**Synthesizing the spatial functionality of contemporary stock assessment software to identify future needs for next generation assessment platforms**

**Running header:**
Spatial capabilities in stock assessment

**Authors:**
Aaron M. Berger[1*], Caren Barceló[2‡], Daniel R. Goethel[3], Simon D. Hoyle[4,5], Patrick Lynch[6], Jeremy McKenzie[7], Alistair Dunn[8], André E. Punt[9], Richard D. Methot[10], John Hampton[11], Clay Porch [12], Richard McGarvey[13], James Thorson[14], Teresa A'mar [15,16], Jonathan Deroba[17], Bjarki Þór Elvarsson[18], Steven J. Holmes [15], Daniel Howell [19], Brian J. Langseth[20], Craig Marsh[3], Mark N. Maunder[21], Sophie Mormede[22], Scott Rasmussen[23]

**Affiliations:**
[1] Fishery Resource Analysis and Monitoring Division, Northwest Fisheries Science Center, NMFS-NOAA, 2032 S.E. OSU Drive, Newport, OR, USA.
[2] ECS Federal LLC, Fairfax, VA, USA.
[3] Auke Bay Lab, Alaska Fisheries Science Center, National Oceanic and Atmospheric Administration, Juneau, AK, USA.
[4] National Institute of Water and Atmospheric Research, 217 Akersten Street, Port Nelson, Nelson, New Zealand.
[5] Department of Statistics, University of Auckland, Private Bag 92019, Auckland, New Zealand.
[6] Office of Science and Technology, National Marine Fisheries Service, National Oceanic and Atmospheric Administration, Silver Spring, MD, USA.
[7] National Institute of Water and Atmospheric Research, 41 Market Place, Viaduct Harbour, Auckland, New Zealand.
[8] Ocean Environmental, Ltd., Wellington, New Zealand.
[9] School of Aquatic and Fishery Sciences, University of Washington, Seattle, WA, USA.
[10] National Marine Fisheries Service, NOAA, Seattle, WA, USA.
[11] Secretariat of the Pacific Community, Oceanic Fisheries Programme, Noumea, New Caledonia.
[12] Southeast Fisheries Science Center, Sustainable Fisheries Division, 75 Virginia Beach Drive, Miami, 4600 Rickenbacker Causeway, Miami, FL 33149, USA.
[13] South Australian Research and Development Institute (SARDI), Department of Primary Industries and Regions, Government of South Australia, 2 Hamra Ave, West Beach, SA, Australia.
[14] Habitat and Ecological Processes Research Program, Alaska Fisheries Science Center, NOAA, Seattle, WA, USA.
[15] National Institute of Water and Atmospheric Research, 301 Evans Bay Parade, Wellington, New Zealand.
[16] Dragonfly Data Science, Wellington, New Zealand.
[17] Population Dynamics Branch, Northeast Fisheries Science Center, NMFS-NOAA, 166 Water St, Woods Hole, MA, USA.
[18] Marine and Freshwater Research Institute (MFRI), 220 Hafnarfjordur, Iceland.
[19] Institute of Marine Research, Bergen, Norway.

[20] Fishery Resource Analysis and Monitoring Division, Northwest Fisheries Science Center, NMFS-NOAA, 2725 Montlake Blvd E, Seattle, WA, USA.
[21] Inter-American Tropical Tuna Commission, 8901 La Jolla Shores Drive, La Jolla, CA, 92037-1508, USA.
[22] SoFish Consulting Ltd., Wellington, New Zealand.
[23] Zaita Design, 29 Burbank Crescent, Churton Park, Wellington, New Zealand.

[ǂ] Current address: University of Washington, Puget Sound Institute, 326 East D Street, Tacoma, WA, USA.

[*] Corresponding author – aaron.berger@noaa.gov

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**ORCID:**
Aaron Berger: https://orcid.org/0000-0002-1408-7122
Caren Barcelo: https://orcid.org/0000-0002-3336-5052
Daniel Goethel: https://orcid.org/0000-0003-0066-431X
Simon Hoyle: https://orcid.org/0000-0002-1787-6565
Patrick Lynch: https://orcid.org/0000-0001-7121-6181
Jeremey McKenzie:
Alistair Dunn:
Andre Punt: https://orcid.org/0000-0001-8489-2488
Richard Methot: https://orcid.org/0000-0002-5606-6944
John Hampton:
Clay Porch:
Richard McGarvey: https://orcid.org/0000-0001-8698-8774
James Thorson:
Teresa A'mar: https://orcid.org/0000-0002-8634-1142
Jonathan Deroba: https://orcid.org/0000-0003-4269-6790
Bjarki Þór Elvarsson: https://orcid.org/0000-0001-5855-1188
Steven Holmes: https://orcid.org/0000-0002-3011-2017
Daniel Howell: https://orcid.org/0000-0002-1716-5456
Brian Langseth: https://orcid.org/0000-0002-9901-6146
Craig Marsh:
Mark Maunder:
Sophie Mormede: https://orcid.org/0000-0003-4668-2046
Scott Rasmussen:

**Abstract:**
Marine fishes are heterogeneously distributed across their ranges according to population dynamics governed by complex spatiotemporal relationships between ontogenetic habitat usage, species interactions, environmental variability, and harvest patterns. However, few stock assessments incorporate spatial population structure in the determination of population status and sustainable catch limits. A small number of generalized stock assessment software platforms are utilized worldwide to assess a large number of marine fish populations. Although each platform relies on similar underlying population dynamics, the spatial capabilities and functionality often differ among them. We catalogue spatial dynamics and capabilities across stock assessment platforms to leverage collective experiences and identify future needs for next generation assessment software packages. Despite commonalities across platforms (e.g., most models allow for a single population with spatial heterogeneity, apportionment of recruitment, and age-varying connectivity), no single platform is flexible enough to address the full breadth of spatial dynamics observed for managed marine fish species. Our review clarifies spatial assessment design and modeling 'good practices', while emphasizing the need for more generalizable and modular next generation assessment platforms that can account for the spatiotemporal complexity of marine resources (such as natal homing and spawning migrations, ontogenetic movement patterns, metapopulation structure, and complex fleet dynamics). Generalized, spatially-integrated assessment platforms will be key decision-tools to account for spatiotemporal species and fishery interactions, particularly as managers attempt to address climate change and implement ecosystem-based fisheries management.

**Keywords:**
Spatial population structure, spatial stock assessment, software design good practice, movement, mark-recapture, next generation stock assessments

## 1. Introduction

Spatiotemporal distributions of living marine resources arise from productivity, movement, harvest, and environmental interactions that collectively influence population structure and dynamics at multiple scales (Ciannelli et al. 2008, 2013; Link 2018). Observations of complex spatial dynamics for many marine species have increased recognition that data to monitor and preserve spatial population structure is critical for sustainable fisheries management (Smedbol and Stevenson, 2001; Hilborn et al., 2004). In particular, the availability of high-resolution data has led to important advancements in understanding fine-scale connectivity dynamics and increased explorations into spatial population models (Nathan et al., 2008; Goethel et al., 2011). Spatial stock assessment models are a type of integrated population model that directly incorporates spatial processes to estimate population parameters by fitting to available data to determine stock status (Hilborn and Walters, 1992; Maunder and Punt, 2004). Such models are increasingly recognized as imperative for preserving ecosystem function and managing biocomplexity (Cadrin et al., 2020). Yet, most stock assessments utilized for management advice do not explicitly account for spatial heterogeneity, despite wide recognition of the importance of spatial structure for buffering against stock collapses (Berger et al., 2017b). A comprehensive understanding of spatial modeling tools, along with existing capabilities and knowledge gaps, is a first step towards increased use of spatial stock assessments in fisheries management.

Spatial assessment models have a rich history as research tools, but have limited 'operational' (directly used for determining harvest regulations) applications in fisheries management (Quinn et al., 1990; Porch et al., 1998; Goethel and Cadrin, 2021). Simulations show that spatially explicit models are typically more robust than spatially-aggregated or spatially-implicit (e.g., areas-as-fleets) counterparts when there is enough informative data (e.g., Porch et al., 1998, Ying et al., 2011; Goethel et al., 2019; Bosley et al., 2022). In general, spatial stock assessments can better match the scale of biological processes, incorporate a broad spectrum of data sources at the scale of collection, and directly inform spatiotemporal management actions (Maunder, 2001; Berger et al., 2017b; Punt et al., 2020).

In some cases, spatial assessments may not be required, or practical, to develop adequate management advice (e.g., Punt et al., 2017; Lee et al., 2017). For instance, spatial models are often complex, data intensive, and limited by the quantity, quality, and availability of georeferenced data (Berger et al., 2017b; Cadrin, 2020; Punt et al., 2020). As spatial resolution increases, data are increasingly partitioned, which reduces the sample sizes available to estimate important spatial parameters (e.g., movement and strata-specific recruitment or fishing mortality; Cope and Punt, 2011; Punt, 2020). Other impediments to implementing spatial stock assessments include low-resolution historical catch data, limited information regarding connectivity, and unresolved hypotheses about spatial processes (Berger et al., 2017b). Institutional inertia, such as within regional fisheries management organizations (RFMOs), may also prevent or delay the adoption of spatial management procedures due to added model complexities and unfamiliarity (Berger et al., 2017b; Punt, 2019a,b). Nonetheless, the tradeoffs of using a spatial stock assessment model should be explored through simulation testing to directly examine potential benefits and limitations (Guan et al., 2013; Punt, 2019b; Cadrin et al., 2023; Goethel et al, 2023b).

The practicality of implementing spatial assessments has increased over the last decade, largely spurred by a rapid evolution in data collection technologies with high spatiotemporal resolution (Hidalgo et al., 2016; Lowerre-Barbieri et al., 2019; Goethel et al., 2023b). Thus, the desire and ability to evaluate operational spatial assessments is expected to increase in the coming years (Goethel and Cadrin, 2021; Thorson et al., 2021), and contemporary modeling tools will need to be developed to meet growing demands (Dichmont et al., 2016; Punt et al., 2020). Roughly twenty generalized stock assessment platforms (i.e., standalone software packages) are currently used to assess the population status and trends of many global fish stocks, but only five are known to explicitly account for spatial processes (Punt et al., 2020; Dichmont et al., 2021). While some commonalities exist among the five (hereafter referred to as the 'platforms'), each platform was mostly developed independently to address specific needs for a given stock or management framework. Thus, there are unique assumptions and approaches to incorporating spatial processes and population structure across platforms. A comprehensive understanding of existing spatial assessment capabilities and limitations (e.g., what dynamics cannot yet be addressed) need to be identified to effectively guide the development of the next generation of stock assessment software platforms (Lynch et al., 2018, Punt et al., 2020).

