

Drawing the lines: resolving fishery management units with simple fisheries data

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Abstract: The task of assessing marine resources should begin with defining management units. Often this step is overlooked or defined at temporal scales irrelevant to management needs. Additionally, traditional methods to define stock structure can be data intensive and (or) cost prohibitive and thus not available for emerging or data-limited fisheries. We present an approach that uses commonly available fisheries data (catch and effort) to delineate management units for dynamically independent populations. Spatially explicit standardized indices of abundance are grouped using a two-step partitioning cluster analysis that includes abundance index uncertainty. This “management unit estimator” is tested via simulation and found generally to recover the true number of management units across data of different temporal length, sample size, and quality. Management units are then determined for four species with varying ecologies, fishery histories, and data issues that exemplify the challenges of applying this method to messy data sets. Defining management units via relative abundance incorporates changes in population connectivity in relation to current removals and environmental conditions and creates consistency of index use within assessments. The two-step clustering approach is simple and widely applicable to situations wherein the clustering metric contains uncertainty.

Résumé : La tâche d'évaluer les ressources marines devrait débiter par une définition des unités de gestion. Cette étape est souvent négligée ou alors définie à des échelles temporelles qui ne sont pas pertinentes aux besoins de la gestion. De plus, les méthodes traditionnelles de définition de la structure des stocks peuvent exiger beaucoup de données et (ou) représenter un coût inabordable et donc ne pas être accessibles aux pêches en émergence ou aux pêches pauvres en données. Nous présentons une méthode qui utilise des données de pêche couramment disponibles (capture et effort) pour définir les unités de gestion chez des populations dynamiquement indépendantes. Une analyse de groupement avec partition en deux étapes qui inclut un indice d'incertitude de l'abondance sert à regrouper des indices standardisés d'abondance qui sont spatialement explicites. Cet « estimateur des unités de gestion » a été testé par simulation; il arrive généralement à retrouver le nombre réel d'unités de gestion dans des ensembles de données différant par leur étendue temporelle, la taille des échantillons et la qualité. Nous avons ensuite déterminé les unités de gestion pour quatre espèces qui sont distinctes par leur écologie, leur histoire passée de pêche et leurs problèmes de données afin de mettre en lumière les défis qu'il y a à appliquer la méthode à des ensembles d'éléments désordonnés. La définition des unités de gestion au moyen de l'abondance relative incorpore des changements dans la connectivité de la population en relation avec les retraits actuels et les conditions environnementales; elle crée aussi une cohérence dans l'utilisation des indices au cours des évaluations. La méthode de groupement en deux étapes est simple et peut s'appliquer facilement à des situations dans lesquelles la métrique de regroupement contient de l'incertitude.

[Traduit par la Rédaction]

Introduction

Fundamental to natural resource assessment, management, and conservation is defining the basic resource unit (Begg et al. 1999a; Waldman 1999). While the species level may be a convenient starting point, intraspecific subpopulations are commonly far from homogenous. It is widely recognized

that several factors (e.g., demographic and life history variability, habitat patchiness, environmental change, genetic structuring, and adaptability) may result in temporally-spatially structured populations with unique population dynamics (Secor 1999; Hilborn et al. 2003; Kritzer and Sale 2006). Defining resource units in relation to future removals without regard to such population structuring may lead to poor model assumptions (e.g., assuming complete diffusivity of individuals and fishing mortality effects (Booth 2000; Seijo et al. 2004)), unsustainable population interactions (e.g., localized depletions or extinctions), and ultimately fruitless management (Gauldie 1991; Stephenson 1999; Laikre et al. 2005).

There are various definitions for the resource unit (generally referred to as a “stock”) in fisheries and marine conservation (Nielsen 1995; Begg and Waldman 1999; Waples and Gaggiotti 2006). The dizzying array of stock definitions exists primarily because stocks are an inherently fuzzy measure of nature (Dizon et al. 1992). One therefore needs an explicit notion of context — why is one defining a stock in

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the first place? The reasons generally vary with the objectives of conservation and management. Specific to marine fisheries, management objectives often look to maximize yield while conserving aspects of the population that will enable such persistent yield on a continual basis (Punt et al. 2006). Stock designation should therefore promote these goals and look to unite groups of populations with similar characteristics relevant to achieving such goals.

There are two elements common to most definitions of a stock in fisheries, although they are not always combined. The first element frames the stock definition in relation to measures of reproductive isolation or dispersal (i.e., reproductive stock; Dizon et al. 1992; Jennings et al. 2001), while the second defines a stock in relation to human-mediated removals (i.e., harvest stock; Gauldie 1991; Jennings et al. 2001). Synthesizing the two viewpoints creates a nonlinear continuum of stock types dimensioned on connectivity and removals (Gulland 1983; Moritz 1994) with no discrete boundaries.

