from objective analyses to produce weights based on the best available data to subjective expert judgment being used to set weights based on beliefs. Dormann et al. (2018) describe four analytical approaches to setting model weights to improve predictive accuracy: equal weighting, Bayesian, information-theoretic, and tactical approaches. Each of these approaches differs in their assumptions, data requirements and treatments of individual candidate models as well as their numerical algorithms, e.g., bootstrap aggregation. In general, evaluating the relative benefits and costs of applying each of these approaches to generate robust scientific advice from model ensembles is an ongoing investigation.

5.4 Management Strategy Evaluation

Management strategy evaluation (MSE) is a simulation experiment technique that was developed to implement adaptive environmental assessments for renewable resources (Walters 1986, Smith et al. 1999, Punt et al. 2014). The MSE approach is flexible and general and can be adapted for application to any fishery system. There is, in fact, an entire book devoted to case studies of MSE applications in management science for fishery systems. In general, it is best to take a broad view of MSE and note that it is always situation-specific. Regardless, the key features of an MSE algorithm can be described in a set of general steps as follows (e.g., Punt et al. 2014).

5.4.1 Specify Management Objectives

The first step of the MSE algorithm proceeds by establishing the concepts of what the set of management objectives for the fishery system should be. Each chosen objective must then have one or more performance metrics, which represent the objective in a tangible manner. Similarly, the set of constraints on management of the fishery system should be identified in order to ensure that objectives are feasible.

5.4.2 Identify Important Uncertainties

The second step begins with a broad overview of the types of uncertainties that have an important effect on the understanding and prediction of the fishery system dynamics. The set of important uncertainties will typically include observation errors for data inputs, process errors for system dynamics, and structural uncertainties about how the system operates. The structural uncertainties for models of system processes, including the implementation of management strategies, are particularly important in determining the role of uncertainty and risk for decision making. Overall, the goal of the MSE algorithm is to find the management strategies that are robust to the important uncertainties, which will be simulated through the evaluation process.

5.4.3 Construct Operating Models

The third step is to build a set of mathematical models to represent the fishery system. These operating models represent the dynamics of the fishery system and will include components for the population dynamics fishery resources and the fleet dynamics of the fishery. These models will specify boundaries of the fishery system and will need to specify how information is gathered from the fishery system including the data observation processes, the likelihood components relating the dynamics to the observations, and the implementation of management measures to control the fishery system. Multiple operating models are expected to be needed because fishery systems are complex, i.e. have many components and interrelationships among components, and have some components that are typically not observable with a high degree of certainty.

5.4.4 Set Operating Model Parameters

The fourth step is to set the parameters of each operating model and characterize parameter uncertainty. This is typically accomplished by fitting the operating models to observed or simulated data from the fishery system. The fitting process is typically constructed to optimize the likelihood of the set of observations of the fishery system within a frequentist or Bayesian or random effects estimation framework.

5.4.5 Identify Management Strategies

The fifth step is to identify the set of feasible management alternatives that could be implemented to influence the dynamics of the fishery system to achieve the management objectives. Typically, the individual management strategies will be feedback or closed-loop policies that depend on the dynamic state of the fishery system. Alternatively, some of the management strategies may be open loop policies in which the management actions do not depend on changes in the fishery system state. The specification of the management strategies will also need to identify the sequence of steps or stages in decision making. Overall, some strategies may be less flexible and adaptive to uncertainty than others under alternative operating models and the set of constraints on the management process.

5.4.6 Conduct Simulation Experiment

The last step requires that the set of paired combinations of an operating model and a management strategy be simulated with sufficient randomization and replications to assess the relative performance for achieving the management objectives. The information from these simulated combinations is summarized and contrasted to understand the characteristics of the management strategies and their relative performance. The last step can be expected to lead to revisions of previous steps in an iterative process of scientific refinement for public policy analysis. This is analogous to one cycle in the adaptive management for fishery systems, which consists of planning, implementation, and evaluation.

6. USER INTERFACE DESIGN

6.1 Overview of User Interface

Some key design features of the MAS user interface are listed below.

- List of MAS Library Objects
    - Individual Models
    - Set of Models
    - Templates for Model Component Configurations
        - Population Component
            - e.g., Movement Matrices, Life History Parameters
        - Observation Component
        - Environment Component
        - Analysis Component
    - Analytical Templates for Quantities of Interest
        - Central Tendency
        - Dispersion
        - Time Series of Joint Distributions
- List of MAS User Actions
    - Create Model
    - Get Model
    - Copy Model
    - Modify Model
    - Save Model
    - Delete Model
    - Evaluate Model(s) Fit to Data
    - Change Data for Model(s)
    - Compare Models
- List of MAS User Tools
    - Read Existing Model Tool
    - Construct New Model Tool
    - Model Set Construction Tool, Variations on a Theme
        - Using Different Data
        - Using Different Structure
        - Using Different Data and Structure
    - Random Model Set Construction Tool
    - Model Document Generation Tool

- Text
- Tables
- Figures
- Appendices

6.2 Screen Objects and Actions

- Single or Multiple Windows
- Model Property Sheet
    - Nested Pull Down Menus
- Action Panel
    - Model Definition GUI Interface
    - Nested Pull Down Lists
- Visualization and Graphics
    - Model Inputs
    - Model Outputs
        - Write Model Results to Output File
          Predicted Fishery Selectivities
          Predicted Survey Selectivities
          Predicted Fishing Mortality Rates
          Predicted Total Mortality Rates
          Calculate Predicted Total Mortality Rates
          Predicted Spawning Biomass
          Predicted Recruitment by Population
          Predicted Fishery Observations
          Predicted Survey Observations
          Predicted Quantities of Interest by Population
          Predicted Population Numbers at Age at the Start of the Year
          Predicted Population Mean Lengths and Weights at Age for the Plus Group at the Start of the Year
    - Model Diagnostics
    - Model Projections

7. ANALYTICAL REQUIREMENTS AND SYSTEM MAINTENANCE

7.1 Analytical Requirements

The key system analytical requirements are listed below.

- Numerical Optimization Routine Library
- MCMC Sampling Routine Library

- Bootstrap Routine Library
- Probability Distribution Library
    - Univariate Distributions
    - Multivariate Distributions
    - Mixture Distributions
- Negative Loglikelihood Function Library
- Growth Function Library
- Recruitment Function Library
- Maturity Function Library
- Fecundity Function Library
- Movement Function Library
- Input Data Function Library
- Output Function Library
- Prior Distribution Library
- Hyperprior Distribution Library
- Operating Model Template Library

7.2 System Maintenance

The key system maintenance requirements are listed below.

- Standard Operating Protocol for Testing Models.
- Standard Operating Protocol for Total Quality Improvement (Figure 14).
  General principles of system maintenance through a continuous evaluation cycle from Deming (1960) include:
  (i) How can the system be improved? What change would improve quality?

  (ii) Make the change and observe the results through simulation or sampling.

  (iii) Are the results better? If yes, implement the change. If no, then identify why the results were not better.

  (iv) Repeat.

- Standardized MAS model library with primary actors and ATL interface (Figure 15)
    (i) Access control to MAS library is provided for primary actors.
    (ii) Users can search and download models.
    (iii) Contributors can create and submit models.
    (iv) Managers can manage the model library and allocate resources.

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FIGURES

Figure 1. A schematic diagram of three age-structured populations (blue, green, red) in three natal areas with different feeding migration rates between areas (colored arrows) and different habitat characteristics by area.

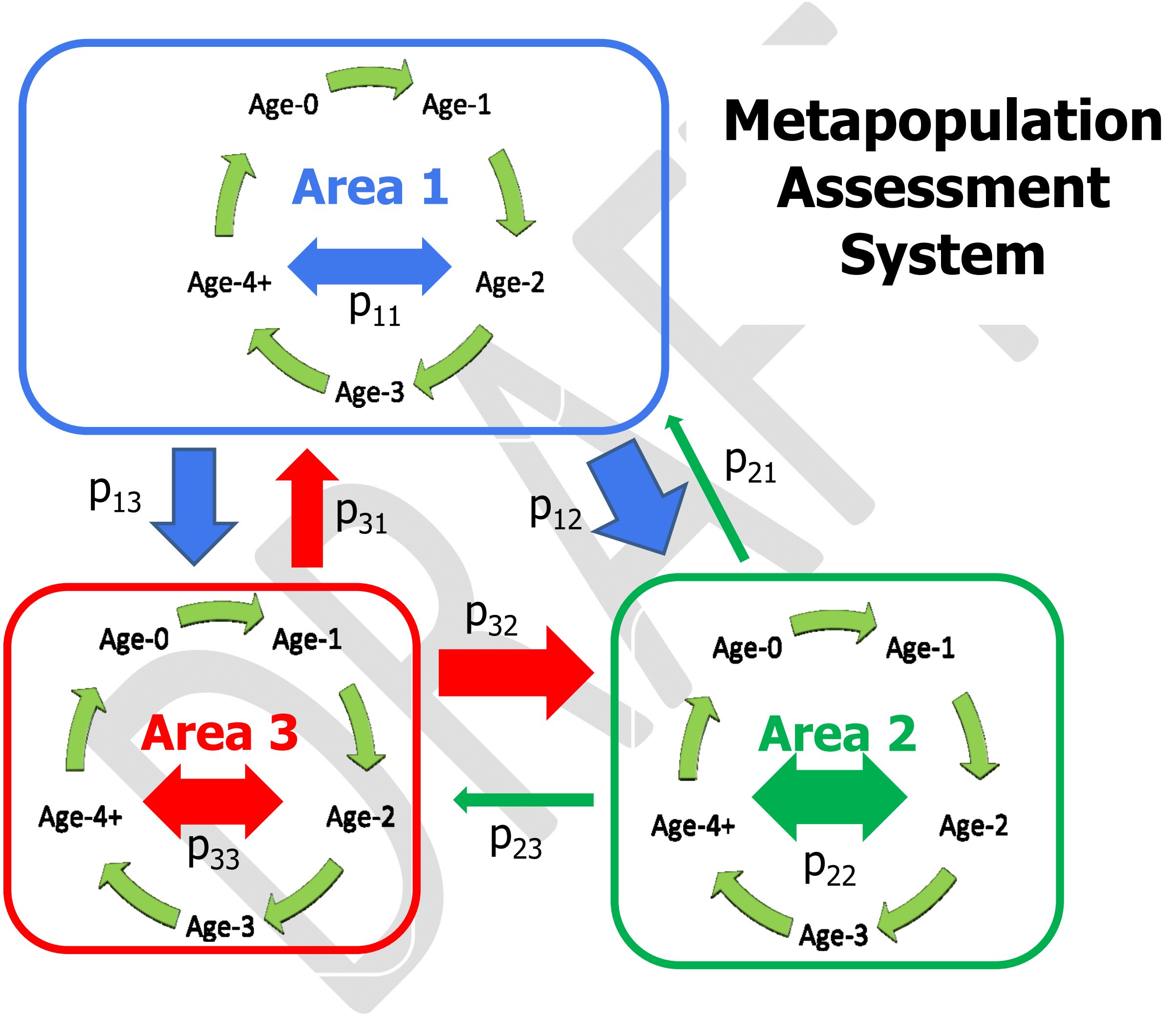


Figure 2. A schematic diagram of two fish populations harvested by seasonal fishing fleets on a common fishing ground where private views are used to encapsulate data operations and public views are used to share data outputs.