The purpose of this paper is to expand upon the work of Punt et al. (2020) who reviewed the modeling capabilities of nine generalized assessment software packages. Here, we review the spatial capabilities of platforms to highlight commonalities, systematic differences, and provide insight into regional differences in spatial modeling approaches. Based on our review, we identify current challenges that remain and provide good practice guidance towards the adoption of spatial stock assessments. The focus of this paper is on the spatial dimension of population models, but we acknowledge the correlative and interactive nature of all model structure decisions (e.g., space, time, age, sex, and life-stage partitions), which are implicitly considered in our analysis. The ability to better incorporate climate change impacts and ecosystem dynamics into stock assessment and management frameworks will require spatial assessment tools. This review provides a prospective of where the stock assessment discipline currently is and where we should aim to go in the coming years to ensure changing distributions, species' spatiotemporal overlap, and other scale-dependent management exigencies can be adequately addressed.

## 2. Spatial capabilities of generalized stock assessment platforms

A useful starting point for comparing spatial assessment capabilities is to develop a common vocabulary (Goethel et al., 2023a). The literature on marine population structure suffers from inconsistent use of spatial terminology (Kritzer and Sale, 2004; Cadrin, 2020), and many of the reviewed software packages use different terms for the same spatial processes. Although previous studies have defined important terms applicable to spatial assessment models (e.g., Goethel and Berger, 2017; Cadrin, 2020), no comprehensive unified nomenclature has been developed. For this paper, we define a common set of spatial terms and use them to compare and contrast platform spatial capabilities (Table 1). While a comprehensive, rigorous treatment of spatial stock assessment terms is beyond the scope of this review, the provided definitions can form a basis for developing a unified nomenclature to combat pervasive linguistic uncertainty and vagueness associated with spatial population modeling.

There are five primary generalized stock assessment platforms, which can readily incorporate spatial population structure and connectivity. Each of the five platforms have been used to provide tactical management advice for national and international RFMOs across the globe (Fig. 1). The platforms included in this review are Casal2 (Doonan et al., 2016) – the successor to CASAL ($C^{++}$ Algorithmic Stock Assessment Laboratory; Bull et al., 2012), the Globally-applicable area-disaggregated general ecosystem toolbox (Gadget; Begley 2005), MULTIple length Frequency ANalysis-Catch at Length (MULTIFAN-CL or MFCL; Fournier et al. 1998), Stock Synthesis (SS3; Methot and Wetzel, 2013), and Virtual Population – 2 Box (VPA 2-Box; Porch 2018).

Although each platform was originally built to address specific objectives or assess a given species (or species group), all have undergone iterative development to generalize versatility across an array of life histories, spatial dynamics, and data availability (Punt et al., 2020). Casal2 is a statistical age- or length-structured population dynamics modeling platform designed to be structurally flexible and user-friendly. The user can easily define alternative population categories (e.g., sex, life-stage, spatial strata) for single or multiple stocks. Casal2, and its predecessor CASAL, have been primarily used for New Zealand and Australian stock assessments, and for toothfish assessments for the Commission for the Conservation of Antarctic Marine Living Resources. Gadget is based on an age-, length-, or age-length-structured statistical population model, which tracks growth, fishing, predation, and migration processes for multiple species (or multiple groups within a species) using a general ecosystem structure framework. Gadget is primarily used to assess stocks in the North Atlantic Ocean. MFCL is a statistical age-structured population model optimized to fit to length or weight data and is scalable according to data availability. MFCL is used to assess large pelagic species in the Pacific and Indian Oceans. SS3 is a statistical age- and length-structured population dynamics modelling framework, which is scalable according to data availability (data-weak to data-rich). Thus, it supports broad application in the United States and around the world. VPA 2-Box was designed to extend the general cohort reconstruction methods of virtual population analysis (e.g., the adaptive framework, ADAPT; Gavaris 1988) to two spatial strata ('boxes'), particularly for the case of Atlantic Bluefin tuna population assessments.

Each platform has unique underlying spatial population dynamic assumptions, data options, and available spatial model configurations. We first overview the primary spatial features and modeling options that a platform should consider. The specific spatial capabilities of each modeling platform are then reviewed to highlight unique features along with commonalities among platforms. We conclude this section by discussing current developmental features, because these are useful for understanding future directions for spatial models. Focus is placed on modeling options related to spatial and population structure, productivity dynamics, connectivity, spatial variation in demographics, fleet structure, and biological reference points. Model features were identified based on a literature review and input from lead platform developers.

*2.1 Primary features of spatial stock assessment methods*

There are several key considerations that arise when developing spatial stock assessment models, including the type of spatial population structure, how connectivity occurs among spatial strata or population units, the spatial scale of recruitment and other demographic processes, and the calculation of appropriate reference points (Table 2; Punt, 2019b; Goethel et al., 2023a). All features of an integrated stock assessment are necessarily intertwined, and parameters can be increasingly co-dependent when the model has spatial dimensions (Sampson, 2014). Each modeling choice influences parameters and dynamics across the spatiotemporal domain, often with feedback loops (e.g., movement parametrizations influence spatial recruitment estimation and vice versa). In addition, the quantity, quality, and resolution of available data plays a critical role when structuring a model.

Population structures that can be modeled include panmictic (a single reproductive population), spatial heterogeneity within a single reproductive population, a metapopulation, and multiple populations with limited reproductive mixing and natal homing (see Table 1 for definitions). The productivity dynamics and stock-recruit assumptions (i.e., scale of density-dependence) are typically features of the population structure (Table 1). For instance, a single population will assume global density-dependence using a single stock-recruit relationship without (panmictic) or with (spatial heterogeneity) apportionment. A metapopulation typically assumes local density-dependence with a stock-recruit relationship for each population component (i.e., sub-population). Natal homing implies local density-dependence, with each population maintaining a unique stock-recruit relationship due to lack of reproductive mixing.

The number of spatial strata within the biological domain should be determined by the degree of heterogeneity in fishing dynamics and demographics, while balancing data availability with spatial strata resolution. Connectivity among spatial strata should account for dispersal among population units, directed migrations (e.g., natal homing spawning migrations), mixing among population units, or movement among strata or sub-populations. The principle of parsimony is often necessary when developing models with biological connectivity patterns due to the rapid expansion of parameters with increasing numbers of spatial strata. For example, a variety of simplifying assumptions can be utilized for describing movement dynamics in spatial assessments, such as ignoring movement, estimating time- and age-invariant movement, or implementing various functional forms or preference functions to model the primary drivers of movement while reducing the number of estimated parameters.

Fleet structure and the degree of demographic (or life history) variation should also guide the number of spatial strata within an assessment model (Punt, 2019b). Spatiotemporal variation in fishing dynamics across the model domain will impact age-specific harvest, which is driven by the availability of fish in a given strata and to a gear type (i.e., the strata-specific selectivity). Fleets can either be modeled independently by stratum or parameters (e.g., selectivity or availability) can be shared across strata when there are commonalities in harvest patterns. In some cases, spatial patterns in fishing reflect spatial patterns in the targeted population such that modeling spatial stratifications by fleet can be advantageous (Berger et al., 2012; Waterhouse et al., 2014). Spatial demographic assumptions are another important consideration, because they influence estimates of spawning stock biomass (via maturity), mortality (through natural mortality), and depletion (as determined by growth and size- or age-based harvest; Punt, 2023). Similar to fleet structure, the degree of spatial complexity associated with demographic parameters (e.g., growth, maturity, fecundity, and natural mortality) can differ, be shared, or correlated across strata. Demographic complexity can be determined by ecosystem drivers (e.g., be phenotypic and based on area of inhabitance, such as in a subpopulation of a metapopulation) or due to genetic differences (i.e., be genotypic and based on natal population).

Biological reference points are used to determine the current status of the stock, which are key components of harvest control rules (HCRs) used to specify (and project) future catch limits. Spatially-explicit reference points can be non-intuitive to calculate and difficult to interpret when there is non-stationarity in population dynamics (e.g., movement occurs across mortality and demographic regimes or connectivity varies over time; Goethel and Berger, 2017). However, under the assumption of time-invariant movement rates, equilibrium reference points can be derived by population or stratum assuming either global or local density-dependence in recruitment dynamics (Porch, 2018; Kapur et al., 2021; Cardinale et al., 2023).

### *2.2 Spatial data integration*

A variety of unique data types can provide information on spatial processes (Punt et al., 2019b; Goethel et al. 2023a), such as tagging data for migration pathways (Goethel et al., 2011; Sipple et al., 2015) or oceanographic data for drivers of movement (Malick et al., 2020). However, the utility, information content, and processes that can be informed by a given data source depend on how a platform integrates the information (e.g., the scale at which it is applied and assumptions utilized in the observation model; Punt, 2019b). All of the platforms allow integration of typical fishery and survey data (e.g., biological inputs, catch, abundance indices, and age- or length-composition data) by stratum or population (depending on population structure). Explicit data weighting options or iterative reweighting procedures (i.e., depending on assumed probability distributions) to account for uncertainty among data sets is also possible. External knowledge can be incorporated through the use of priors on specific parameters or bounds. Examples of novel spatially-explicit data sources that can be integrated into assessment platform include stock composition information (Casal2, Gadget, SS3, and VPA 2-Box), environmental covariates (MFCL, Gadget, and SS3), and predation information (Casal2, Gadget, and SS3).

### 2.2.1 Tagging data

Tagging (e.g., conventional, genetic, or chemical) data is one of the most common auxiliary data sources used in spatial stock assessments, which can help inform mortality, distribution, connectivity, or abundance. There are some key differences among platforms in how these data are used to inform population dynamic processes. All platforms utilize the Hilborn (1990) tag-attrition modeling approach, which models tag cohorts (i.e., a combination of release stratum, population unit, and age or length) through time using a spatial Brownie estimator. Observed recaptures across space are predicted based on mortality and movement estimates by fitting the tagging data in the combined objective function. Casal2 can also utilize a Petersen estimator to directly inform predictions of absolute abundance (i.e., population scale; Doonan et al., 2016). Casal2, Gadget, and MFCL additionally allow age to be assigned implicitly through size-age matrices and growth parameters. When using conventional tagging data, all platforms use release-conditioned tagging sub-models (as opposed to recapture-conditioned approaches; McGarvey et al., 2010). This implies that spatially-explicit recapture probabilities are a function of the number of releases in each stratum or population-unit (Punt et al., 2020). Tag recaptures are then defined by spatially-explicit fleet dynamics (i.e., fleet-specific fishing mortality and associated selectivity).