An important insight that distinguishes these two general definitions is not just breeding units versus fishing units, but rather the concept of time. While conservation tends to focus more on evolutionary sustainability (e.g., extinction probabilities of lineages, loss of genetic diversity) and thus the reproductive or evolutionarily significant stock, fisheries objectives focus largely on ecological sustainability (e.g., biocomplexity (Hilborn et al. 2003) and population resiliency (Salt and Walker 2006), maintaining yield) under resource use and thus the traditional harvest or management stock (Ihssen et al. 1981; Gauldie 1991; Begg and Waldman 1999). Neither time scale nor stock term is mutually exclusive, but defining stocks on one time scale (evolutionary) may be insufficient for management on another (ecological) (Taylor and Dizon 1996). Given the goals of managing marine fisheries, stock units defined on ecological scales are therefore considered most appropriate (Lande 1988; Dizon et al. 1992; Begg and Waldman 1999).

Many methods have been proposed to distinguish stocks on ecological scales (Ihssen et al. 1981; Begg et al. 1999b), though genetic approaches garner great attention (Ovenden 1990; Booke 1999; Palsbøll et al. 2007). Although genetic methods have improved substantially to capture population differences on increasingly finer time scales, these approaches remain challenged when resolving demographic independence or population structure over decades or shorter (Waples and Gaggiotti 2006). In particular, most current genetic methods attempt to define demographic connectivity via estimation of dispersal or migration rates. Not only are these rates difficult to measure genetically, but the relationship between demographic independence and migration remains poorly defined (Waples and Gaggiotti 2006). And while understanding the genetic component of a stock may be necessary, it may not be sufficient for short- and even long-term goals of resource conservation and management (Taylor and Dizon 1996; Gunderson and Vetter 2006). Whether through reproductive isolation, dispersal, life history traits, or phenotypic characteristics, an effective method of stock designation for management needs to capture stock population dynamics (Carvalho and Hauser 1995; Begg and Waldman 1999; Quinn and Deriso 1999). Additionally, stock dynamics may also change given the current combined

effects of environment and removals (Gauldie 1991). For instance, one level of fishing under a particular climate regime may create a particular population structuring, but changes to either fishing practices or climate may induce further fragmentation or coalescence of populations, thereby altering abundance trends and management needs. The approach used to identify a stock needs to be sensitive to such natural fluidity.

In addition, many of the current methods of stock identification require substantial and potentially cost-prohibitive sampling protocols in addition to the fishery information that is traditionally collected. This is especially true for data-limited or emerging fisheries, where timely management decisions early during fishery development may be critical to successful long-term persistence of populations and associated fisheries, but sampling effort and resources for research are low (Perry et al. 1999). Ideally, a stock identification technique should focus directly on population dynamics without much additional cost beyond that associated with monitoring the fishery.

In pursuit of this goal, we introduce a method (hereafter referred to as the management unit estimator or MUE) of stock identification that uses spatially resolved standardized relative measures of abundance (either of a fishery-independent or -dependent origin) and a simple two-step clustering approach to combine areas with similar abundance trends to designate putative stocks, which are demographically nonhomogeneous. The major assumption is that areas clustered together behave as one stock with the same population dynamics, an assumption consistent with that made when abundance indices are incorporated into traditional stock assessment models (Gauldie 1991; Quinn and Deriso 1999; Maunder and Punt 2004). In addition, the MUE incorporates uncertainty about the clustering units (in this case, the abundance indices) and proves robust to high levels of such uncertainty. The estimator is tested using simulation and then applied to the spatial abundance data of four Northeast Pacific groundfish species.

Materials and methods

General approach

The major objective of the MUE is to identify groups of areas with similar population dynamics using spatially resolved time series of abundance data with associated uncertainty. Such abundance indices can come from fishery-dependent and -independent sources and vary greatly in quality and quantity. Similarities among areas are then defined by distance measures, and groups are determined by clustering algorithms.

Common to both simulation testing of the estimator and application to the species examples are four tasks that describe the general methodological approach: (i) develop abundance indices from raw data, (ii) generate simulated data from abundance indices and their inherent uncertainty, (iii) cluster simulated data, and (iv) interpret the resultant clusters. The basic approach is to create a large number of data sets based on index uncertainty, each of which contains standardized indices of abundance by area. For each data set, a clustering algorithm is used to cluster and subsequently assign areas to management units. A second cluster-

ing algorithm then clusters the resultant management unit assignments for each simulated data set to get the final management unit designations. This second clustering step accounts for variability in the clustering assignments and theoretically recovers management units most supported by the data, avoiding individually spurious relationships while still incorporating the uncertainty of the abundance metric.

Data preparation (Fig. 1, step A) involves constructing standardized indices of abundance for each area along with measures of their uncertainty (e.g., coefficients of variation (CVs)). Methods for constructing indices of abundance and their CVs are not covered in this paper, as they are specific to the indices concerned (e.g., survey estimates or catch per unit effort (CPUE)) and are covered in detail elsewhere (Punt et al. 2000; Maunder and Punt 2004; Helser et al. 2007).