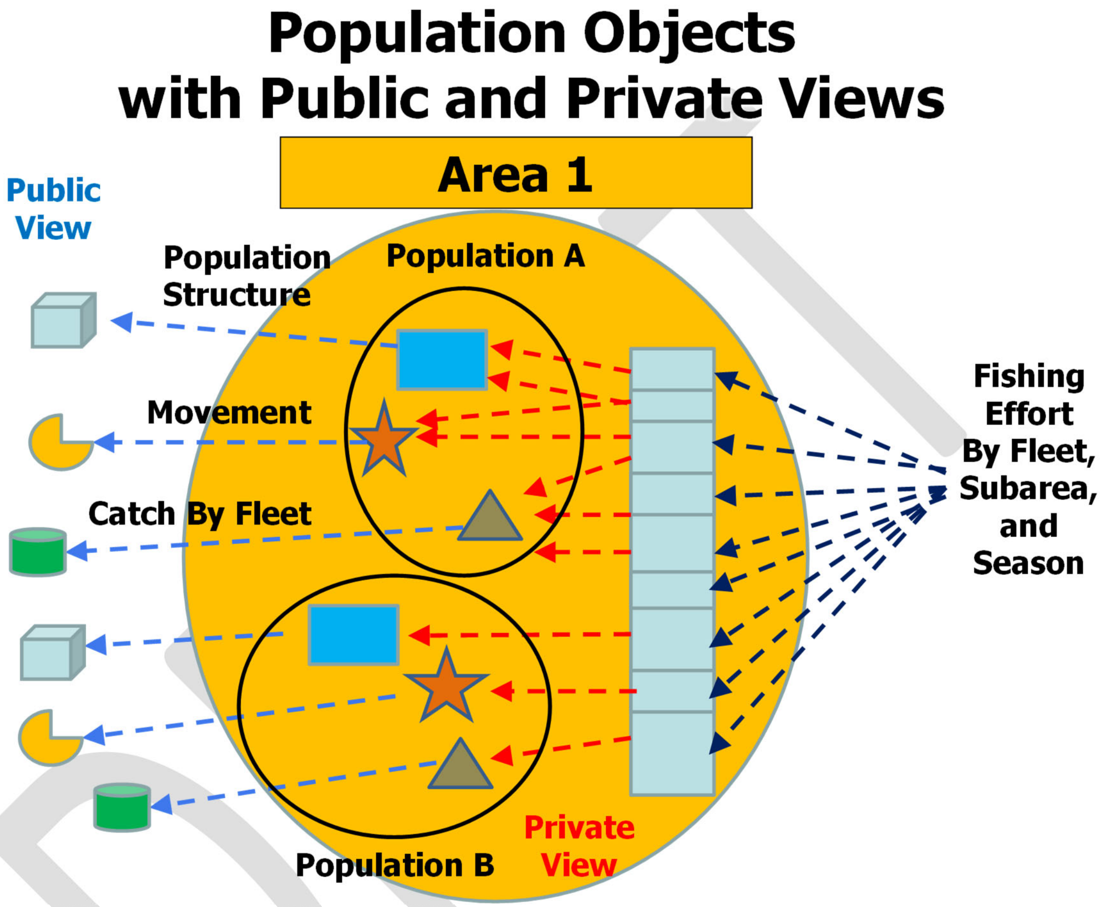


Figure 3. A schematic diagram of the analysis layers for MAS including model construction $\left(M_j\right)$, ensemble construction $\left(\underline{M}\right)$, information objects for model forecasting $\left(f\left(\underline{M}\right)\right)$, as well as information for management strategy evaluation that produces analytical information based on the sets of operating models $\left(\underline{M}_O\right)$, estimation models $\left(\underline{M}_E\right)$ and management strategies $\left(\underline{S}\right)$.

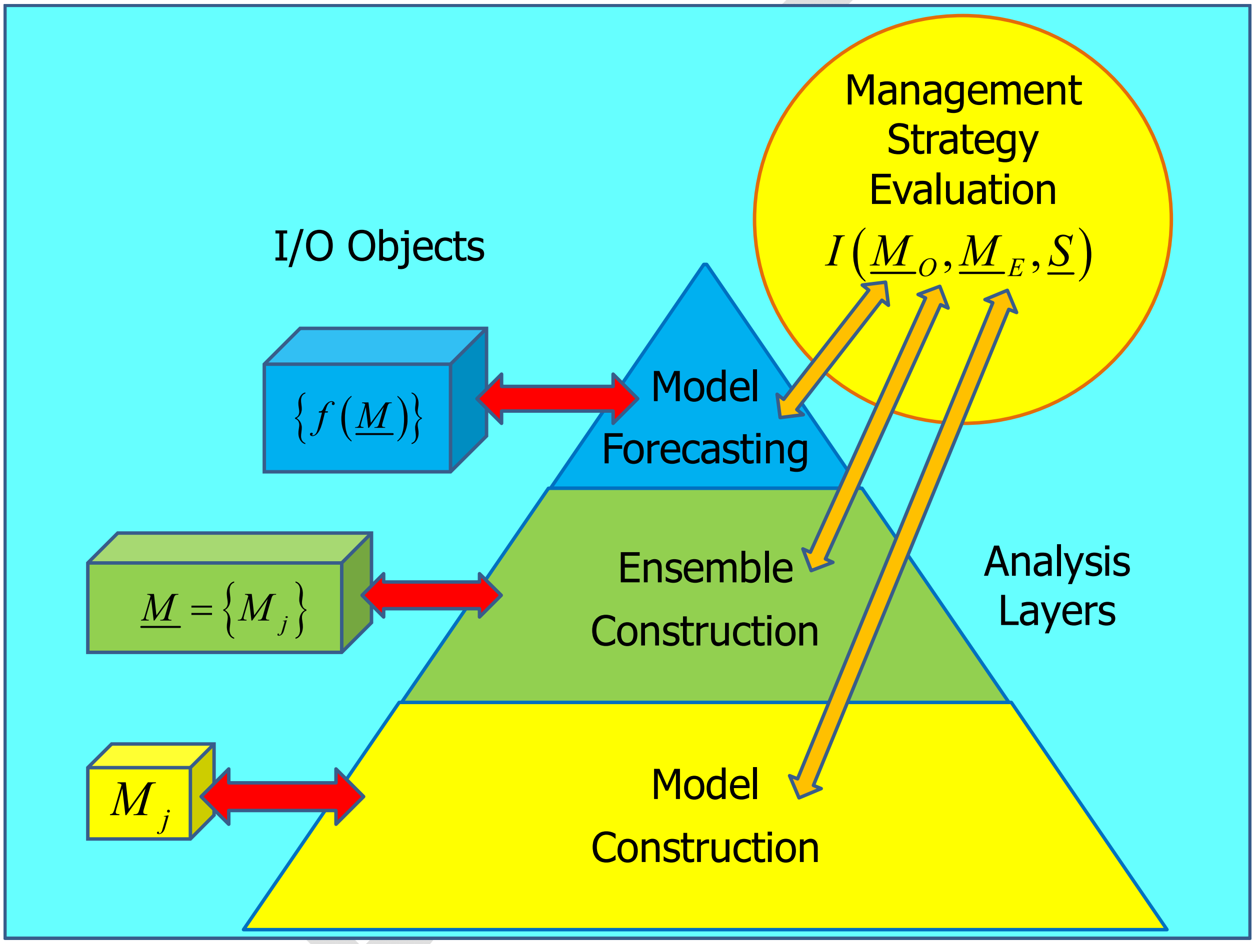


Figure 4. A schematic diagram of the abstraction for MAS model class structure showing the four primary components (Population, Observation, Environment and Analysis) along with information flows between subcomponents of population structure, habitat location and movement.

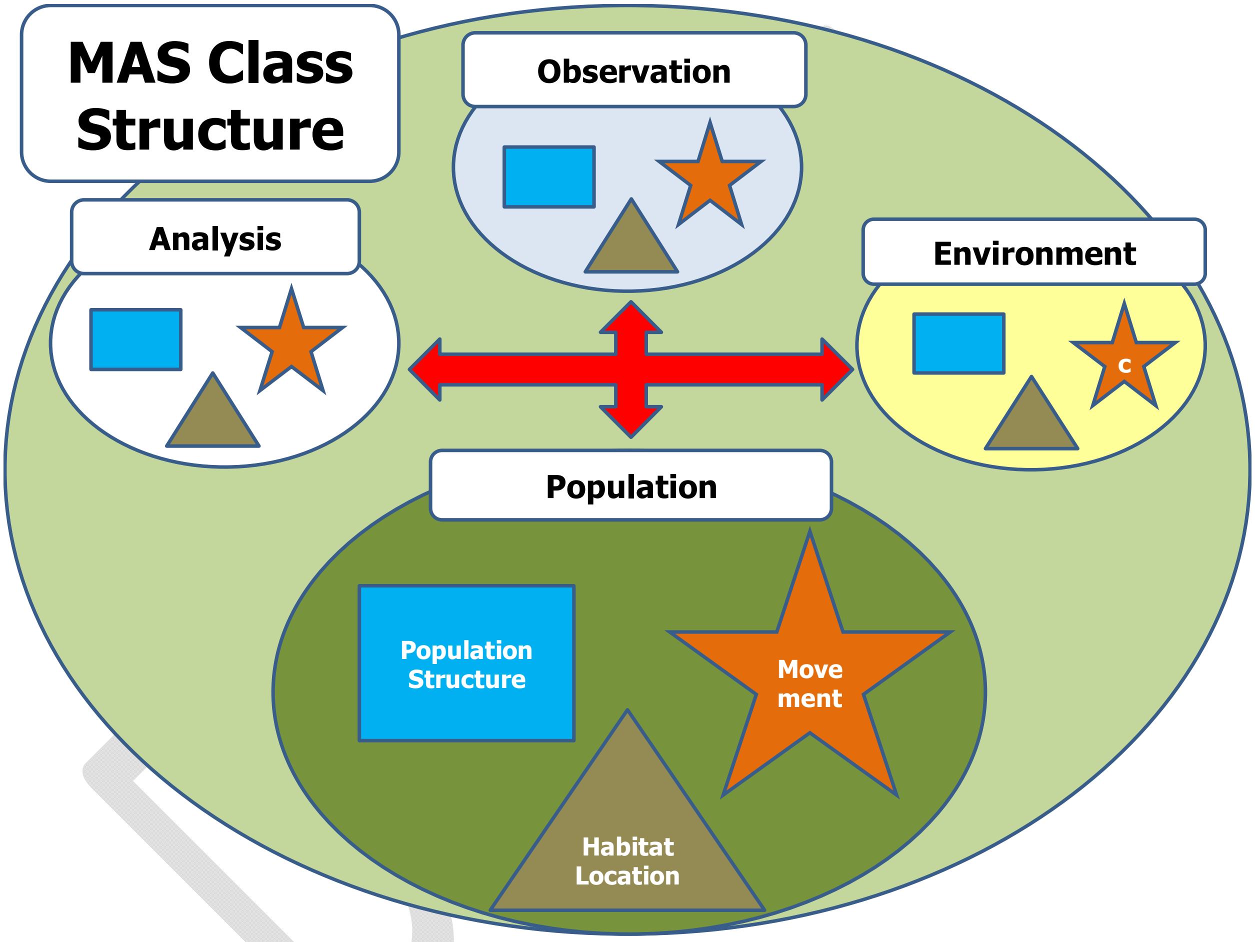


Figure 5. A schematic diagram of the array dimensions needed for a two-gender, age-structured population represented by numbers at age by time and area.