Software that integrates tag-recovery data (or mark-recapture data more generally) into a stock assessment must include methods to adequately account for tag model 'nuisance' parameters (i.e., tag non-reporting rate, tag shedding rate, and tag-induced mortality) and tag mixing assumptions to ensure inference from tagged individuals is representative of non-tagged individuals (Goethel et al. 2019). All platforms have the capability to address these needs by incorporating additional tag parameters that may be input or estimated. For instance, tag reporting rates can be input or estimated (e.g., with priors) by fleet and stratum for all platforms. Reporting rates may also vary by tag cohort (Casal2) or tagging program (MFCL) when multiple tagging experiments have been conducted. Casal2 can model the recapture process based on a detection probability defined by user inputs for the number of fish that were scanned for tags and the rate of detection. The detection probability can be based on a subset of the catch and can be fleet or strata specific. Each platform also allows specification of tag loss due to initial tag shedding, tag-induced mortality, or chronic tag loss. Incomplete tag mixing can be accounted for by adjusting fishing mortality for recently tagged fish (Casal2, MFCL, and VPA 2-Box) or defining a mixing period during which recaptures are not fit (Casal2 and SS3). For MFCL, the fishing mortality for tag recaptures during the mixing period, which can be specified by release cohort, is determined using numerical methods (e.g., Newton-Raphson) in a similar way as is commonly done to evaluate models conditioned on a given catch.

The structure of tagging sub-models in stock assessment, such as distributional assumptions and the capacity to pool tag recoveries, can influence estimation and computing overhead. For example, MFCL and SS3 allow the user to specify a maximum time at liberty before tags enter a pooled state where cohort is no longer tracked to improve run times. SS3 requires the assignment of age-at-release, instead of modeling multiple ages based on length-at-release, as is the case for MFCL. Platforms have different options for specifying the probability distribution assumptions (i.e., likelihood functions) used for mark-recapture data, including binomial (Casal2), negative binomial (MFCL, SS3, and VPA 2-Box), Poisson (Gadget, MFCL, SS3, and VPA 2-Box), or multinomial (MFCL, SS3, and VPA 2-Box).

Although not as commonly integrated, other tag types (e.g., satellite, telemetry, natural, or gene) can be incorporated using existing mark-recapture frameworks within each platform, but they require alterations to data format (e.g., Taylor et al., 2011). For example, it may be required to aggregate information by cohort and time step in the assessment when using satellite tags. Otherwise, simplifying assumptions may need to be devised, such as assuming 100% reporting for genetic tags. VPA 2-Box is the only platform that explicitly includes a generalized tag-attrition model that differentiates the fitting procedure for satellite pop-off tag observations and conventional tag release and recoveries.

*2.3 Spatial modeling options*

2.3.1 Population and spatial structure

All platforms are capable of accommodating a panmictic (i.e., single population) structure, along with at least one other spatially-defined population structure (Table 3). For instance, all platforms except VPA 2-Box are capable of modeling spatial heterogeneity within a single population paired with a global density-dependent recruitment assumption. In fact, the majority of spatially-explicit models used for management advice assume a single population with spatial heterogeneity (Punt, 2019a,b).

Both MFCL and SS3 only allow a single population with or without spatial heterogeneity. However, the development pathways for MFCL and SS3 were quite different. MFCL was designed for highly migratory large pelagic species, where most spatial models have directly incorporated post-settlement connectivity (e.g., western and central Pacific Ocean yellowfin tuna, *Thunnus albacares*; Vincent et al., 2020). Conversely, SS3 was initially designed for Pacific hake in a natal homing context (Methot and Dorn, 1995), and has been more widely implemented for demersal species where adult connectivity is often ignored (e.g., Gulf of Mexico red snapper, *Lutjanus campechanus*; SEDAR, 2018). However, SS3 has been increasingly applied to migratory species with movement estimated (e.g., Indian Ocean yellowfin tuna; Fu et al., 2021). For both MFCL and SS3, the inability to incorporate local density-dependence in stock-recruitment functions has been identified as a primary limitation.

MFCL and SS3 cannot fully accommodate either metapopulation or natal homing structures, given the inability to model local density-dependence. However, for assessments that do not use a spawner-recruitment relationship, the capability to incorporate time-varying apportionment of recruits among strata may compensate in MFCL and SS3 for the lack of strata-specific density-dependence because the apportionment parameters can be density-dependent in response to global abundance. SS3 can accommodate natal spawning groups (or other specified population contingents, termed 'morphs') with unique demographics. However, all morphs are derived from a global stock-recruitment relationship and subsequently apportioned (input or estimated) across spatial strata. Thus, natal homing dynamics can be partially emulated in SS3 by assigning a different morph to each natal stratum and applying a seasonal model structure to create a seasonal movement pattern between breeding areas and feeding areas.

Gadget and Casal2 have the greatest flexibility in population structure. In addition to spatial heterogeneity within a single population, Gadget can also model metapopulations, whereas CASAL2 can accommodate natal homing. Both platforms can incorporate either local or global density-dependence in productivity based on the assumed population structure. CASAL, the precursor to Casal2, was initially developed for demersal species around New Zealand and then extended to include natal homing dynamics (e.g., New Zealand snapper, *Pagrus auratus*; Francis and McKenzie, 2015). Gadget was developed for pelagic and demersal species in Europe, which required integrating metapopulation structure (Stefánsson and Pálsson, 1997). Both natal homing and metapopulation structure require population unit specific stock-recruit functions. The associated local density-dependence assumption for recruitment might have important implications when developing biological reference points and associated catch recommendations (Goethel and Berger, 2017; Kapur et al., 2021).

As a result of the mathematical limitations inherent in VPA frameworks, VPA 2-Box is limited to modeling a maximum of two population units. However, VPA frameworks, in general, do not implement an explicit stock-recruit function, because a backward recursion calculation through time and age is utilized. Nonetheless, projections using the companion Projection 2-Box (PRO 2-Box) can assume a population unit specific stock-recruit function for the available metapopulation or natal homing structures (ICCAT, 2003).

Aside from VPA 2-Box, all other platforms are theoretically scalable to any number of strata (and population units for Casal2 and Gadget), but these will be effectively limited by data and computing power. Currently, the maximum number of spatial strata used in an operational assessment are 4, 6, and 9 for Casal2, SS3, and MFCL, respectively (Langley and Methot, 2008; Doonan et al., 2016; Day et al., 2023). All platforms can incorporate strata closed to fishing (e.g., marine reserves) within the confines of available population structures. Explicitly modeling the dynamics within closed areas may be difficult, though, if a fishery-independent survey (or other closed-area data set) is not available (McGilliard et al., 2015).

Each platform provides a unique set of options for parametrizing and estimating dispersal and movement. Options may be constrained pending decisions about population structure (e.g., natal homing spawning migrations are only possible in a natal homing model; Table 3). All platforms use a box-transfer sub-model for connectivity with the assumption of instantaneous movement rates at the start or end (SS3) of the time step. Spawning migrations are directly incorporated into platforms that can handle natal homing population structure (Casal2 and VPA 2-Box) to enable natal return to spawning populations. For these models, natal spawning migrations are enforced at a specific age and time such as instantaneously in the middle of a time step, resulting in the need to estimate only non-spawning mixing rates (i.e., the degree of overlap among natal populations in a given stratum based on estimated migration rates out of the spawning area). Dispersal among populations can also be input or estimated in both Casal2 and VPA 2-Box , which results in small amounts of reproductive mixing among natal populations. For the metapopulation version of VPA 2-Box and Gadget, dispersal (or reproductive mixing) among sub-populations is implied when fish move to another population-unit. All platforms also allow for larval dispersal via recruit apportionment (i.e., under the assumption of global density-dependence in stock-recruit dynamics). SS3 and Casal2 are the only platforms that enable estimation of age-0 movement, because population dynamics begin at birth, whereas most other models begin at the age of recruitment to the fishery.

All platforms allow estimation of time- and age- or length-variation in movement parameters, and each includes parameter blocking or functional form options to reduce parameter load (Table 3). For example, simplifications for age-based connectivity include using a linear ramp (MFCL and SS3), ogive or logistic relationships (Casal2 and MFCL), and/or partition-based (e.g., immature compared to mature age classes) preference functions linked to depth, distance, density, or other habitat variables (Gadget). Casal2 and SS3 also have the ability to model density-dependent connectivity (e.g., relative to population density). The general movement formulation for most platforms (besides MFCL) is a gravity model, which estimates residence diagonals of the movement matrix and then derives movement off-diagonals from all residence-gravity parameters to reduce the number of estimated parameters (as compared to the traditional box-transfer approach; Carruthers et al., 2011; Punt, 2019b). MFCL uses a unique, implicit transition matrix, which first estimates connectivity among adjacent strata. Connectivity among non-adjacent strata is then implicitly calculated if connectivity occurs among common strata (e.g., if connectivity occurs between a stretch of adjacent strata, then connectivity will also occur between the non-adjacent strata in that stretch; Kleiber et al., 2018; Punt, 2019b), thereby reducing the number of parameters to be estimated.

All platforms allow for spatially-invariant demographics, but only some (Casal2, Gadget, and VPA 2-Box) allow the analyst to switch between tracking phenotypic- and genotypic-based differences among strata (Cadrin et al., 2023). Spatially-invariant demographics are often assumed to avoid complications resulting from movement across demographic regimes (i.e., changes in growth or maturity as fish move between strata or join new population units). When a natal homing structure is assumed (as available in Casal2 and VPA 2-Box), demographics are often linked to genetic population and do not change based on stratum occupied. For Casal2, a partition category must be defined for each natal origin stratum to ensure that individuals can be tracked by their origin population as they move across space and through time. For Casal2, Gadget, and VPA 2-Box, demographic parameters can be linked to stratum in a spatial heterogeneity model structures or sub-population in a metapopulation model structure, where the new demographic regime is instantaneously adopted once a fish moves to the new unit.

### 2.3.2 Fleet spatial structure

Across platforms, fleet structure is defined by known (i.e., observed) fleet dynamics and data availability, then linked to the number of strata or population units modeled. Each of the platforms has the ability to include multiple fleets (with theoretically no upper limit to the number that can be specified by stratum), and most can include an unlimited number of abundance indices. VPA 2-Box is the most constrained of the five platforms, because data (e.g., the catch-at-age matrix) from multiple sectors or countries must be combined into a single stratum-specific matrix (i.e., multiple fleets or surveys must be aggregated by population unit). All the other platforms allow fleet-specific parameters to vary by stratum or to share parameters (e.g., selectivity) for common fleets across strata. However, a single fleet cannot technically operate across multiple strata (except in Casal2), because a new fleet must be defined for each stratum with associated strata-specific observed and predicted values. However, sharing or mirroring parameters for a specific fleet across multiple strata effectively emulates a single fleet operating across multiple strata. On the other hand, multiple fleets within a stratum are common (e.g., in Casal2, MFCL, and SS3), especially for large pelagic assessments. In application, a degree of aggregation is often necessary (e.g., across gear types within a sector or across countries within a gear type) due to limited sampling of length- or age-composition in many high seas fisheries.

### 2.3.3 Biological reference points

For the calculation of biological reference points, all platforms make similar equilibrium assumptions regarding spatial dynamics (e.g., movement, recruit apportionment, and relative removals by fleet are based on average values from a specified time block and held constant for the projection period). Many platforms can also calculate multiple types of biological reference points (e.g., MSY- or depletion-based), and some platforms calculate them as strata- or population-explicit (MFCL and Gadget). PRO 2-Box, the extension to VPA 2-Box for implementing projections, similarly allows for a single reference point for the entire domain or population unit-specific reference points. SS3 calculates domain-wide reference points, while accounting for spatial dynamics and reporting stratum-specific depletion estimates. However, global density-dependence is assumed for all platforms that model spatial heterogeneity structure and implement strata-specific reference points (MFCL and SS3 along with spatial heterogeneity implementations of Casal2 and Gadget). Otherwise, local density-dependence is assumed when population-specific reference points are calculated for metapopulation and natal homing implementations of Casal2, Gadget, or VPA 2-Box using PRO 2-Box. Typically, spatially-aggregated reference points are then calculated by summing population-specific values (e.g., $B_0$ values as in Casal2) or performing a domain-wide yield- or spawner-per-recruit analysis using a weighted average (across population units) of the biological parameters (e.g., as in PRO 2-Box).

2.3.4 Platform selection and development

No current platform can address all (or even most) of the possible formulations across the primary decision-points for a spatially-explicit stock assessment (see section 2.1; Table 2). For instance, none of the platforms can incorporate every common type of population structure or movement pattern. Thus, when developing a spatial assessment, a platform should be chosen that can incorporate the available data, address the spatial drivers and primary uncertainties for the species being modeled, and produce outputs in a format that coalesce with the given management framework. In general, there are tradeoffs among platforms between population structure and connectivity complexity (Fig. 2). Casal2 and Gadget can be useful options when local density-dependence needs to be addressed when metapopulation or natal homing population structures exist. Conversely, MFCL and SS3 are likely to be useful modeling options when global density-dependence can be assumed. Casal2 and SS3 tend to allow for more complexity in connectivity options (e.g., age-0 movement and natal homing migrations, respectively). VPA 2-Box is constrained in terms of flexibility in spatial structure to a maximum of two modeled population units and options for movement dynamics. However, it is the only platform that can accommodate both metapopulation and natal homing population structure. Additionally, VPA 2-Box is the quickest of the platforms to initialize and provides a useful research tool for explorations of spatial dynamics (e.g., a comparison tool against single population assessments, such as for Atlantic bluefin tuna, *Thunnus thynnus*; Cadrin et al., 2019).

Many of the reviewed platforms have been in development for a decade or longer and undergone iterative refinements to keep pace with research and development needs (Punt et al., 2020). While many developmental features have yet to be used in operational applications, they highlight research priorities that can be achieved in the near-term. In particular, current research and development of spatial modeling features provides a window into future platform capabilities, opportunities, and ensuing challenges for next generation stock assessments (Table 3; Fig. 3).

## 3. Current challenges implementing spatial stock assessments

Despite the successful application in a few operational management settings (e.g., Indian and Pacific Ocean highly migratory species; Punt, 2019a), considerable challenges remain for broader adoption of spatial stock assessments. We highlight major challenges that remain, with emphasis on common issues noted across platforms.

### *3.1 Lack of appropriate generality*

Next generation assessment platforms need to be developed where spatial population structure and associated spatial dynamics are a primary consideration from the outset (with the ability to aggregate to one-strata panmictic assessments; Goethel et al., 2023a). Spatial structure is not always a primary consideration during initial platform development (except in a handful of instances), resulting in reactive developmental adaptations to spatial processes that govern stock dynamics. The development of new platforms should be fully flexible to accommodate all common population structures and enable modular additions and new parametrizations (e.g., connectivity modeling options).

Bespoke spatial stock assessment models (e.g., Taylor et al., 2011; Punt et al., 2017; Goethel et al., 2019, 2021) are useful and often necessary research tools to guide the development of next generation assessment platforms. However, emphasis must be placed on overcoming the tendency to solely design bespoke spatial assessment frameworks, because they are often developed in isolation for a specific species or region, and have limited or specific dimensionality. Further, this can lead to a lack of communication within the modeling community, thereby limiting synergistic research and development opportunities. Improving communication and knowledge sharing when developing spatial assessments is necessary to further operational applications (Goethel et al., 2023a). Next generation platforms will need to be well documented, reproducible (i.e., use open source code), and provide tutorial examples of spatial applications to ensure that potential analysts can implement spatial models and develop new modular code, as necessary, to fit specific and unique spatial dynamic applications.

### *3.2 The challenge of too much or too little data*

Overcoming the curse of dimensionality (Bellman, 1961), while concomitantly ensuring parsimonious model parameterizations, remains an obstacle when constructing models with increasing spatial (and temporal) dimensions (Cope and Punt, 2011). For instance, the number of pairwise connectivity parameters increases proportional to the square of the number of units modeled. State-space methods can help reduce the parameter load associated with increasing model resolution, but have yet to be widely implemented for spatial stock assessments. Rapidly increasing scientific and technological advances along with associated decreases in collection costs for many data types have helped to improve understanding of spatiotemporal dynamics for marine species (Goethel et al., 2023b). Non-traditional data types (e.g., electronic tags, omics, vessel monitoring systems, and citizen science data) are often spatially-explicit, and should be integrated into spatial assessment models in the near future (e.g., Taylor et al., 2011; Oremland et al., 2022).

Theoretically, tag data can provide important information on growth, abundance, mortality, and movement. Medium- to long-term tagging data sets can be informative about changes in biological processes over time, potentially enabling estimation of spatiotemporal variation in assessment parameters. However, most tagging studies are unable to uniformly release tags across a species' range, which can possibly lead to large (and hard to detect) biases (Kolody and Hoyle, 2015). Given the importance of conventional tagging data for informing spatial assessments, improving methods to account for tag non-reporting, tag loss or mortality, and incomplete mixing need to be a research priority (e.g., Goethel et al., 2019). New tagging approaches that reduce or eliminate common biases from unmet design-based methodological assumptions need to be incorporated into stock assessment model workflows and associated objective functions (e.g., genetically-based mark recapture techniques and spatiotemporal movement models; Skaug, 2001; Bravington et al., 2016; Mildenberger et al., 2023).

The decomposition of a stock into defined spatial components, such as individual populations or strata, can introduce data complications. While the spatial resolution of some fishery monitoring data has improved in recent years and supports stratified or more continuous spatiotemporal approaches to assessment modeling, historical fishery data typically has lower spatial resolution leading to increased model structure uncertainty or ad hoc spatial assignments. On the other hand, fishery independent surveys tend to be spatially explicit but have less spatial density and limited seasonality. The spatial integration of biological samples (e.g., size at age) and stock composition information needs to be considered for metapopulation and natal homing population structures but is often not straightforward (Taylor et al., 2011; Punt et al., 2020; Goethel et al., 2023a).

*3.3 Challenges with the management and review process*

Operational use of spatial assessments for management decision-making requires the calculation of spatial reference points. However, equilibrium assumptions that have traditionally formed the basis for reference point calculations become tenuous when spatial population dynamics are modeled, especially connectivity. Closed-form solutions for stratum-specific or population-specific MSY-based (or proxies thereof) reference points are feasible under assumptions of constant movement and other time-averaged (e.g., recent prevailing conditions) biological and fishery parameters (Porch et al., 2018; Kapur et al., 2021). Similarly, long-term simulations can be implemented to identify the fishing mortality that achieves a spatially-aggregated MSY (e.g., Goethel and Berger, 2017). However, additional considerations and potential complications exist for the calculation of spatial reference points, which are not necessarily present in spatially-aggregated approaches. For instance, connectivity among strata often impedes the ability to achieve a constant reference point for multiple strata or population units simultaneously (Goethel and Berger, 2017; Bosley et al., 2019; Kapur et al., 2021). There is rarely a unique solution for attaining maximum sustainable yield across multiple spatial strata, because multiple combinations of fleet- and stratum-specific fishing mortality rates can achieve nearly identical levels of total yield (Bosley et al., 2019). Accordingly, additional strata-specific management objectives would be required to obtain unique and tractable solutions.

Summarizing fishing mortality rates across spatial units is not straightforward, yet it is often a required metric for management action (e.g., fishing mortality is often a fundamental aspect of reference points or harvest control rules). No single measure of overall fishing mortality across all fleets and strata exists for spatial models that sufficiently represents fishing intensity. Langseth and Schueller (2017) contrasted several alternative approaches for synthesizing spatial fishing mortality estimates using simulation, which highlighted that considerable differences in projected stock status occur depending on the fishing mortality metric utilized and the relative sizes of the strata. While the development of a spatially-integrated fishing mortality metric for management remains an unresolved issue, further testing within a management strategy evaluation would be informative (Langseth and Schueller, 2017).

Similarly, when assessment strata boundaries differ from management strata boundaries, resulting reference points may be incompatible or irrelevant for operational use. For instance, a common approach has been to apportion catch from a single-stratum panmictic assessment to multiple management strata. However, apportioned catches may not align with local dynamics, resulting in localized depletion within some management strata (Bosley et al., 2019). A priority focus should be to resolve inconsistencies across population, management, and policy dimensions to avoid unintended consequences (Freire and García-Allut, 2000; Cope and Punt, 2011; Kerr et al., 2017; Berger et al., 2021), and align outputs with the spatiotemporal scales that best reflect management objectives.

Overcoming institutional inertia also remains a paramount challenge to advancing the operational use of spatial stock assessments for the provision of management advice (Berger et al., 2017a,b). The process by which scientific advice is developed, presented, and used by fishery managers has historically been slow to change, and adoption of new scientific methods can be time-consuming. The need for annual harvest specifications informed by stock assessments is often an additional obstacle to the development, testing, and application of complex spatial stock assessment models. Therefore, there needs to be sufficient capacity or training opportunities to enable adequate peer review of new spatial models as well as well-defined processes for the development of spatial assessments within the constraints of existing assessment cycles (Goethel et al., 2023a).