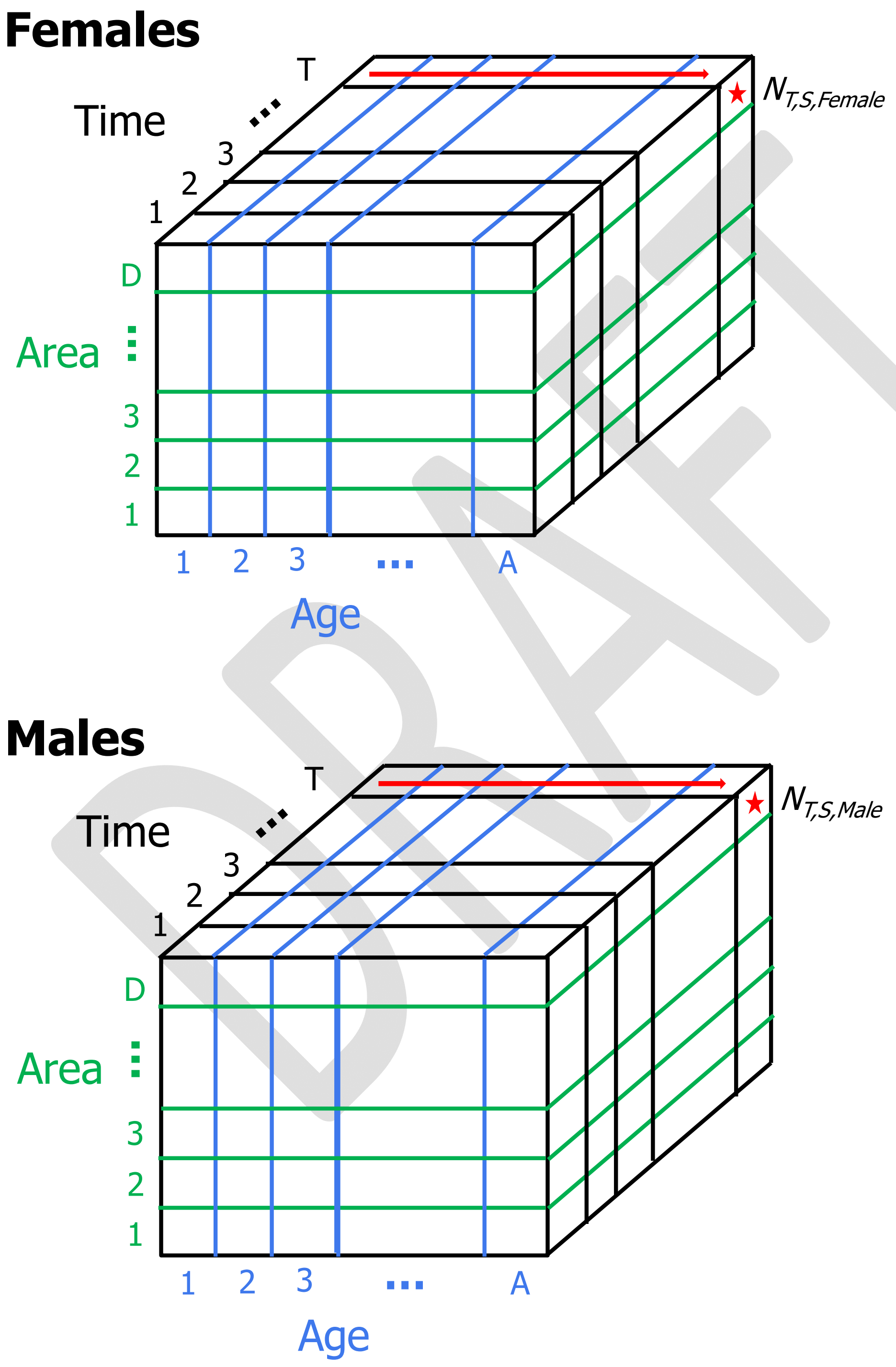


Figure 6. A schematic diagram of the directed movements of a spatially-structured population inhabiting five areas (V_1, V_2, V_3, V_4, and V_5) along with the associated movement probabilities among areas $\left(T_{ij}\right)$, as represented by the directed graph of the transfer matrix $\underline{\underline{T}} = \left(T_{ij}\right)$.

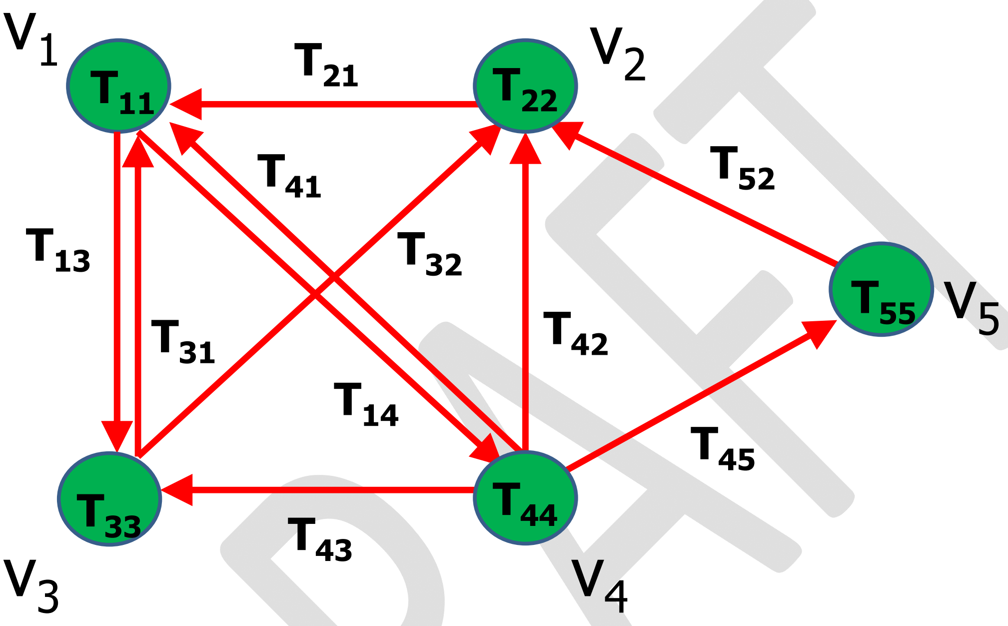


Figure 7. A schematic diagram of the annual cycle of fish catch and movement for a population with three seasons.

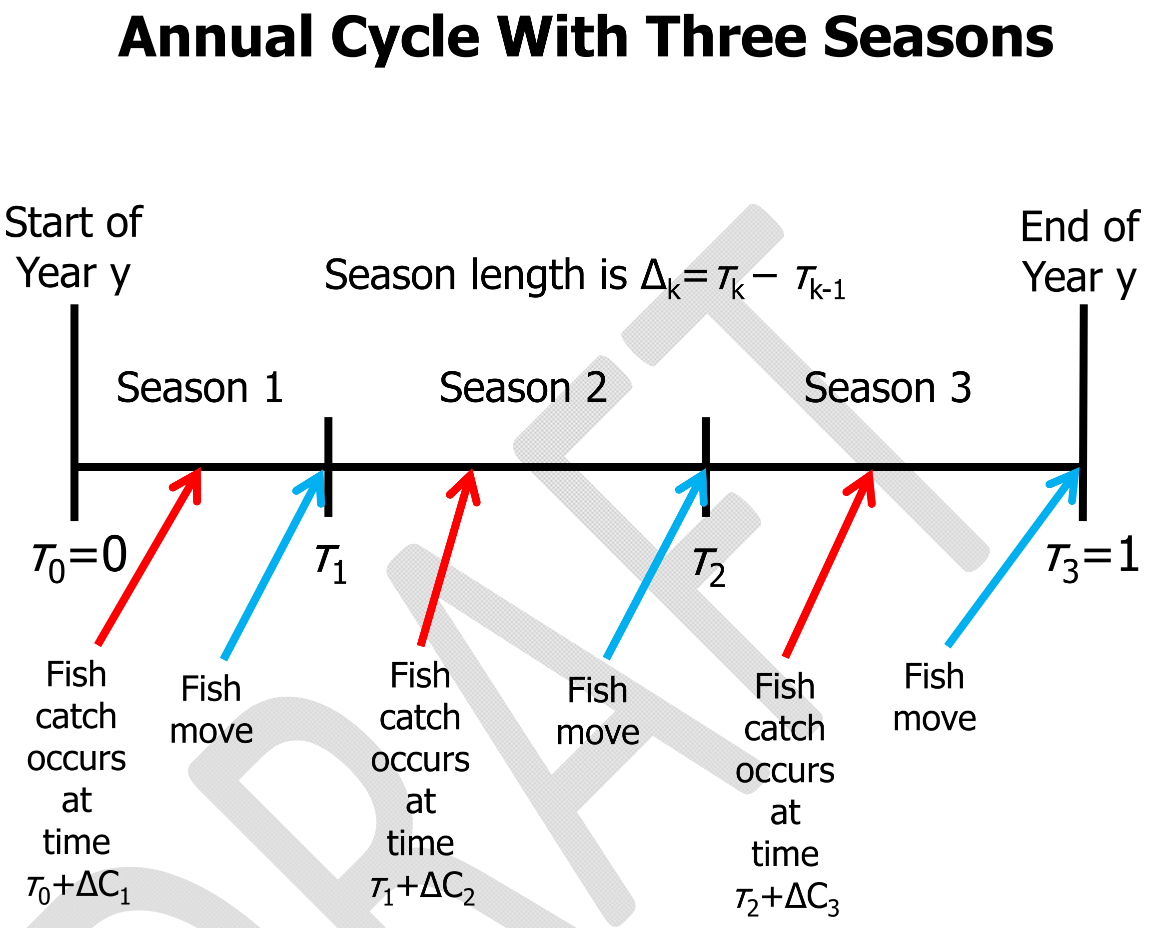


Figure 8. A schematic diagram of the exponential decrease in initial population numbers in area *s* by gender *g* of an age-*a* cohort at the start of season *t*, $N^{(p)}_{(y,t),s,a,g}$, to population numbers at age-*a* at time $t^* = t + \Delta^*$, $N^{(p)}_{(y,t^*),s,a,g} = N^{(p)}_{(y,t),s,a,g} \cdot \exp\left(-\Delta^* \cdot Z^{(p)}_{(y,t),s,a,g}\right)$, as a function of total instantaneous mortality at age-*a*, $Z^{(p)}_{(y,t),s,a,g}$.

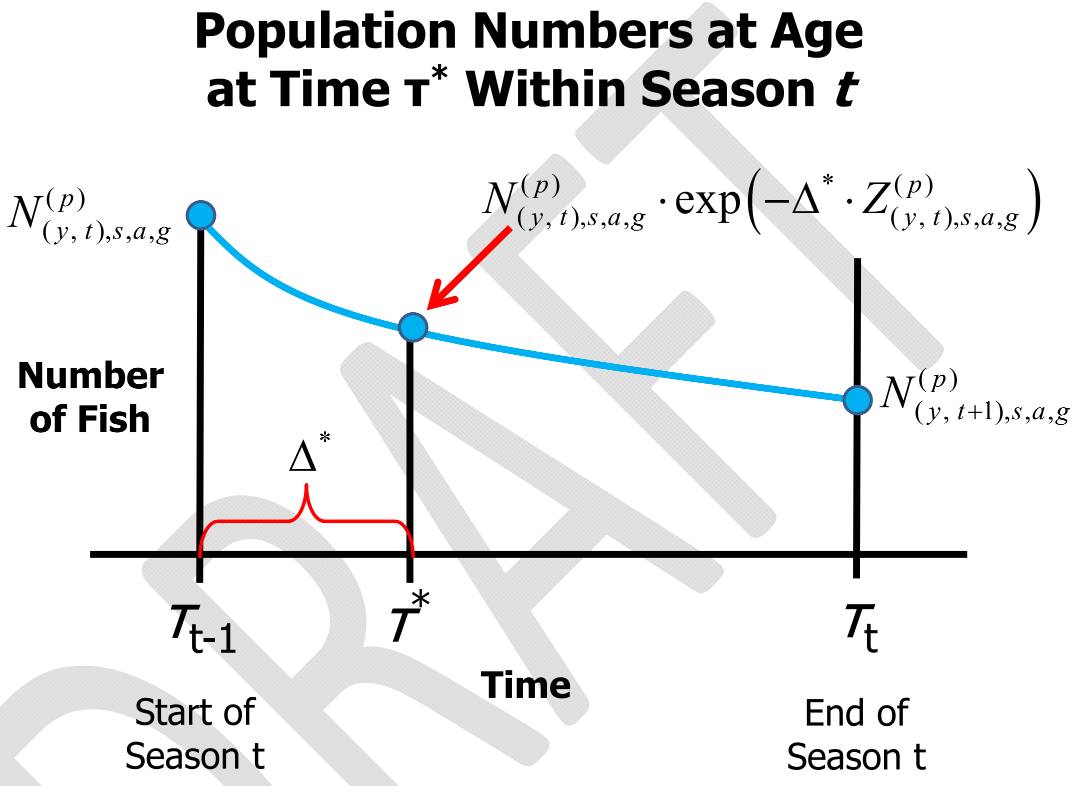


Figure 9. A schematic diagram of the empirical mean weights at age by season for a population in an annual cycle with three seasons.