## 4. Recommendations for good practices and the next generation of spatial assessment platforms

Software design and modeling capabilities of next generation stock assessment platforms need to incorporate input from the global stock assessment community to build upon lessons learned and leverage research and developmental advancements (Hoyle et al., 2022). Here, we expand on Hoyle et al. (2022) and provide a set of good practice recommendations for developing spatial assessment platforms based on our review of current spatial capabilities (section 2), identify gaps and insufficiencies, and highlight general spatial modeling recommendations (e.g., Punt et al., 2020; Goethel et al., 2023a). From a holistic design perspective, we focus on considerations that emphasize incorporation of spatial options from the onset of model development (Table 4). Although often overlooked, we recommend continued development of a common nomenclature (e.g., Table 1) as a first step when developing next generation stock assessment platforms to ensure unified understanding across frameworks, regions, and disciplines (e.g., Wetzel et al., In Review).

### *4.1 Space – A basic (if not 'the') principle of design*

Space is the footprint within which we interpret ecological function and patterns over time, and there is "no single scale at which models should be constructed" (Levin, 1992). The development history of many assessment platforms has highlighted that spatial structure should be a foundational design consideration for next generation frameworks (Goethel et al., 2023a). From a flexible coding perspective, it is much easier to implement (and adapt) a model structure that starts with the most disaggregated spatial structure, then allows for aggregation of data or implementation of models at lower resolution, as needed. The same logic applies to population and partition structure, because allowing for the most complex partitioning from the outset allows for straightforward aggregation to less complex population structures (e.g., aggregation across natal strata for metapopulation or spatial heterogeneity structures). Spatial flexibility will require a fully generalized stock-recruit function, which allows for global or local density-dependence and spatiotemporal variability in recruitment (i.e., recruitment deviations and apportionment; Punt, 2019a). The ability to implement multistage stock-recruit functions (e.g., Brooks et al., 2019) would also be beneficial. Integrating spatial structure across the life cycle would enable explicit modeling of larval connectivity and dispersal dynamics that are a primary driver of metapopulation structure (e.g., Goethel et al., 2011; Archambault et al., 2016) and a critical component of the reproductive resilience paradigm (Lowerre-Barbieri et al., 2016).

### *4.2 Modularity and software development good practices*

Future platforms should be designed using software development good practices (e.g., including unit tests and post-compile model checks to validate the source code) and managed collaboratively by individuals with a background in software engineering, open-source tools, and project development (Hoyle et al., 2022). Enhancements should come from open-source contributions by an interdisciplinary development team to ensure that model capabilities transparently plan for evolving needs, improving ecological knowledge, and novel data sources. Resources will also be necessary to ensure that documentation of platform capabilities, available methods, and worked examples remains up to date. A user-friendly interface will also facilitate understanding of data input and modeling option layouts and specifications. Workflows should include rapid, automated model summaries, diagnostics, and management outputs in graphical and tabular form to streamline productivity and improve assessment completion timelines (Hayashi et al., 2021; Goethel et al. 2023a).

Modular programming, or utilizing a network of independent functions that are easily interchangeable, adaptable, and flexible to evolving needs, will be essential for evolving platform maintenance and developmental needs. This is particularly necessary when considering flexibility in the spatial and temporal model domain to facilitate explorations of alternative model configurations, performance, diagnostics, and parsimony across a spatiotemporal continuum. Flexibility is paramount because it is difficult to predict how new ecosystem-level information will translate to spatial modeling and management needs, especially given climate change. Hence, a modular framework wherein partitions can be readily added and new spatial parametrizations coded (e.g., spatial linkages within connectivity preference functions) is necessary to ensure modeling tools remain effective, efficient, and have an extensive shelf life (Punt et al., 2020). Methods for parallelizing optimization routines and resources to simultaneously run multiple models (e.g., model ensembles or sensitivity explorations) to reduce computational time must concomitantly be improved (Punt et al., 2020; Hoyle et al., 2022).

4.3 *Efficient exploration of alternative spatial configurations*

Developing code that can efficiently implement multiple spatial structures will be necessary to conduct sensitivity or robustness tests and characterize structural uncertainty. Ideally, platform design should include the capacity to explore and simulation test hybrid and multi-scalar model structures, where the full complement of stock assessment types (i.e., spatially-aggregated, areas-as-fleets, spatially-stratified, and spatiotemporal; Goethel et al., 2023a) could be implemented. The ability to nest a fine-scale spatiotemporal sub-model within an overarching spatially-stratified population model would enable fitting high-resolution tagging data at the scale it was collected to better inform estimates of movement parameters (e.g., Thorson et al., 2021). Nested, or hierarchical, spatial designs are conducive to integrating data types and population dynamics that act at fine (e.g., connectivity) and coarse (e.g., reproductive mixing) resolutions (Cao et al., 2020; Punt et al., 2020).

The application of contemporary statistical methods to stock assessment models can also offer considerable gains in efficiency, practicality, and parsimony. For example, state-space methods offer flexibility with parameter estimation, especially for space- or time-varying demographic processes (e.g., movement; Stock and Miller, 2021). The Woods Hole Assessment Model (WHAM; https://github.com/timjmiller/wham) currently includes state-space features, but does not yet contain spatial capabilities (though a spatial Beta version of WHAM is in development; T. Miller, pers. comm.). Future research should explore how best to incorporate spatial processes and data collection at multiple, interacting resolutions. One avenue of exploration is the use of artificial intelligence (AI) through machine learning to explore hidden geostatistical structures and efficiencies in large data sets (De Iaco et al., 2022).

4.4 *Improved connectivity parametrization*

Designing a robust, flexible, and efficient set of connectivity parametrizations is recommended to promote broad use of spatial data and assessment options, because connectivity is typically one of the most difficult spatial population dynamic features to estimate. For example, increased utilization of preference functions and connectivity kernels that can generate a wide-range of pairwise connectivity values with comparatively few parameters represents a potential solution. Connectivity information derived from preference functions are related to information content, such as *in situ* or remotely-sensed environmental data described in geographic layers, and thus can remove the scale-dependency issues inherent with estimating discrete box-transfer connectivity parameters (Goethel and Cadrin, 2021; Thorson et al., 2021). A generalized connectivity parametrization based on preference functions and connectivity kernels needs to satisfy several requirements:

1) Integrated – applicable to both Lagrangian and Eulerian structures so that integrated models can include individual-tracking (i.e., Lagrangian models for individual archival tags) and density-tracking (i.e., Eulerian models for point-count samples) components;
2) Versatile – the ability to incorporate a combination of three distinct connectivity processes:
    a) Passive advection: undirected transport following an ocean or tidal current;
    b) Taxis: directed movement of individuals towards preferred habitat, as learned behaviorally or ingrained evolutionarily based on local and past information, as well as behavioral cues and capacities; and
    c) Diffusion: residual and otherwise unexplained movement of Lagrangian particles away from a given location or Eulerian densities away from a grid cell;
3) Scalable – data fitted at multiple spatiotemporal scales using the same structure and parameters across those scales (e.g., hours-to-days for 1-100m scales for acoustic arrays and predation experiments; days-to-months at 100m-10km scales for archival and electronic tags; and months-to-years at 10km-1000km scales for population or community models);
4) Tractable – can be implemented with differing numbers of parameters (parsimony) and modular (flexible);
5) Interpretable - defined according to ecological processes or theory such that research (targeted laboratory and field experiments) and monitoring (long-term surveys) can be used to identify model performance and applicability; and
6) Functional – can be applied as an estimation model (i.e., efficiently calculate the inverse-probability and using Bayesian or maximum likelihood methods to identify parameters conditional upon data) or an operating or projection model (i.e., sample from connectivity probabilities while projecting dynamics forward through time).

Resource selection functions (RSFs) and potential functions (PFs) are analytical approaches that satisfy all of these requirements. With the former, movement probability between two time-steps is defined as the product of a preference component (i.e., representing whether a given location is preferred or not) and an availability component (i.e., representing constraints about movement distance given speed as well as physical barriers; Manly et al., 2002). Diffusion is represented via the availability component, while passive advection and taxis are represented via the preference component of the RSF (Johnson et al., 2008). For the PF parametrization, movement probability is defined by integrating movement processes using a stochastic differential equation within a reaction-advection-diffusion model. In this case, taxis is defined as advection along the gradient of a PF, which is itself typically estimated as a function of covariates (Brillinger, 2012; Thorson et al., 2021; McClintock et al., 2021). Both approaches are functionally similar as the time-interval approaches zero, but they differ for practical applications as modeled time intervals increase. Both also define taxis based on environmental layers and a reduced set of habitat preference parameters, which can greatly reduce model complexity relative to estimating pairwise movement rates between every modeled location (Lehodey et al., 2008; Mormede et al., 2017; Thorson et al., 2021). Next generation platforms should strive to incorporate these approaches, in addition to more common functional forms, to enable connectivity modeling with fewer parameters and more direct habitat and ecosystem linkages.

*4.5 Improved integration of demographic change*

Transitions among demographic regimes are complex and can be a nuisance (at best) or intractable (at worst) in spatial assessments owing to the interactive nature of population structure, demographic gradients, and connectivity across the spatial domain. A first step to improve modeling of spatially-explicit biological parameters is a better understanding of the environmental forcing variables that influence changes in demography. With continued investments and associated advancements in the field of omics, tools to disentangle genetic and phenotypic contributions to observed demographic patterns will lessen the need to make uninformed assumptions about spatial demography and lead to improved spatial assessments. For instance, modeling spatially-varying growth will likely require additional model partitions (e.g., tracking natal population, current stratum, length, and age), which would allow tracking maximum size by stratum (or population) and enable calculating growth increments as individuals move among strata (Punt, 2019a). Similar approaches could be used for other demographic parameters, such as maturity, though computing resources can drastically increase with the number of model partitions as noted for integrated length-age models that additionally partition by numerous tag release events (e.g., MFCL-based tuna assessments). Alternatively, weighted averages of demographic rates can be applied to populations that overlap according to the source of variation (genetic, phenotypic, or both) if natal origin and movement are tracked in combination.

*4.6 Keeping pace with novel data*

The estimation of spatial population parameters requires increasing amounts of informative data as nonstationary processes are uncovered at finer-scales. Next generation spatial platforms need to be amenable to incorporating novel data sets (e.g., information on connectivity; White et al., 2019), as well as novel methods that use traditional data sets, to inform the suite of spatial model features that should be considered (Table 4; Goethel et al., 2023b). For instance, vessel monitoring systems can provide high-resolution information on spatial patterns in fishery removals, which can be linked to habitat or environmental features (e.g., Gardner et al., 2022). Unstaffed or remotely-operated vehicles can collect a suite of fishery-independent data, including video- or acoustic-based indices of abundance and oceanographic data (e.g., de Robertis et al., 2021; Bolser et al., 2023). Self-reported digital data and citizen science information can help improve catch statistics and biological samples across sectors and strata that may be difficult to otherwise sample. Local or traditional ecological knowledge can provide unique perspectives that help to refine model structure and hypotheses regarding system or fishery dynamics (e.g., Duplisea, 2018).

Omics data are well suited to help identify mixing rates (i.e., population composition data from otoliths or genetic samples) and high-resolution spatiotemporal distribution (e.g., from environmental DNA data). The recent development of close-kin genetic data to implement mark-recapture methods (Skaug, 2001; Bravington et al, 2016) seemingly has much potential to inform and improve spatial assessment models (Marcy-Quay et al., 2020). For instance, close-kin mark-recapture (CKMR) can provide estimates of absolute adult abundance based on genetic sampling, while providing estimates of other parameters, such as adult natural mortality and reproductive contributions. The genetic information used in CKMR can also be used to identify stock-structure and potentially even movement rates (Trenkel et al., 2022). Implementation of CKMR generally requires the use of a population dynamics model, so it is conceptionally amenable to being incorporated into a generalized stock assessment platform (see developmental features, Table 3). Alternatively, CKMR analyses could be conducted outside of the assessment model and the resulting population estimates fit by strata or population unit in a spatial population dynamics model (though careful consideration of uncertainty should be considered; Brooks and Deroba, 2015).

Flexibility in existing tagging sub-models will also be necessary, such that conventional tags can be modeled as either Petersen estimators or as tag-attrition models. The capability for either release or recapture conditioning, depending on tagging experiment design, could also help to minimize bias caused by partial-reporting, tag shedding, and tag-induced mortality (e.g., McGarvey and Feenstra, 2002; McGarvey et al., 2010). Spatiotemporal tagging sub-models are amenable to incorporating a variety of fine-scale data sets (e.g., electronic tag tracks, biotelemetry, operational oceanographic data, and habitat mapping), which can be used to parametrize connectivity preference functions within RSF or PF connectivity models (e.g., Marsh et al., 2015).

*4.7 Improve model performance diagnostics*

Diagnosing model performance and misspecifications are increasingly difficult as stock assessments become more complex (e.g., as the number of data sets or model partitions and strata increase). In a spatial context, analyzing data fits may not be feasible solely based on visual diagnostics, such as multi-dimensional residual patterns. There is an increased need to develop robust methods for data weighting that integrates information across the spatial domain with the increasing quantities and types of data used to support spatial models. Use of self-weighting likelihoods can help (e.g., Thorson et al. 2022), but more ad hoc iterative approaches will also likely need to be adapted (e.g., extend recommendations in Carvalho et al., 2017, 2021 to spatial situations). Determining model robustness as a function of model complexity will need to be routinely conducted using simulation testing, including an evaluation of variance-bias tradeoffs and considerations related to management implementation time lags. Recent recommendations to test the robustness of various model configurations to system or model uncertainties (Punt et al., 2020), such as with a management strategy evaluation (MSE), will be more readily realized by incorporating easily accessible simulation capabilities into next generation platforms. Ensemble modeling approaches that develop inference by integrating outputs from multiple plausible models to account for model structure uncertainties are likely to have an increasing role as management procedures include spatial processes (Stewart and Martell, 2015; Jardim et al., 2021).

*4.8 Embrace spatial reference points*

Next generation platforms need to embrace tiered or nested approaches to developing reference points. Spatial assessments, and related management procedures, can further complicate traditional reference point considerations because equilibrium assumptions can become even less tenable (though see Kapur et al. 2021), calculations rarely have closed form or unique solutions, and allocations of catch or ratios of effort are often specified by stratum as well as fleet. Existing approaches from the reviewed platforms include stratum- and population-specific depletion estimators, MSY-based approaches, SPR proxies, and multi-scalar methods that account for both domain-wide reference points and strata-specific depletion. Along with the optimization routine for local density-dependence developed by Kapur et al. (2021), these methods are likely adequate to support management in the near-term. However, next generation assessments need to consider alternate approaches such as empirical density or habitat-occupied approaches (e.g., Reuchlin-

Hugenholtz et al., 2015, 2016) to define reference points. Methods that account for nonstationary (or non-equilibrium) temporal dynamics need to be concomitantly examined across spatial strata. It is expected that increased application of spatial assessments and easier implementation of MSE frameworks that incorporate spatial dynamics will accelerate the movement away from solely using equilibrium- and model-based reference points towards minimally complex management strategies based on directly measurable empirical or hybrid indicators (e.g., CKMR abundance estimators; Hillary et al., 2019; Goethel et al., 2023b).

**5. Conclusions**

Spatially-explicit stock assessments can represent a stepping stone towards ecosystem-based fishery management (Plaganyi et al., 2014; Karp et al., 2019). Research investments are warranted for spatial assessments that increase awareness of the impacts of climate on species redistribution, examine the implementation of marine protected areas, identify local changes in abundance (i.e., 'localized depletion'), and elicit the explicit biotic and abiotic spatial-linkages that drive ecosystem processes and function (Cury et al., 2003; Nye et al., 2009; McClure et al., 2023). Relatively few generalized stock assessment software packages support spatial modeling approaches, and those that do were largely developed in relative isolation to address the specific needs of a stock or region, with little cross-collaboration. The reviewed platforms demonstrate some similarities in general stock assessment features, but specific spatial capabilities differ in many instances. Overall, no single platform in use today is fully generalizable to all (or even most) of the common spatial population structures and connectivity dynamics required to broadly assess marine resources that exhibit spatial structure.

Based on our review of existing spatial model capabilities, it is recommended that next generation stock assessment platforms need to take a unified, modular software development approach that incorporates spatial layers (partitions or strata) as a foundational feature and are generalizable across common population and model structures. For example, a generalizable model should be able to implement spatially-aggregated and spatially-explicit models, while also enabling hybrid and multi-scalar sub-models. Utilizing the fundamentals of spatiotemporal approaches (e.g., spatial autocorrelation and random effects) will result in parametrization efficiencies that create space for the integration of high-resolution movement and tagging modules. Guidance on spatial stock assessment development and pragmatic workflows can help to overcome institutional impediments (Goethel et al., 2023a).

Increased collaboration in the assessment development community through open source and group efforts has aided knowledge transfer and refined good practices for stock assessment tools. For example, recent collaborative workshops have aimed to develop international good practices for stock assessment (e.g., those held by the Center for Advancement of Population Assessment Methodology, CAPAM; http://www.capamresearch.org/Workshops) and specifically spatial modeling (via a global simulation experiment aimed at identifying and disseminating good practices in spatial stock assessment; https://aaronmberger-nwfsc.github.io/Spatial-Assessment-Modeling-Workshop/; Goethel et al., In Review). Much of what has been learned through these international forums is guiding the development of new stock assessment modeling platforms that aim to incorporate a wide array of spatial capabilities (e.g., the Fisheries Integrated Modeling System; https://github.com/NOAA-FIMS). Ultimately, such efforts will help counter institutional inertia and increase operational application of spatial stock assessments to meet evolving marine resource spatial planning demands.

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## 8. Figures

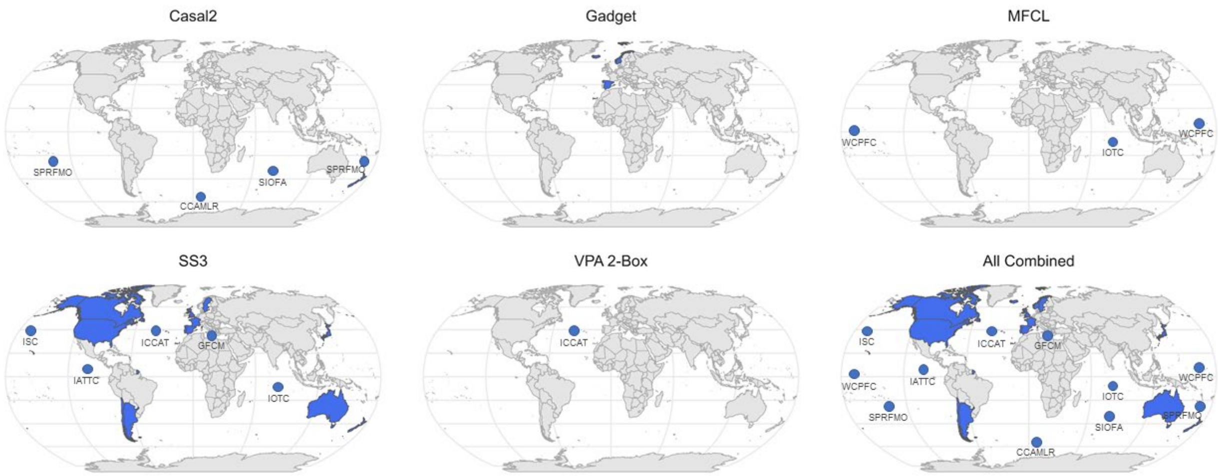


**Figure 1.** Countries (blue fill) and regional fisheries management organizations (RFMOs) or similar oceanic entities (blue dots) that have used Casal2, Gadget, MFCL, SS3, or VPA 2-Box to develop operational management advice. Coloration is a representation at the time of publication and not exhaustive due to widespread use of these platforms and changes over time. CCAMLR: Commission for the Conservation of Antarctic Marine Living Resources; GFCM: General Fisheries Commission for the Mediterranean; IATTC: Inter-American Tropical Tuna Commission; ICCAT: International Commission for the Conservation of Atlantic Tunas; IOTC: Indian Ocean Tuna Commission; ISC: International Science Committee for Tuna and Tuna-like Species in the North Pacific Ocean; SIOFA: Southern Indian Ocean Fisheries Agreement; SPRFMO: South Pacific Regional Fisheries Management Organisation; WCPFC: Western and Central Pacific Fisheries Commission.