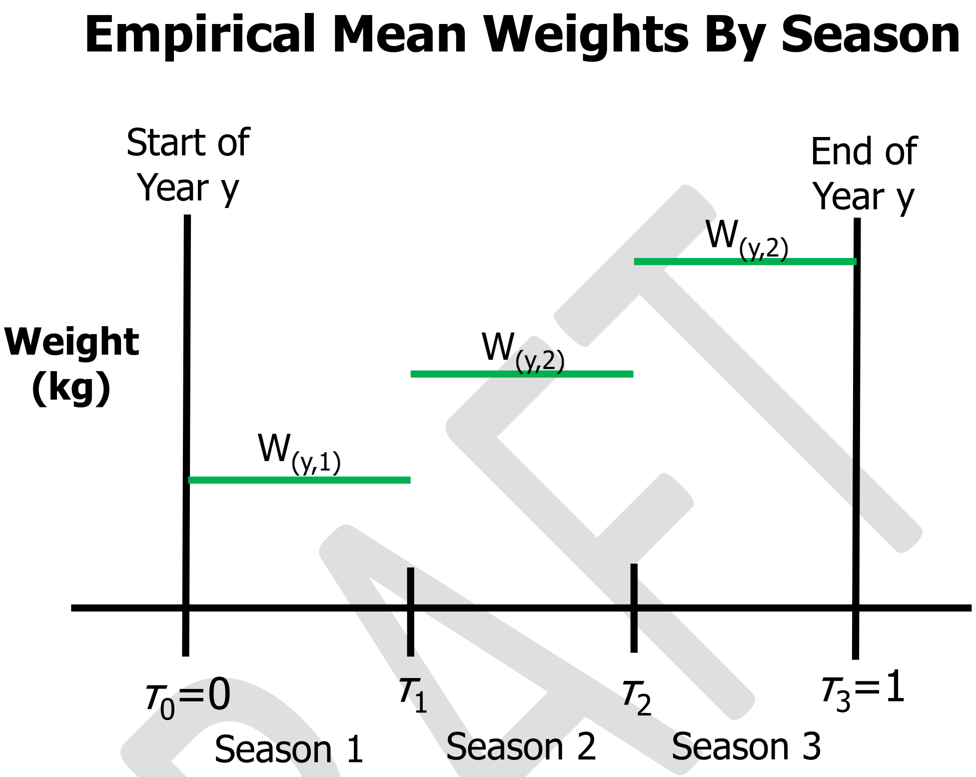


Figure 10. A schematic of the timing of the processes of recruitment, fishery catch, tag recovery, and spawning within season *t* where the season length is Δ_t.

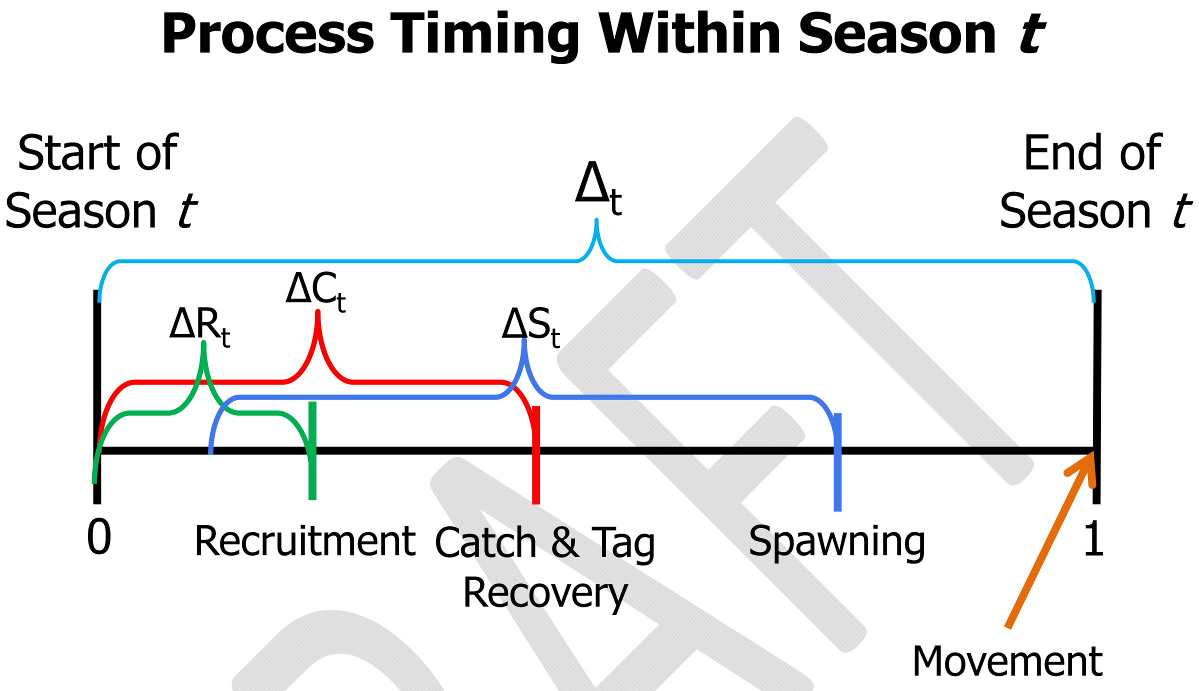


Figure 11. A schematic diagram of the seasonal changes in the number of fish in the *j*th area from population *p* based on the number of survivors from the previous season across all areas.

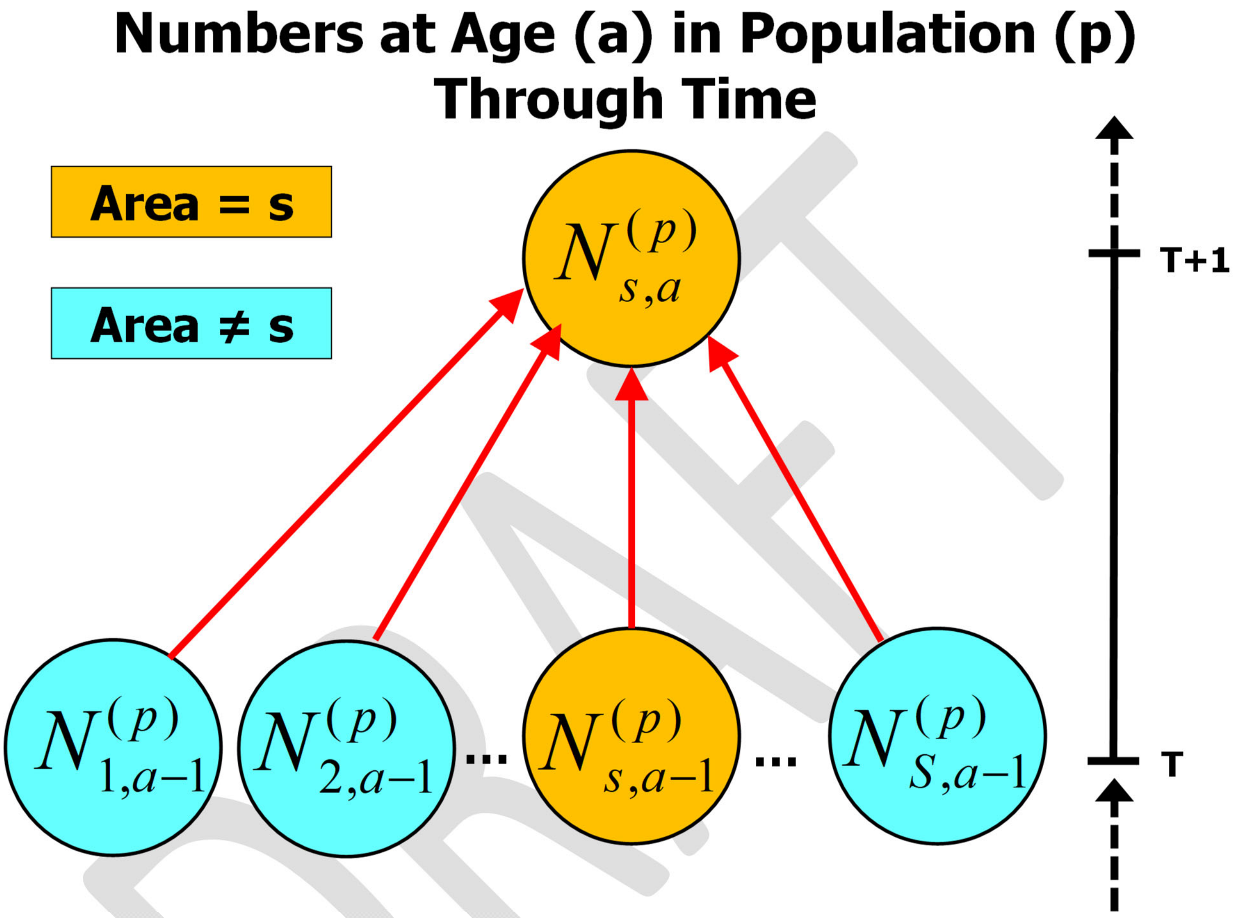


Figure 12. A schematic diagram of the proportion simplex for an ensemble model with 3 contributing models (blue lined triangle) and a model weight vector $\underline{w}^*$ that represents a unique point in the model space or hypothesis about the relative credibilities of the candidate models (red star).

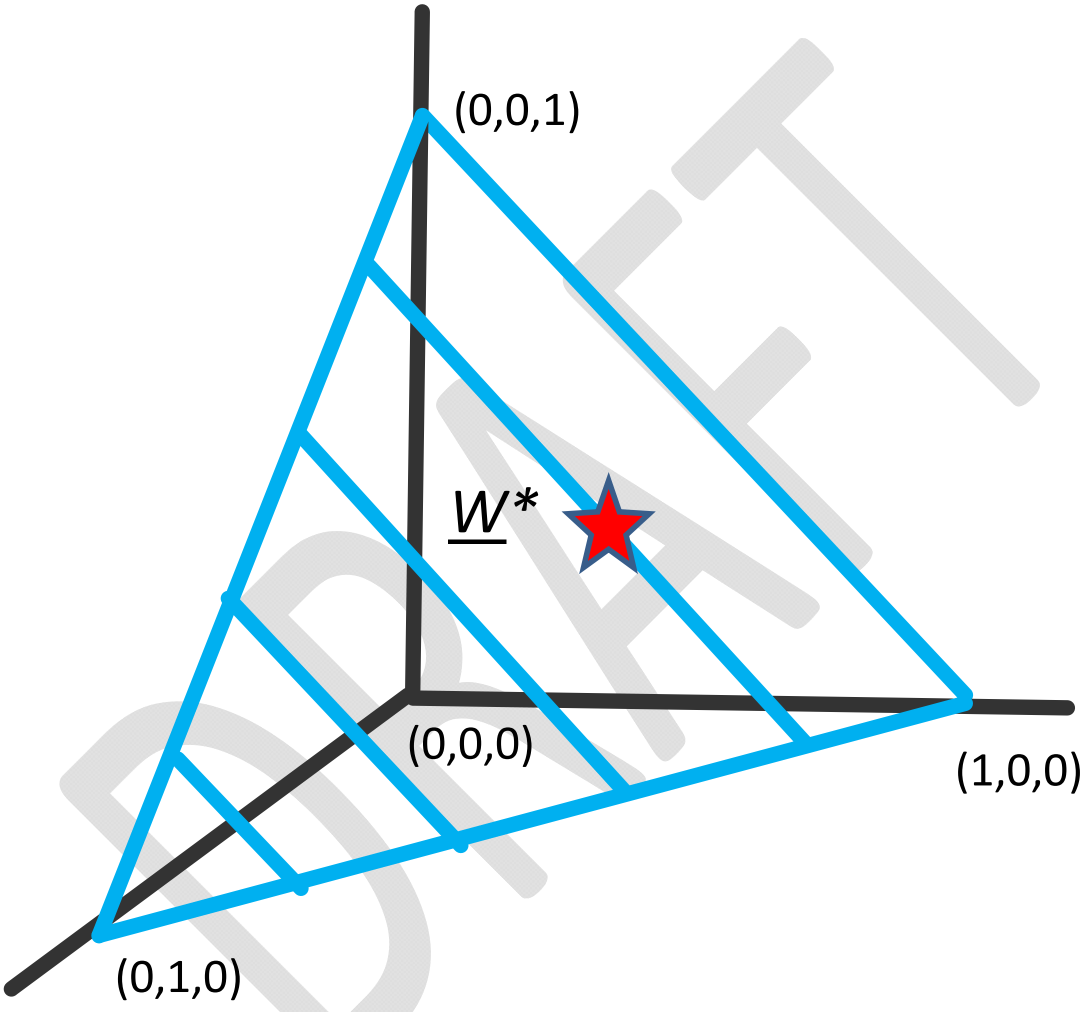


Figure 13. A schematic diagram of the relationships between the processes of model validation, verification, and uncertainty quantification for evaluating fishery system impacts on quantities of interest.

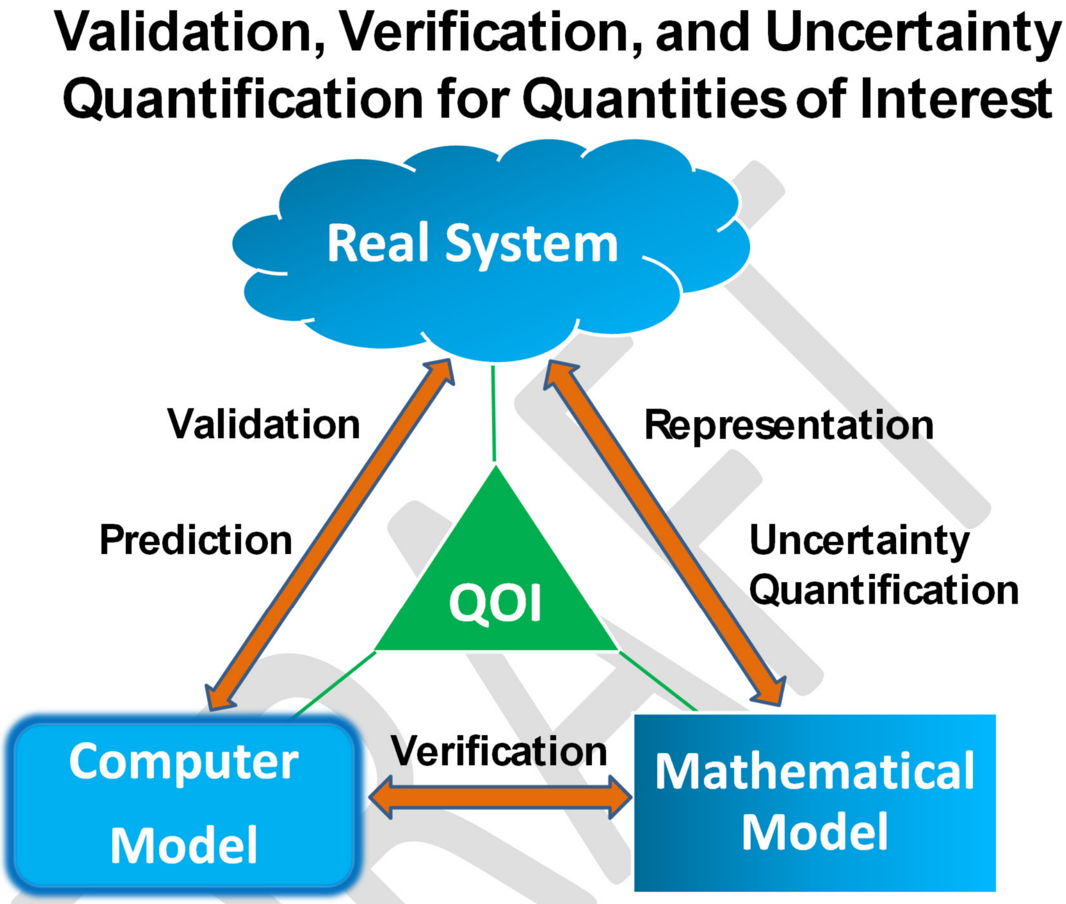


Figure 14. A schematic diagram of the Deming cycle for total quality improvement (Deming 1960).

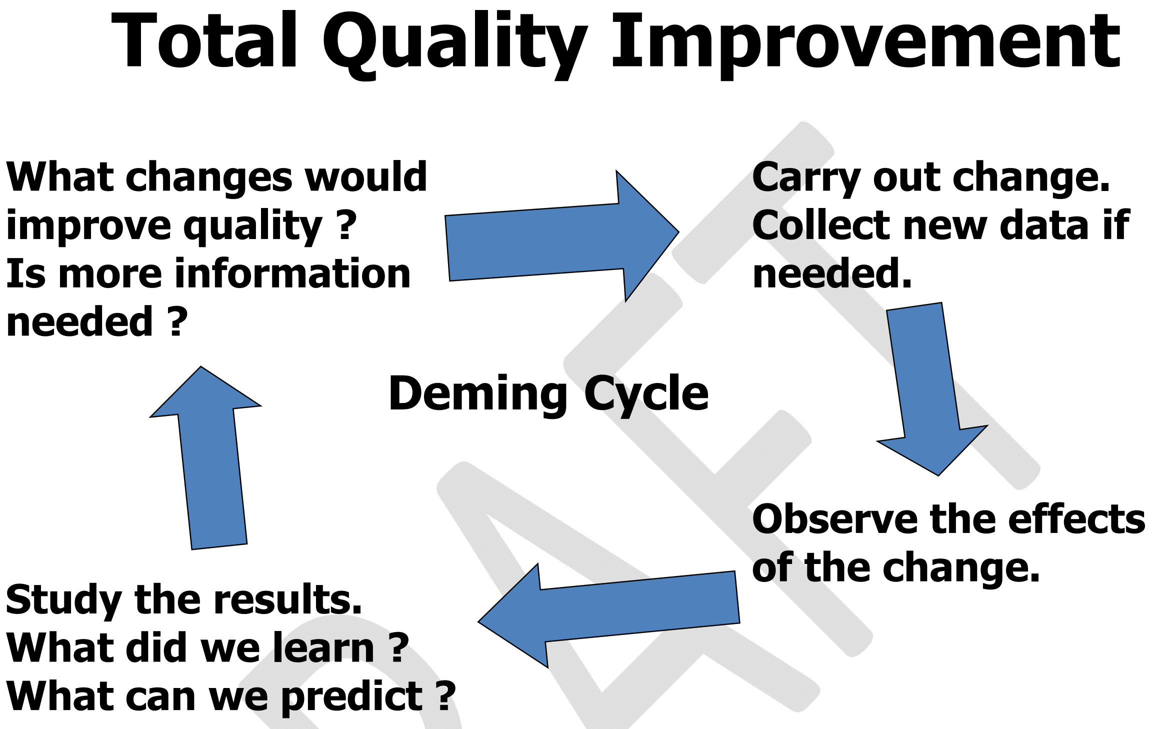
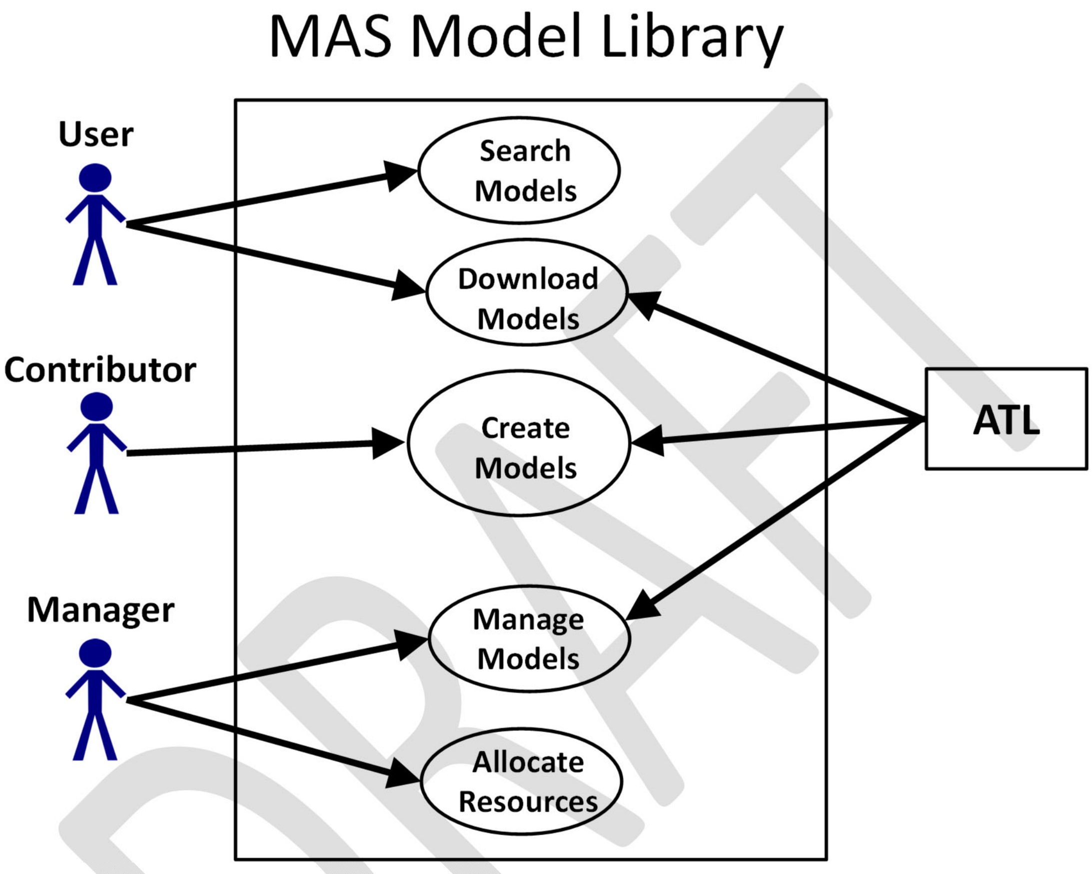


Figure 15. A schematic of a use-case diagram for Metapopulation Assessment System (MAS) model library including the primary actors which are the users, contributors, and managers along with analytical support based on the Analytics Template Library (ATL).



APPENDICES

APPENDIX 1. Unfished Equilibrium Numbers at Age Algorithm for MAS.

In this Appendix we provide details of an algorithm to iteratively calculate unfished equilibrium numbers at age, conditioned on the existence of an equilibrium solution. That is, we need to calculate unfished numbers at age in equilibrium by population, area, and gender $\left(N^{(p)}_{unfished,s,a,g}\right)$ to determine the values of unfished female spawning biomasses by population and area to inform the recruitment process models. Here note that the unfished numbers at age by population, area, and gender depend on the population movement and recruitment distribution matrices and are needed to compute the unfished spawning biomasses by population and area, which in turn, are needed to implement the recruitment submodels by population and area for the initial fished equilibrium time period and assessment time horizon. That is, this algorithm will determine the values of the unfished equilibrium female spawning biomasses for the recruitment submodels by population and area, which are derived quantities that depend on the unfished recruitment parameters by population and area.