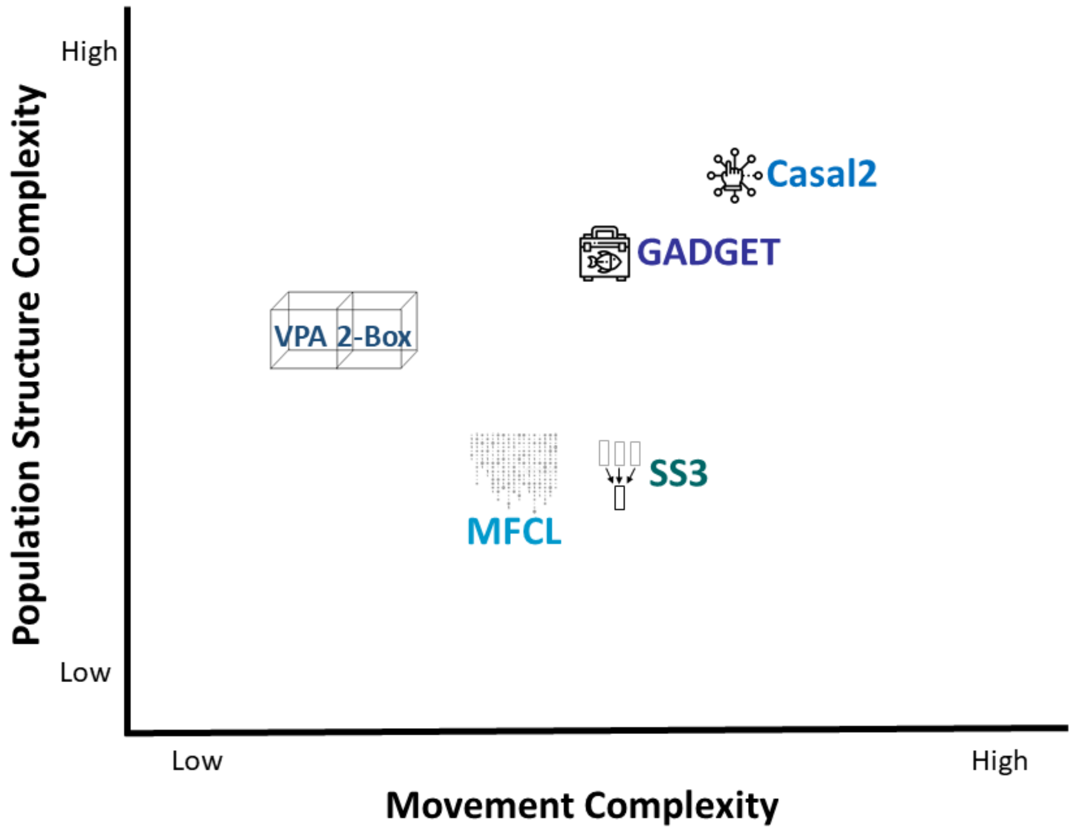


**Figure 2.** Conceptualization of tradeoffs between movement and population structure options for five assessment platforms that integrate spatial processes. Tradeoffs among other important drivers of spatial dynamics (e.g., recruitment, demographic variation, and fleet structure) are captured in Table 3. Symbols are shown for display purposes only and do not reflect trademarks or contain proprietary rights.

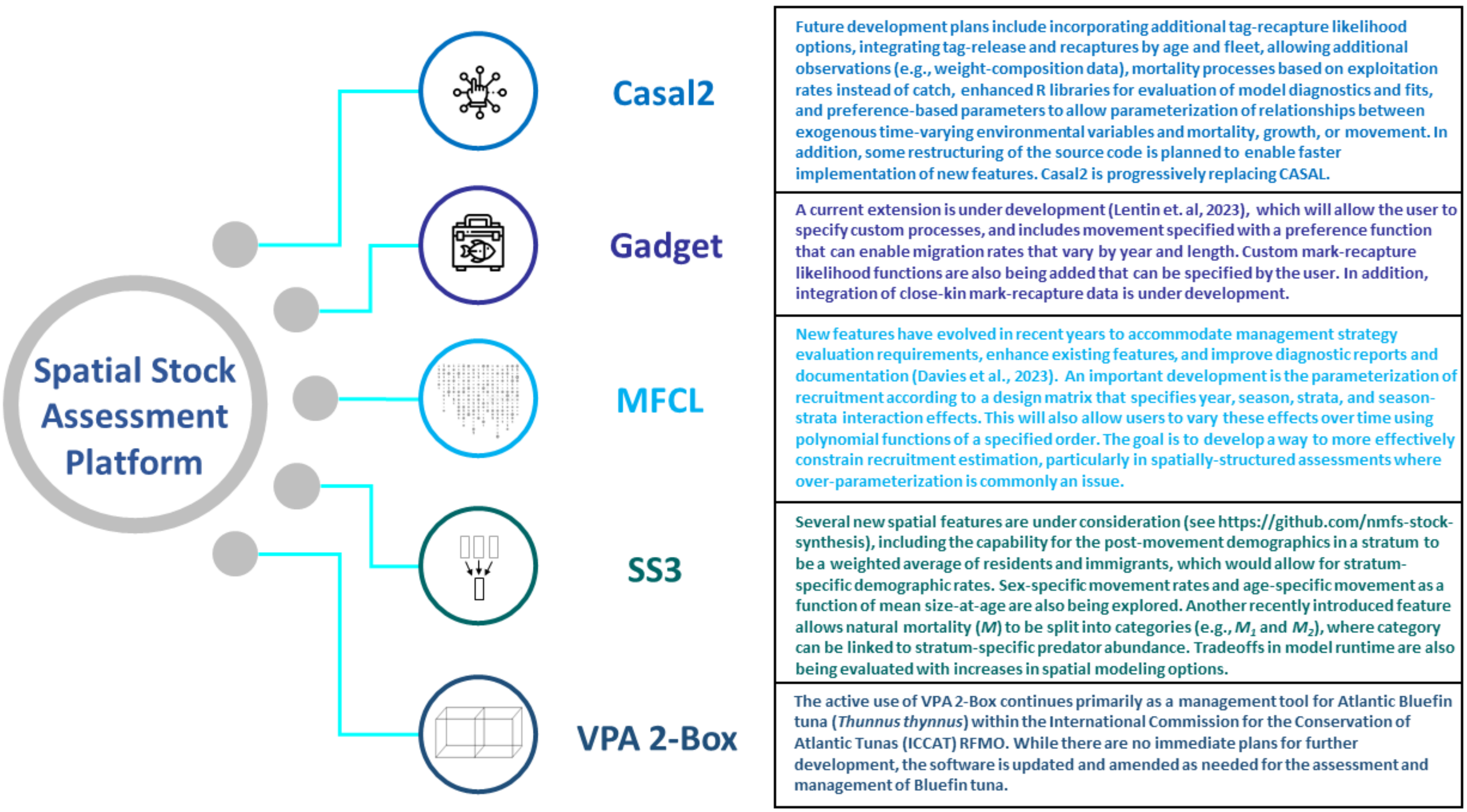


**Figure 3.** Select model features related to spatial dynamics that are under development for each platform. Many of these features may not yet be available in the publicly released versions of each platform. Symbols are shown for display purposes only and do not reflect trademarks or contain proprietary rights.

## 9. Tables

**Table 1.** Definitions of spatial terminology used throughout the paper.

| Term | Definition |
|---|---|
| Allocation | The partitioning of a total catch quota (or limit) from a spatially-aggregated or panmictic assessment model to specific strata or management areas. |
| Apportionment | The partitioning of population-level recruitment across sub-populations or other spatial strata. |
| Area-as-fleets | A type of spatially implicit stock assessment wherein multiple fleets are modeled to account for spatial differences in age or length structure across the population, usually due to spatiotemporal variability in availability (i.e., movement patterns) or selectivity (i.e., fishery patterns) across the biological domain. Also referred to as 'fleets-as-areas'. |
| Biological domain | The full spatial extent of a biological resource or species' range. |
| Connectivity | Demographic linkage between spatial strata or population units as a result of larval dispersal, directed migrations, straying, or mixing. |
| Dispersal | Connectivity resulting in transition to another population unit, which includes the exchange of genes through reproduction, typically in the form of larval dispersal or movement of juveniles or adults. |
| Local depletion | Overexploitation within a strata or sub-population (or other critical subset of the biological domain), which may have negative biological or economic impacts, but may not be detectable within a panmictic or spatially-aggregated assessment. |
| Metapopulation | Population structure wherein a network of interacting sub-populations exists, each with unique stock-recruitment relationships and quasi-independent demographics, but which demonstrate high rates of dispersal and reproductive mixing (i.e., often resulting in a single genetic population within a species). |
| Mixing | Connectivity resulting in multiple population units temporarily co-occurring in a spatial stratum (i.e., overlap associated with natal homing population structure). |
| Movement | Connectivity resulting in transition to and reproductive mixing with a new population unit (i.e., dispersal within a metapopulation) or transition to a new spatial stratum (i.e., within a single population with spatial heterogeneity). |
| Natal homing | Population structure wherein limited reproductive mixing occurs outside of a natal population and defined by return spawning migrations to natal spawning locations, often resulting in genetic populations within a species. Mixing often occurs amongst multiple genetic populations during non-spawning periods, but with very limited dispersal. Also, commonly referred to as natal return or overlap structure. |
| Panmictic | Population structure wherein a single, reproductively well-mixed population occurs for a species that demonstrates limited spatial structure or spatial dynamics. |
| Population | A self-reproducing biological entity within which all fish are able to reproductively mix and have the potential to contribute to recruitment, often resulting in a distinct genetic biological entity. Depending on whether demographics are genetically or environmentally determined, individuals may or may not share a common set of biological parameters. The population is often the demographic unit of concern for conservation. |
| Population structure | The degree and type of biocomplexity within a species resulting from connectivity, reproductive dynamics, and other processes that influence spatial ecology (e.g., ecosystem interactions). |
| Spatially-aggregated | In assessment nomenclature, a model that does not account for spatial dynamics (i.e., panmictic assessment). |
| Spatially-explicit | In assessment nomenclature, a model that mechanistically accounts for spatial dynamics (i.e., a spatially-stratified or spatiotemporal assessment). |
| Spatially-implicit | In assessment nomenclature, a model that accounts for spatial dynamics implicitly through the spatial assignment of non-spatial processes (i.e., areas-as-fleets). |
| Spatially-stratified | In assessment nomenclature, a coarse resolution spatially-explicit assessment model that models broad-scale population units or spatial strata assuming box-transfer movement across strata (as opposed to high resolution spatiotemporal assessment models). |
| Spatial heterogeneity | Population structure wherein strong spatial structure exists within an otherwise panmictic population due to differences across the biological domain in demographics, exploitation, habitat usage, connectivity, or other ecosystem drivers. Reproductive dynamics assume a single reproductive population (i.e., stock-recruit relationship) with apportionment to strata. |
| Spatial strata | A unit of spatial delineation (i.e., area or region) within a population, typically corresponding to common fishery (e.g., management area) or biological (e.g., phenotypically distinct) conditions. |
| Spatiotemporal | In assessment nomenclature, a high resolution spatially-explicit assessment model that uses spatial autocorrelation and random effects to enable modeling fine-scale spatial strata and spatiotemporal dynamics (as opposed to coarse resolution spatially-stratified assessment models). |

| | |
|---|---|
| Stock | An ambiguous delineation often utilized to define management units, but which may constitute a population, metapopulation, sub-population, fishery unit, or a mixture of entities. |
| Straying | Permanent adult dispersal to a new population or sub-population. |
| Sub-population | A reproductive unit of a metapopulation, which demonstrates unique demographics, but that is not genetically independent. Sub-populations are the key biological entities within a metapopulation. |

**Table 2.** Overview of the primary modeling framework options available for each of six key population dynamic and management criteria (columns) when incorporating spatial population structure into decision-making. Identified spatial options are considered, or refined, within a defined model time-step and other necessary partitions (e.g., age, sex, life-stage). The range of functionality for each of the reviewed platforms is provided in Table 3.