Iteration i=1: Calculate the initial unfished numbers at age estimates by population, area, and gender based on unfished recruitment, the recruitment distribution, equilibrium natural mortality and no movement, where $(x)^{[k]}$ denotes the k^{th} iterate of an estimate of a quantity x.

i. In general, population recruitment by area and gender is a function of area-specific recruitment production and the recruitment distribution matrix $\underline{\underline{Q}}^{(p)} = \left(Q^{(p)}_{i\to j}\right)_{s\,x\,s}$. Set age-0 recruits as a function of unfished recruitment and recruitment distribution by area and gender via

$$\left(N^{(p)}_{unfished,s,a=0,g}\right)^{[1]} = \rho^{(p)}_g \sum_k R^{(p)}_{unfished,k} \cdot Q^{(p)}_{k\to s}$$

ii. Set age-a survivors by area and gender for ages a=1 to A-1 via

$$\left(N^{(p)}_{unfished,s,a,g}\right)^{[1]} = \left(N^{(p)}_{unfished,s,a-1,g}\right)^{[1]} \cdot \exp\left(-M^{(p)}_{unfished,a-1,g}\right)$$

iii. Set age-A group of survivors by area and gender via

$$\left(N^{(p)}_{unfished,s,A,g}\right)^{[1]} = \frac{\left(N^{(p)}_{unfished,s,A-1,g}\right)^{[1]} \cdot \exp\left(-M^{(p)}_{unfished,A-1,g}\right)}{1-\exp\left(-M^{(p)}_{unfished,A,g}\right)}$$

iv. Set unfished spawning biomass by population, area and gender via

$$\left(SB^{(p)}_{unfished,s,g}\right)^{[1]} = \sum_{a} P^{(p)}_{mature,a,g} \cdot W^{(p)}_{spawn,a,g} \cdot \left(N^{(p)}_{unfished,s,a,g}\right)^{[1]} \cdot \exp\left(-\Delta_S \cdot M^{(p)}_{unfished,a,g}\right)$$

<u>Iteration i=2</u>: Calculate the next iterate of unfished numbers at age estimates by population, area, and gender based on unfished recruitment, the recruitment distribution, equilibrium survival, movement probabilities by area, age, and gender, and the previous iterate. Unfished recruitment production by area is a function of area-specific spawning biomasses which need to be iteratively calculated to account for the movement probabilities that redistribute fish.

i. Set age-0 recruits as a function of unfished recruitment and recruitment distribution by area and gender (Note that this calculation of unfished recruitment by population, area and gender does not change between iterations and can be done once, but is listed here to show the iterative process and emphasize the dependence on the unfished recruitment parameters by population and area, $R^{(p)}_{unfished,k}$) via

$$\left(N^{(p)}_{unfished,s,a=0,g}\right)^{[2]} = \left(N^{(p)}_{unfished,s,a=0,g}\right)^{[1]} \equiv \rho^{(p)}_{g} \sum_{k} R^{(p)}_{unfished,k} \cdot Q^{(p)}_{k \to s}$$

ii. Set age-*a* survivors for ages *a*=1 to *A*-1 by population, area, and gender that did not emigrate plus age-*a* surviving immigrants from other areas via

$$\left(N^{(p)}_{unfished,s,a,g}\right)^{[2]} = \sum_{k} \left(N^{(p)}_{unfished,k,a-1,g}\right)^{[1]} \cdot \exp\left(-M^{(p)}_{unfished,a-1,g}\right) \cdot T^{(p)}_{k \to s,a-1,g}$$

iii. Set age-(*A*-1) survivors that did not emigrate plus age-(*A*-1) immigrants from other areas plus age-*A* group survivors that did not emigrate plus age-*A* group immigrants from other areas via

$$\begin{aligned}\left(N^{(p)}_{unfished,s,A,g}\right)^{[2]} = &\sum_{k} \left(N^{(p)}_{unfished,k,A-1,g}\right)^{[1]} \cdot \exp\left(-M^{(p)}_{unfished,A-1,g}\right) \cdot T^{(p)}_{k \to s,A-1,g} \\ &+ \sum_{k} \left(N^{(p)}_{unfished,k,A,g}\right)^{[1]} \cdot \exp\left(-M^{(p)}_{unfished,A,g}\right) \cdot T^{(p)}_{k \to s,A,g}\end{aligned}$$

v. Set unfished spawning biomass by population, area and gender via

$$\left(SB^{(p)}_{unfished,s,g}\right)^{[2]} = \sum_a P^{(p)}_{mature,a,g} \cdot W^{(p)}_{spawn,a,g} \cdot \left(N^{(p)}_{unfished,s,a,g}\right)^{[2]} \cdot \exp\left(-\Delta_R \cdot M^{(p)}_{unfished,a,g}\right)$$

Iteration i=j+1: Calculate the (j+1)st iterate of equilibrium fished numbers at age estimates by population, area, and gender based on unfished recruitment, the recruitment distribution, equilibrium survival, movement probabilities by area, age, and gender, and the *j*th iterate.

i. Set age-0 recruits by population, area, and gender via

$$\left(N^{(p)}_{unfished,s,a=0,g}\right)^{[j+1]} = \left(N^{(p)}_{unfished,s,a=0,g}\right)^{[j]}$$

ii. Set age-*a* survivors for ages *a*=1 to *A*-1 by population, area, and gender that did not emigrate plus age-*a* surviving immigrants from other areas via

$$\left(N^{(p)}_{unfished,s,a,g}\right)^{[j+1]} = \sum_k \left(N^{(p)}_{unfished,k,a-1,g}\right)^{[j]} \cdot \exp\left(-M^{(p)}_{unfished,a-1,g}\right) \cdot T^{(p)}_{k\to s,a-1,g}$$

iii. Set age-(*A*-1) survivors that did not emigrate plus age-(*A*-1) immigrants from other areas plus age-*A* group survivors that did not emigrate plus age-*A* group immigrants from other areas via

$$\begin{aligned}\left(N^{(p)}_{unfished,s,A,g}\right)^{[j+1]} &= \sum_k \left(N^{(p)}_{unfished,k,A-1,g}\right)^{[j]} \cdot \exp\left(-M^{(p)}_{unfished,A-1,g}\right) \cdot T^{(p)}_{k\to s,A-1,g} \\ &\quad + \sum_k \left(N^{(p)}_{unfished,k,A,g}\right)^{[j]} \cdot \exp\left(-M^{(p)}_{unfished,A,g}\right) \cdot T^{(p)}_{k\to s,A,g}\end{aligned}$$

vi. Set unfished spawning biomass by population, area and gender via

$$\left(SB^{(p)}_{unfished,s,g}\right)^{[j+1]} = \sum_a P^{(p)}_{mature,a,g} \cdot W^{(p)}_{spawn,a,g} \cdot \left(N^{(p)}_{unfished,s,a,g}\right)^{[j+1]} \cdot \exp\left(-\Delta_S \cdot M^{(p)}_{unfished,a,g}\right)$$

Continue the iterations until the convergence criteria below is achieved or the maximum number of iterations has been reached.

Convergence Criterion

Calculate the distance between successive sets of unfished equilibrium spawning biomass estimates by population, area and gender, denoted by $D^{[j]}$, by applying the L_1, or least absolute deviations norm, to the set of estimates as

$$D^{[j]} = \sum_{p} \sum_{d} \sum_{g} \left| \left(SB^{(p)}_{unfished,s,g} \right)^{[j+1]} - \left(SB^{(p)}_{unfished,s,g} \right)^{[j]} \right|$$

Stop the iterations when the set of unfished spawning biomass estimates have converged. That is, stop when $D^{[j]} < \varepsilon \;\; for\ a\ \ small\ value\ \varepsilon > 0$.

If the iterations converge, then one has determined the unfished numbers at age by population, area, and gender $\left(N^{(p)}_{unfished,s,a,g} \right)$ along with the unfished spawning biomass by population, area, and gender $\left(SB^{(p)}_{unfished,s,g} \right)$.

APPENDIX 2. Equilibrium Fished Numbers at Age Algorithm for MAS.

Similarly, one needs to calculate fished numbers at age in equilibrium prior to the start of the assessment time horizon by population, area, and gender $\left(N^{(p)}_{fished,s,a,g}\right)$ as a function of population recruitment distribution by area, movement probabilities, and the equilibrium total mortality at age. The equilibrium fished numbers at age by population, area, and gender depend on the population movement and recruitment distribution matrices and are needed to compute the fished equilibrium spawning biomasses by population and area, which in turn, are needed to calculate the equilibrium numbers at by population, area, and gender for the initial fished equilibrium time period to the start of the assessment time horizon.

Iteration i=1: Calculate the initial equilibrium fished numbers at age estimates by population, area, and gender based on unfished recruitment, the recruitment distribution, equilibrium total mortality and no movement, where $(x)^{[j]}$ denotes the j^{th} iterate of an estimate of a quantity *x*.

i. In general, population recruitment by area and gender is a function of area-specific recruitment production and the recruitment distribution matrix $\underline{\underline{Q}}^{(p)} = \left(Q^{(p)}_{i \to j}\right)_{s x s}$. Set the initial age-0 fished recruits as a function of unfished recruitment and recruitment distribution by area and gender via

$$\left(N^{(p)}_{fished,s,a=0,g}\right)^{[1]} \equiv \left(R^{(p)}_{fished,k,g}\right)^{[1]} = \rho^{(p)}_{g} \sum_{k} Q^{(p)}_{k \to s} \cdot R^{(p)}_{unfished,k}$$

ii. Set initial age-*a* survivors by area and gender for ages *a*=1 to *A*-1 from the initial fished recruits and equilibrium total mortality by area and gender via

$$\left(N^{(p)}_{fished,s,a,g}\right)^{[1]} = \left(N^{(p)}_{fished,s,a-1,g}\right)^{[1]} \cdot \exp\left(-Z^{(p)}_{fished,s,a-1,g}\right)$$

iii. Set initial Age-*A* group of survivors from the initial fished recruits and equilibrium total mortality by area and gender via

$$\left(N^{(p)}_{fished,s,A,g}\right)^{[1]} = \frac{\left(N^{(p)}_{fished,s,A-1,g}\right)^{[1]} \cdot \exp\left(-Z^{(p)}_{fished,s,A-1,g}\right)}{1-\exp\left(-Z^{(p)}_{fished,s,A,g}\right)}$$

iv. Set equilibrium fished spawning biomass by population, area and gender via

$$\left(SB_{fished,s,g}^{(p)}\right)^{[1]} = \sum_a P_{mature,a,g}^{(p)} \cdot W_{spawn,a,g}^{(p)} \cdot \left(N_{fished,s,a,g}^{(p)}\right)^{[1]} \cdot \exp\left(-\Delta_S \cdot Z_{fished,s,a,g}^{(p)}\right)$$

Iteration i=2: Calculate the next iterate of the equilibrium fished numbers at age estimates by population, area, and gender based on the recruitment submodel, the recruitment distribution, equilibrium total mortality, movement probabilities by area, age, and gender, and the previous iterate. Equilibrium fished recruitment production by area is a function of area-specific spawning biomasses which need to be iteratively calculated to account for the movement probabilities that redistribute fish.

i. Set age-0 recruits as a function of the recruitment submodel $f_s^{(p)}$ and recruitment distribution by area and gender (Note that this is effectively turning on the recruitment dynamics) via

$$\left(R_{fished,s}^{(p)}\right)^{[2]} = f_s^{(p)}\left(\left(SB_{fished,s,g=female}^{(p)}\right)^{[1]} \mid \underline{\theta}_s^{(p)},\ SB_{unfished,s,g=female}^{(p)}\right) \quad \text{and}$$

$$\left(N_{fished,s,a=0,g}^{(p)}\right)^{[2]} = \rho_g^{(p)} \sum_k Q_{k\to s}^{(p)} \cdot \left(R_{fished,k}^{(p)}\right)^{[2]}$$

ii. Set age-*a* survivors for ages *a*=1 to *A*-1 by population, area, and gender as survivors that did not emigrate plus age-*a* surviving immigrants from other areas (Note that this is effectively turning on the movement dynamics) via

$$\left(N_{fished,s,a,g}^{(p)}\right)^{[2]} = \sum_k \left(N_{fished,k,a-1,g}^{(p)}\right)^{[1]} \cdot \exp\left(-Z_{fished,k,a-1,g}^{(p)}\right) \cdot T_{k\to s,a-1,g}^{(p)}$$

iii. Set age-(*A*-1) survivors that did not emigrate plus age-(*A*-1) immigrants from other areas plus age-*A* group survivors that did not emigrate plus age-*A* group immigrants from other areas via

$$\begin{aligned}\left(N_{fished,s,A,g}^{(p)}\right)^{[2]} &= \sum_k \left(N_{fished,k,A-1,g}^{(p)}\right)^{[1]} \cdot \exp\left(-Z_{fished,k,A-1,g}^{(p)}\right) \cdot T_{k\to s,A-1,g}^{(p)} \\ &\quad + \sum_k \left(N_{fished,k,A,g}^{(p)}\right)^{[1]} \cdot \exp\left(-Z_{fished,k,A,g}^{(p)}\right) \cdot T_{k\to s,A,g}^{(p)}\end{aligned}$$

iv. Set equilibrium fished spawning biomass by population, area and gender via

$$\left(SB_{fished,s,g}^{(p)}\right)^{[2]} = \sum_a P_{mature,a,g}^{(p)} \cdot W_{spawn,a,g}^{(p)} \cdot \left(N_{fished,s,a,g}^{(p)}\right)^{[2]} \cdot \exp\left(-\Delta_S \cdot Z_{fished,s,a,g}^{(p)}\right)$$

<u>Iteration i=j+1</u>: Calculate the (*kj*1)$^{\text{st}}$ iterate of equilibrium fished numbers at age estimates by population, area, and gender based on the recruitment submodels and recruitment distribution, equilibrium total mortality, movement probabilities by area, age, and gender, and the *j*$^{\text{th}}$ iterate.

i. Set age-0 recruits as a function of the recruitment submodel $f_s^{(p)}$ and recruitment distribution by area and gender via

$$\left(R^{(p)}_{fished,s}\right)^{[j+1]} = f_s^{(p)}\left(\left(SB^{(p)}_{fished,s,g=female}\right)^{[j]} \mid \underline{\theta}_s^{(p)},\ SB^{(p)}_{unfished,s,g=female}\right) \text{ and}$$

$$\left(N^{(p)}_{fished,s,a=0,g}\right)^{[j+1]} = \rho_g^{(p)} \sum_k Q^{(p)}_{k\to s} \cdot \left(R^{(p)}_{fished,k}\right)^{[j]}$$

ii. Set age-*a* survivors for ages *a*=1 to *A*-1 by population, area, and gender that did not emigrate plus age-*a* surviving immigrants from other areas via

$$\left(N^{(p)}_{fished,s,a,g}\right)^{[j+1]} = \sum_k \left(N^{(p)}_{fished,k,a-1,g}\right)^{[j]} \cdot \exp\left(-Z^{(p)}_{fished,k,a-1,g}\right) \cdot T^{(p)}_{k\to s,a-1,g}$$

iii. Set age-(*A*-1) survivors that did not emigrate plus age-(*A*-1) immigrants from other areas plus age-*A* group survivors that did not emigrate plus age-*A* group immigrants from other areas via

$$\begin{aligned}\left(N^{(p)}_{fished,s,A,g}\right)^{[j+1]} &= \sum_k \left(N^{(p)}_{fished,k,A-1,g}\right)^{[j]} \cdot \exp\left(-Z^{(p)}_{unfished,k,A-1,g}\right) \cdot T^{(p)}_{k\to s,A-1,g} \\ &+ \sum_k \left(N^{(p)}_{fished,k,A,g}\right)^{[j]} \cdot \exp\left(-Z^{(p)}_{unfished,k,A,g}\right) \cdot T^{(p)}_{k\to s,A,g}\end{aligned}$$

v. Set unfished spawning biomass by population, area and gender via

$$\left(SB^{(p)}_{fished,s,g}\right)^{[j+1]} = \sum_a P^{(p)}_{mature,a,g} \cdot W^{(p)}_{spawn,a,g} \cdot \left(N^{(p)}_{fished,s,a,g}\right)^{[j+1]} \cdot \exp\left(-\Delta_S \cdot Z^{(p)}_{fished,s,a,g}\right)$$

Continue the iterations until convergence is achieved or the maximum number of iterations has been reached.

If the algorithm converges, then one has determined the unfished numbers at age by population, area, and gender $\left(N^{(p)}_{fished,s,a,g}\right)$ along with the unfished spawning biomass by population, area, and gender $\left(SB^{(p)}_{fished,s,g}\right)$. This population-specific information sets the initial conditions at the start (first year) of the initialization time period, prior to the stock assessment time horizon. These initial conditions, along with recruitment deviation parameters, determine the population dynamics for the initialization time period.

APPENDIX 3. Dynamic Fished Numbers at Age Algorithm for MAS.

3.1 Set Initial Numbers at Age

Set initial numbers at age in year *y*=1 of the assessment time horizon equal to the equilibrium fished numbers at age by population, area and gender as $N_{y=1,s,a,g}^{(p)} = N_{fished,s,a,g}^{(p)}$

Loop over years (*y*=1,…,*Y*)

3.2 Calculate predicted fishery selectivities at age by population, fleet, and gender (Logistic submodel example):

$$S_{v,g}^{(p)}(a) = \frac{1}{1+\exp\left(-\frac{\left(a-a_{50,v,g}^{(p)}\right)}{\sigma_{v,g}^{(p)}}\right)}$$

3.3 Calculate predicted survey selectivities at age by population, survey, and gender (Logistic submodel example):

$$S_{I,g}^{(p)}(a) = \frac{1}{1+\exp\left(-\frac{\left(a-a_{50,I,g}^{(p)}\right)}{\sigma_{I,g}^{(p)}}\right)}$$

3.4 Calculate predicted total mortality rates at age by year, population, fleet, and gender (Example with optimized selectivity and mortality parameters):

$$Z^{(p)}_{y,s,a,g} = M^{(p)}_{s,a,g} + S^{(p)}_{v,g}\left(a\right)F^{(p)}_{v,y,s}$$

3.5 Calculate predicted female spawning biomass by year, population, and area (Example with optimized selectivity and mortality parameters):

$$SB^{(p)}_{y,s,g=female} = \sum_{a} P^{(p)}_{mature,a,g=female} \cdot W^{(p)}_{spawn,a,g=female} \cdot N^{(p)}_{y,s,a,g=female} \cdot \exp\left(-\Delta_S Z^{(p)}_{y,s,a,g=female}\right)$$

Where $N^{(p)}_{y,s,a,g=female} \cdot \exp\left(-\Delta_S Z^{(p)}_{y,s,a,g=female}\right)$ is the number of surviving adult female spawners

3.6 Calculate predicted recruitment by year, population, and area (Example with optimized selectivity and mortality parameters):

$$R^{(p)}_{y,s,g} = \rho^{(p)}_{g}\left(Q^{(p)}_{s\to s}R^{(p)}_{y,s} + \sum_{k\neq s} Q^{(p)}_{k\to s}R^{(p)}_{y,k}\right)$$

Where $R^{(p)}_{y,s} = \dfrac{4h^{(p)}_{s} \cdot R^{(p)}_{unfished,s} \cdot SB^{(p)}_{y,s}}{SB^{(p)}_{unfished,s}\left(1-h^{(p)}_{s}\right) + SB^{(p)}_{y,s}\left(5h^{(p)}_{s}-1\right)}$ is the number of recruitment produced by year, population and area, and

Where $\underline{\underline{Q}}^{(p)} = \left(Q^{(p)}_{i\to j}\right)$ is the recruitment distribution by area matrix for each population, and

Where $N^{(p)}_{y,s,a=0,g} = R^{(p)}_{y,s,g}$ is the recruitment strength by population, area and gender in year y.

3.7 Calculate predicted fishery observations (Example with optimized selectivity and mortality parameters):

Calculate predicted fishery catch numbers at age by fleet, year, population, area, and gender as

$$C^{(p)}_{v,y,s,a,g} = N^{(p)}_{y,s,a,g}\frac{F^{(p)}_{v,y,s}S^{(p)}_{v,s,g}\left(a\right)}{\left(F^{(p)}_{v,y,s}S^{(p)}_{v,s,g}\left(a\right)+M^{(p)}_{s,a,g}\right)}\left\{1-\exp\left[-\left(F^{(p)}_{v,y,s}S^{(p)}_{v,d,g}\left(a\right)+M^{(p)}_{s,a,g}\right)\right]\right\}$$

Calculate predicted fishery catch proportion at age by fleet, year, population, area, and gender as

$$P_{v,y,s,a,g}^{(p)} = \frac{C_{v,y,s,a,g}^{(p)}}{\sum_{a} C_{v,y,s,a,g}^{(p)}}$$

Calculate predicted fishery catch biomass at age by fleet, year, population, area, and gender as

$$CB_{v,y,s,a,g}^{(p)} = C_{v,y,s,a,g}^{(p)} \cdot W_{v,s,a,g}^{(p)}$$

3.8 Calculate predicted survey observations (Example with optimized selectivity and mortality parameters):

Calculate predicted survey catch numbers at age by year, population, area, and gender as

$$C_{I,y,s,a,g}^{(p)} = S_{I,s,a,g}^{(p)} N_{y,s,a,g}^{(p)} \cdot \exp\left(-\Delta_I \cdot Z_{y,s,a,g}^{(p)}\right)$$

Calculate predicted survey catch proportion at age by year, population, area, and gender as

$$P_{I,y,s,a,g}^{(p)} = \frac{C_{I,y,s,a,g}^{(p)}}{\sum_{a} C_{I,y,s,a,g}^{(p)}}$$

Calculate predicted survey catch biomass at age by fleet, year, population, area, and gender as

$$CB_{I,y,s,a,g}^{(p)} = q_{I,s} \cdot C_{I,y,s,a,g}^{(p)} \cdot W_{I,s,a,g}^{(p)}$$

Where $q_{I,s}$ is the catchability of survey *I* in area *s.*

3.9 Calculate predicted quantities of interest (Example with optimized selectivity and mortality parameters):

Calculate predicted total fishery catch numbers at age summed over populations by fleet, year, area, and gender as

$$C_{v,y,s,a,g} = \sum_{p} C_{v,y,s,a,g}^{(p)}$$

Calculate predicted total fishery catch proportion at age summed over populations by fleet, year, area, and gender as

$$P_{v,y,s,a,g} = \frac{\sum_p C^{(p)}_{v,y,s,a,g}}{\sum_p \sum_a C^{(p)}_{v,y,s,a,g}}$$

Calculate predicted total fishery catch biomass summed over populations by fleet, year, and area as

$$CB_{v,y,s} = \sum_p \sum_a \sum_g CB^{(p)}_{v,y,s,a,g}$$

Calculate predicted total survey catch numbers at age summed over populations by year, area, and gender as

$$C_{I,y,s,a,g} = \sum_p C^{(p)}_{I,y,s,a,g}$$

Calculate predicted survey catch proportion at age by year, area, and gender as

$$P_{I,y,s,a,g} = \frac{\sum_p C^{(p)}_{I,y,s,a,g}}{\sum_p \sum_a C^{(p)}_{I,y,s,a,g}}$$

Calculate predicted total survey catch biomass by fleet, year, and area as

$$CB_{I,y,s} = \sum_p \sum_a \sum_g CB^{(p)}_{I,y,s,a,g}$$

3.10 Calculate population numbers at age at the start of year *y*+1 (Example with optimized selectivity and mortality parameters):

Set age-*a* survivors for ages *a*=1 to *A*-1 by population, area, and gender that did not emigrate plus age-*a* surviving immigrants from other areas via

$$N^{(p)}_{y+1,s,a,g} = \sum_k N^{(p)}_{y,k,a-1,g} \cdot \exp\left(-Z^{(p)}_{y,k,a-1,g}\right) \cdot T^{(p)}_{k\to s,a-1,g}$$

Set age-(*A*-1) survivors that did not emigrate plus age-(*A*-1) immigrants from other areas plus age-*A* group survivors that did not emigrate plus age-*A* group immigrants from other areas via

$$\begin{aligned} N^{(p)}_{y+1,s,A,g} = &\sum_k N^{(p)}_{y,k,A-1,g} \cdot \exp\left(-Z^{(p)}_{y,k,A-1,g}\right) \cdot T^{(p)}_{k\to s,A-1,g} \\ &+ \sum_k N^{(p)}_{y,k,A,g} \cdot \exp\left(-Z^{(p)}_{y,k,A,g}\right) \cdot T^{(p)}_{k\to s,A,g} \end{aligned}$$

APPENDIX 4. Algorithms to Calculate the Equilibrium and Time-Varying Mean Length of the Plus Group in MAS.