| Population Structure | Recruitment Dynamics | Connectivity | Demographic Variation | Fleet Structure | Biological Reference Points |
|---|---|---|---|---|---|
| Panmictic<br>No spatial structure<br>Single stock-recruit relationship | Global density-dependence (single stock-recruitment relationship)<br>Symmetric or no (i.e., if panmictic) apportionment to spatial strata<br>Spatially-invariant temporal deviations (i.e., for apportionment or from the stock-recruit curve) | No movement | Spatially-invariant | Single fleet or survey across all strata<br>No spatial variation in selectivity | Single reference point for entire biological domain<br>Global density-dependence |
| Spatial heterogeneity<br>Multiple spatial strata within a single population<br>Single stock recruit relationship with apportionment to strata | Global density dependence (single stock-recruitment relationship)<br>Estimated apportionment to spatial strata<br>Spatially-varying temporal deviations (i.e., for apportionment or from the stock-recruit curve) | Age-0 movement (larval dispersal) | Phenotypically-based<br>Demographics change with strata or population unit occupied<br>Assumes environment drives demographics | Single fleet or survey per strata<br>No spatial variation in selectivity | Strata-specific reference points<br>Assume global density-dependence |
| Metapopulation<br>Multiple sub-populations with reproductive mixing<br>Each sub-population has a unique stock-recruit relationship | Local density-dependence (stock-recruitment relationship for each spatial strata)<br>Spatially-invariant temporal deviations (i.e., from the stock-recruit curve) | Time- and/or age-varying movement estimated<br>Functional forms widely utilized (e.g., preference functions or linear ramps by age)<br>Parameter blocking possible | Genetically-based<br>Demographics do not change as fish moves<br>Assumes rates are defined at birth and based on natal population | Single fleet or survey per strata<br>Spatial variation in selectivity | Population unit-specific reference points<br>Assume local density-dependence |
| Natal homing<br>Multiple populations with spatiotemporal overlap<br>Each population has a unique stock-recruit relationship | Local density-dependence (stock-recruitment relationship for each spatial strata)<br>Spatially-varying temporal deviations (i.e., from the stock-recruit curve) | Time- and/or age-varying mixing estimated<br>Functional forms widely utilized (e.g., preference functions or linear ramps by age)<br>Parameter blocking possible | Mixture of phenotypic- and genetic-based demography | Multiple fleets and surveys per strata<br>Spatial variation in selectivity<br>No parameter sharing allowed | |
| | | Spawning or feeding migrations to/from natal spawning ground | | Multiple fleets and surveys per strata<br>Spatial variation in selectivity<br>Parameter sharing allowed | |
| | | Straying from natal populations | | | |

**Table 3.** The primary capabilities for incorporating spatial population dynamics into models for each of the five spatial stock assessment platforms. The last column includes select key development features (see Fig. 3 for more details). DD = density dependence; CKMR = closed-kin mark-recapture;

| Model | Number of Population Units, Strata, and Species | Population Structure | Recruitment Dynamics | Connectivity | Demographic Variation | Fleet Structure | Biological Reference Points | Spatial Data Integration | Developmental Features |
|---|---|---|---|---|---|---|---|---|---|
| Casal2 | Population structure and strata limited by data and computing capacity, Multi-species | Panmictic, spatial heterogeneity, or natal homing | Global DD with apportionment or local DD; spatial temporal deviations | Time- and age-varying movement estimated; functional forms (preference functions) and blocking available; natal homing spawning migrations included | Genetically- or phenotypically-based (depends on population structure), *M*, Movement, recruitment patterns | Multiple options available with spatial variation and parameter sharing | Strata- or population-specific, local or global DD | Mark-recapture (Petersen abundance estimator, tag detection independent of fleet, tag attrition, tag mixing periods where no recaptures are fit, sub-fleet recaptures) | Tag-recapture by age and fleet with more likelihood options; preference-based environmental forcing of M, growth, and movement |
| Gadget | Populations, strata, and species limited by data and computing capacity | Panmictic, spatial heterogeneity, or metapopulation | Global DD with apportionment or local DD; spatial temporal deviations | Time- and age- and length-varying movement estimated; functional forms and blocking available | Genetically- or phenotypically-based (depends on population structure) | Multiple with spatial variation and parameter sharing | Strata- or population-specific, local or global DD | Mark-recapture (tag-attrition, reporting rate by fleet), stock composition, environmental covariates, predation | Preference function movement, CKMR, custom tagging likelihoods |
| MFCL | 1 population and species, strata limited by data and computing capacity | Panmictic or spatial heterogeneity | Global DD with spatial temporal deviations in apportionment to strata | Seasonal- and length-varying movement estimated though stationary inter-annually; functional forms and blocking available | Spatially-invariant | Multiple with spatial variation and parameter sharing | Strata- or population-specific, global DD | Mark-recapture (tag-attrition, reporting rate by fleet or cohort, tag mixing period with unique F) | Recruitment parameterization enhancements (time- and strata-varying with interactions) |
| SS3 | 1 population and species, strata limited by data and computing capacity | Panmictic or spatial heterogeneity | Global DD with spatial temporal deviations in apportionment to strata | Age-varying movement with linear ramp; movement rates time-varying and environmentally influenced | Genetic growth morphs with different growth, *M*, Movement, recruitment patterns | Each fleet operates in single strata; can share parameters | Population-specific, global DD | Mark-recapture (tag-attrition, reporting rate by fleet, defined tag mixing period where no recaptures fit), stock composition, environmental covariates | Multiple populations, local DD, population-specific reference points, CKMR |
| VPA 2-Box | 1 or 2 populations (strata match populations), 1 species | Metapopulation or natal homing | Local DD with spatial temporal deviations (default to global if 1 population) | Time- and age-varying movement estimated; blocking and random walk available; natal homing spawning migrations included | Genetically- or phenotypically-based (depends on population structure) | Multiple per stratum, but aggregated by stratum, with spatial variation | Population-specific, local DD | Mark-recapture (tag-attrition, reporting rate by fleet, mixing period with unique F), satellite tags, stock composition, environmental covariates | No active development; custom features added as needed |

**Table 4.** Recommended platform capabilities for next generation stock assessment models that incorporate spatial population dynamic processes. Platform design should include flexibility within the core features of spatial models.

| Feature | Ideal Flexibility | Capability |
|---|---|---|
| Code structure | Modular, easily adaptable and readable | Modular; parallelized optimization; transparent; group development; reproducible; documented |
| Model partition | Model and spatial structure options integrative with data, population dynamic, and management needs | Time-step; age; sex; life-stage |
| Model structure | Fully hybrid with ability to accommodate almost any model type | Spatially-aggregated; areas-as-fleets; spatially-stratified; spatiotemporal |
| Spatial structure | Enable multi-scalar aggregation or disaggregation | 1-stratum; multiple strata (limited only by data); multi-scalar (adjust to scale of individual data sets; e.g., high resolution tagging sub-models) |
| Population structure | Generalizable to all common structures | Panmictic; spatial heterogeneity; metapopulation; natal homing |
| Data integration | Multi-scalar and amenable to novel data sources | Flexible aggregation to fit scale of data collection; population composition data (e.g., otoliths); natural markers (e.g., parasites); close-kin mark-recapture and gene-tagging; vessel monitoring system catch data; operational oceanography; citizen science, digital reporting, and local ecological knowledge; telemetry and electronic tagging |
| Parameterization | Readily reduce effective parameters | Enable random effects; include spatial autocorrelation; share parameters across fleets, strata, time-step, or populations; utilize prior information |
| Parameter estimation | Multiple methods for statistical inference | Maximum likelihood; Bayesian with informative prior information and Markov chain Monte Carlo for posterior distributions |
| Stock-recruit | Match population structure assumed scale of density dependence and include pre-recruit spatial dynamics | Local density-dependence; global density-dependence; multistage stock-recruit function (with ability to model larval dispersal) |
| Recruitment variability | Incorporate spatiotemporal variability options for deviations and spatial apportionment | Fixed input; time-invariant estimation; temporal variation; spatial variation; spatiotemporal variation |
| Movement | Time- and age-varying with new options easily incorporated | No movement; fixed input; time-varying; age-varying; age- and time-varying; flexible parameter blocking; easy manipulation of movement matrix to remove infeasible movement patterns; functional forms (e.g., gravity-based, linear ramps, etc.); preference functions and environmental linkages (e.g., RSF and PF models); seasonal migrations (e.g., feeding and spawning); density-dependent movement; random walk |

| | | |
|---|---|---|
| Dispersal | Matching array of population structures | No interactions among populations; no reproductive mixing, but overlap; larval dispersal only; full reproductive mixing |
| Regional abundance estimation | Potential for data linkages | Regional abundance scaled by empirical data; regional abundance estimated directly |
| Fleet structure | Parametrization that allows aggregation or disaggregation of fleets within strata along with parameter sharing among strata | Common fleet type across strata with parameters shared across strata; common fleet type across strata with unique parameters; unique fleet type across strata with or without shared parameters across strata |
| Demographic variation | Genetic or phenotypic linkages that account for natal demographic regime, previous demographic regime, and current demographic regime (e.g., age-size models with growth increments and tracking of connectivity trajectory) | Constant across model domain; spatially-varying using empirical inputs; genetic-based demographics (i.e., based on natal population); phenotypic-based demographics (i.e., based on occupied strata); combined genetic and phenotypic variation |
| Tagging sub-model | Multiple structures and resolutions | No tag data; aggregated within strata; high resolution (i.e., sub-strata resolution); Petersen estimator by stratum and fleet; Brownie (tag-attrition) release conditioned; Brownie (tag-attrition) recapture conditioned; estimate 'nuisance' parameters (e.g., tag mixing and tag reporting) and incorporate auxiliary Information (e.g., high reward tag reporting information) |
| Data weighting | Likelihood easily adaptable to model partition and structure specification | Data driven and reproducible; spatiotemporal iterative reweighting; random effects estimation; state-space estimation |
| Diagnostics | Multi-scalar evaluation with quantitative and visual aid summaries | Goodness-of-fit; prediction skill; retrospective performance, model consistency; convergence |
| Simulation testing | Readily adapt to operating and estimation model modes across different population structures and spatial strata | Full feedback loops (MSE); data generation and estimation at multiple scales; resampling and other Monte Carlo methods; perform self-tests |
| Biological reference points | Multi-scalar and able to incorporate empirical or directly measured options | Spatially aggregated; strata- and/or population-specific; assuming local or global density-dependence; able to calculate empirical reference points (e.g., based on density or area-occupied); able to incorporate non-equilibrium dynamics and non-stationary connectivity |