5.1. Equilibrium Mean Length of the Plus Group Algorithm

For the plus group which is comprised of all fish with ages greater than or equal to a cutoff age denoted as age-*A*, we want to account for any expected growth in length of plus group fish that occurs beyond age-*A* at equilibrium with total mortality rates at age Z_a. To do this for the equilibrium case, let N^* be the total number of fish at an equilibrium total mortality rate Z_A in the plus group of population *p* in year *y*. Here the plus group consists of ages *A* (the reference or youngest age in the plus group) to *MaxPlusGroupAge* (the oldest possible age of a fish in the plus group) with *MaxPlusGroupAge* >= *A* where the total number of fish in the plus group is the sum of numbers at age *A* to *MaxPlusGroupAge*, $N^* = \sum_{k=A}^{MaxPlusGroupAge} N_k$.

Now we want to approximate the expected length of the plus group when the population is at equilibrium, denoted as $E\left[L_A^*\right] \equiv E\left[L_{A,t=0}^*\right]$ using an abundance-weighted average of the mean lengths of survivors in the plus group, where the mean length of an age-*a* fish is L_a. To do this, assume that (i) all age classes in the plus group have equal abundance at age-*A* when they entered the plus group (N_A) and (ii) all age classes in the plus group experience the same equilibrium instantaneous total mortality rate, denoted by Z_A, where the number of fish at age *A*+*k*+1 is the number of survivors from age *A*+*k*, or $N_{A+k+1} = N_{A+k} \cdot e^{-Z_A}$.

The total number of fish in the plus group can be expressed as the sum of survivors at age for ages *A* to *MaxPlusGroupAge* as

$$N^* = N_A + N_{A+1} + N_{A+2} + \ldots + N_{MaxPlusGroupAge} = N_A \cdot \left(1 + e^{-Z_A} + e^{-2Z_A} + \ldots + e^{-(MaxPlusGroupAge-A-1)\cdot Z_A}\right)$$

Summing the finite geometric series of *MaxPlusGroupAge*+1 terms on the RHS above gives the following expression for the total number of fish in the plus group

$$N^* = N_A \cdot \frac{\left(1 - e^{-(MaxPlusGroupAge-A)\cdot Z_A}\right)}{\left(1 - e^{-Z_A}\right)}$$

As a result, the expected length of the set of fish in the plus group ($E\left[L_A^*\right]$) at equilibrium total mortality rate Z_A can be expressed as a weighted average of mean lengths of survivors at age as

$$E\left[L_A^*\right] = \frac{\sum_{k=A}^{MaxPlusAge} N_k \cdot L_k}{N^*} = \frac{\left(1-e^{-Z_A}\right)}{\left(1-e^{-(MaxPlusGroupAge-A)\cdot Z_A}\right)} \cdot \sum_{k=0}^{MaxPlusGroupAge-A-1} e^{-k\cdot Z_A} \cdot L_{A+k}$$

5.2. Time-Varying Mean Length of the Plus Group Algorithm

As year class strength and survival rates vary across cohorts in the population, the number of new fish entering the plus group will change dynamically. One can improve the accuracy of the plus group dynamics by accounting for the dynamic effects of varying year class strengths and survival rates on the mean length of the plus group through time. To do this, one can approximate the time-varying expected length of the plus group using a weighted average of the mean lengths of the age-(*A*-1) age class entering the plus group at ($N_{A-1,t}$) and the total survivors in the plus group ($N_{A,t}^*$) where the (possibly) time-varying mean length of an age-*A* fish at time *t* is $L_{A,t}$ and the expected length of the entire plus group at time *t* is $E\left[L_{A,t}^*\right]$. Given this, the expected length of the plus group at time *t*+1 can be approximated as a weighted average of the mean length of age-(*A*-1) survivors entering the plus group at time *t*+1 and the expected length of the plus group survivors from the previous time step $E\left[L_{A,t}^*\right]$ as

$$E\left[L_{A,t+1}^*\right] = w_{A,t} \cdot L_{A,t+1} + w_{A,t}^* \cdot E\left[L_{A,t+1}^*\right] = \frac{N_{A-1,t} \cdot e^{-Z_{A-1,t}} \cdot L_{A,t+1} + N_{A,t}^* \cdot e^{-Z_{A,t}} \cdot E\left[L_{A,t}^*\right]}{N_{A-1,t} \cdot e^{-Z_{A-1,t}} + N_{A,t}^* \cdot e^{-Z_{A,t}}}$$

Here the dynamic weights $w_{A,t}$ are the fraction of the incoming age-*A* fish and the complementary fraction of existing age-(*A*+1) and older fish alive at time *t*+1 in the extended plus group.

For example, the expected length of the plus group at equilibrium with total mortality rate $Z_{A,0}$ at time *t*=0 is

$$E\left[L_{A,0}^*\right] = \frac{\left(1-e^{-Z_{A,0}}\right)}{\left(1-e^{-(MaxPlusAge-A)\cdot Z_{A,0}}\right)} \cdot \sum_{k=0}^{MaxPlusAge-A-1} e^{-k\cdot Z_{A,0}} \cdot L_{A+k,0}$$

which is set to be equal to the plus group mean length at time *t*=1 to start the model, or $L_{A,1} = E\left[L_{A,0}^*\right]$.

Given this initial condition, the expression for the expected mean length of the plus group in the initial time period of the assessment time horizon is

$$E\left[L^*_{A,1}\right] = w_{A,1} \cdot L_{A,1} + w^*_{A,1} \cdot E\left[L^*_{A,0}\right] = E\left[L^*_{A,0}\right]$$

While the corresponding dynamic mean lengths at times T=2…Y are

$$E\left[L^*_{A,T}\right] = w_{A,T} \cdot L_{A,T} + w^*_{A,T} \cdot E\left[L^*_{A,T-1}\right] = \frac{N_{A-1,T-1} \cdot e^{-Z_{A-1,T-1}} \cdot L_{A,T} + N^*_{A,T-1} \cdot e^{-Z_{A,T-1}} \cdot E\left[L^*_{A,T-1}\right]}{N_{A-1,T-1} \cdot e^{-Z_{A-1,T-1}} + N^*_{A,T-1} \cdot e^{-Z_{A,T-1}}}$$

And so on for $t>2$ throughout the assessment time horizon.

Note that this time series of calculated dynamic mean lengths of the plus group accounts for the differences in survival and growth for the incoming age-(A-1) cohort to the plus group but not potential changes in mean size at age within the extended plus group due to time-varying growth.

APPENDIX 5. Implementation of the Dirichlet Multinomial Distribution as an Option for Fitting Size Composition Data in MAS.

Here are some notes on the implementation of the multinomial negative loglikelihood (NLL) component for composition data in MAS and on the Dirichlet-multinomial negative loglikeihood as described in the Thorson at al. (2017) article and as it is implemented in SS3.30[1] and MAS[2]. Here also note that each age composition NLL is an additive component of the overall objective function to be minimized to optimize the model parameter estimates.

- The NLL for a multinomial age (or size composition) sample is conditioned on the observed proportions at age $\underline{p}^{OBS} = \left(p_1^{OBS},\ldots,p_{A\max}^{OBS}\right)$ in a total of $A_{\max}$ age bins (or $A_{\max}$ age bins if age-0 individuals are included) and the effective number of fish sampled *N*, noting that cluster sampling effects due to intracluster correlation are expected.
- The NLL for a multinomial sample of ages (or age composition data) for a fishing fleet is a function of the predicted population proportion at age $\underline{p} = \left(p_1,\ldots,p_{A\max}\right)$ where the age categories are ages 1, 2, … *Amax*.
- Given the number of fish sampled *N*, the observed proportions sampled at age p_a^{OBS} for all ages and the predicted proportions at age p_a for all ages, the NLL for a multinomial age composition sample (excluding constants) is

  $$NLL_{Mult}\left(\underline{p} \mid N, \underline{p}^{OBS}\right) = -\sum_{a=1}^{A\max} N \cdot p_a^{OBS} \cdot \log\left(p_a\right)$$

  With $N_{eff} = N$ in the absence of iterative reweighting to estimate N_{eff} and $\underline{p}$ being the proportion at age parameter vector to be freely estimated.
- This $NLL_{Mult}\left(\underline{p}\right)$ is implemented in lines 340-354 of Fleet.hpp (MAS) and in lines 401-407 of SS_objfunc.tpl (SS3.30). This is a one-step model (i.e., not a compound distribution).
- For the Dirichlet-multinomial likelihood (actually the posterior distribution of a conjugate prior Dirichlet with multinomial likelihood), the negative loglikelihood sample is conditioned on the observed proportions at age $\underline{p}^{OBS} = \left(p_1^{OBS},\ldots,p_{A\max}^{OBS}\right)$ and the number of fish sampled *N*.

[1] SS3.30 is the Stock Synthesis 3.30 model. [2] MAS is the Metapopulation Assessment System.

- Here the probability model has two implicit Markov Chain Monte Carlo steps:
  - (i) Randomly sample proportions $\underline{p}^*$ from the Dirichlet distribution with concentration parameters $\underline{\alpha} = \beta \cdot \underline{p}$ and
  - (ii) Randomly sample numbers of fish at age $x_1, ..., x_{A\max}$ from the multinomial distribution with parameters $\underline{p}^*$ and *N*.
  - (iii) Integrate over steps (i) and (ii) to compute the posterior. But in this special case of the Dirchlet-multinomial conjugate distribution relationship, there is an exact analytical solution, so we do not have to do any random MCMC sampling.
- The NLL for a Dirichlet-multinomial sample of ages (or age composition data) for a fishing fleet is a function of the concentration parameter β (β expresses the strength of belief in the prior for the proportion at age vector) and the predicted population proportion at age $\underline{p} = \left(p_1, ..., p_{A\max}\right)$ where the age categories are ages 1, 2, … *Amax*.
- Given the number of fish sampled *N*, the observed proportions sampled at age p_a^{OBS} for all ages and the predicted proportions at age p_a for all ages, the NLL for a Dirichlet-multinomial age composition sample is

$$NLL_{Dir-Mult}\left(\underline{p}, \beta \mid N, \underline{p}^{OBS}\right) = -\log\Gamma\left(\beta\right) + \log\Gamma\left(N+\beta\right) - \sum_{a=1}^{A\max} \log\Gamma\left(N \cdot p_a^{OBS} + \beta \cdot p_a\right) + \sum_{a=1}^{A\max} \log\Gamma\left(\beta \cdot p_a\right)$$

  With β and $\underline{p}$ being freely estimated parameters.
- The effective sample size for the Dirichlet-multinomial (DM) age composition sample in this case is

$$N_{eff} = \frac{N + N\beta}{N + \beta}$$

- If one reparameterizes the DM model by setting $\beta = \theta \cdot N$, then $N_{eff} = \frac{1}{1+\theta} + N \cdot \frac{\theta}{1+\theta}$ and the NLL for the DM model becomes

$$NLL_{Dir-Mult}\left(\underline{p}, \beta \mid N, \underline{p}^{OBS}\right) = -\log\Gamma\left(\theta \cdot N\right) + \log\Gamma\left(N+\theta \cdot N\right) - \sum_{a=1}^{A\max} \log\Gamma\left(N \cdot p_a^{OBS} + \theta \cdot N \cdot p_a\right) + \sum_{a=1}^{A\max} \log\Gamma\left(\theta \cdot N \cdot p_a\right)$$

  This is the linear parameterization #1 listed in equation (10) of Thorson et al (2017).
- This parameterization #1 is implemented in SS3.30 in lines 409-431 of of SS_objfunc.tpl (SS3.30, downloaded on 28-Feb-2018) with similar code used for the length composition data samples, if applicable. Note that parameterization #2 does not appear to be implemented in SS3.30.

- Note that to implement the DM model for age (or size) composition data, one needs to include the β concentration scaling parameter either as a freely estimated parameter or as a fixed/assumed parameter in the objective through the NLL components and that in the limit as $\beta \to \infty$,the DM model simplifies to the Multinomial model.