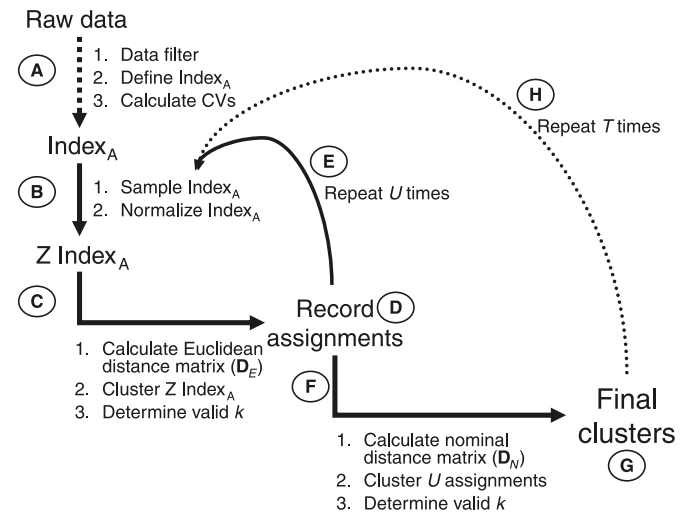
The MUE method requires both the indices of abundance based on the actual data and the number of resampled data sets (U) to account for the uncertainty in the indices (R code to apply the MUE is freely available from the primary author). Each resampled data set (Fig. 1, step B) involves adding sampling error to the actual indices of abundance. For the analyses in this paper, each “new” index for resample i , year y , and area L ($a_{i,y,L}$) is drawn from a normal distribution, $a_{i,y,L} \sim N(\hat{A}_{y,L}, CV_{y,L} \hat{A}_{y,L})$, where $\hat{A}_{y,L}$ is the actual abundance index value, and $CV_{y,L}$ is the CV associated with $\hat{A}_{y,L}$. The abundance indices for each area will not necessarily be on the same scale and need to be normalized so they are in comparable units for clustering (Kauffman and Rousseeuw 1990). For each resampled data set i , this is done by taking the area-specific Z score $Z_{i,y,L}$ for each year in the time series of abundance

$$Z_{i,y,L} = \frac{a_{i,y,L} - \mu_{i,L}}{\sigma_{i,L}}$$

where $\mu_{i,L}$ is the mean index value across years, and $\sigma_{i,L}$ is the associated standard deviation.

There are many clustering methods to consider (Theodoridis and Koutroumbas 2006). We chose to use a “partitioning around medoids” method (k -medoids), an intuitive approach when the goal is to identify specific (or “hard”) groupings in data, rather than a hierarchy of clusters (Berkhin 2006). This approach is more robust to outliers than clustering around centroids (Kauffman and Rousseeuw 1990; Berkhin 2006) and has several associated measures to aid in interpreting the appropriate number and membership of groups (Gordon 1999; Theodoridis and Koutroumbas 2006). The k -medoids approach requires one to specify how many k clusters one seeks to find, then uses measures of dissimilarity to find the best groupings (defined by minimizing the sum of cluster dissimilarities) for the specified k (Kauffman and Rousseeuw 1990). For each resampled data set, the k -medoids approach involves the following steps: (a) calculating the Euclidean distances from the $N(\text{area}) \times M(\text{year})$ matrix, resulting in an $N \times N$ dissimilarity matrix (\mathbf{D}_E ; step C-1 in Fig. 1); (b) applying the k -medoids algorithm (as implemented in the R function *pam*) to cluster areas using \mathbf{D}_E for $k = 2$ to total areas $- 1$ (step C-2 in Fig. 1); (c) applying cluster validity diagnostics to choose the most valid number of clusters k (step C-3 in Fig. 1);

Fig. 1. Order of operation for the hierarchical clustering approach. Steps B–G are general to all applications. The pathway B–H is used for the simulation testing. The pathway A–G is used in the applied examples. Index_A is abundance index by area; Z Index_A is normalized abundance index by area; CV is coefficient of variation; k is the number of clusters (i.e., management units); U is the number of simulated data set iterations; T is the number of trials (for management unit estimator (MUE) simulation testing) of U .



and (d) assigning each area to a cluster based on the cluster results for the value of k selected at step (c) (step D in Fig. 1). Repeating these steps for each of the U resampled data sets leads to a matrix of cluster assignments for each area that accounts for sampling error.

The final task is to determine the k cluster value most descriptive of the assignment matrix. An $N \times N$ dissimilarity matrix (\mathbf{D}_N) is calculated using the U nominal assignments of areas to clusters (using the R function *daisy*) (step F-1 in Fig. 1), and the k -medoids algorithm is used to cluster areas based on \mathbf{D}_N for $k = 2$ to total areas $- 1$ (step F-2 in Fig. 1). Cluster validity diagnostics are then used to choose the most valid number of clusters, and the final grouping of areas within clusters (i.e., areas within management unit) is recorded (steps F-3 and G in Fig. 1).

Five common relative cluster validity diagnostics were considered and evaluated for performance: (i) Dunn's index (Halkidi et al. 2002; Theodoridis and Koutroumbas 2006), (ii) G3 (Gordon 1999), (iii) Goodman–Kruskal's γ (Jain and Dubes 1988; Gordon 1999), (iv) Hubert's Γ (Halkidi et al. 2002; Theodoridis and Koutroumbas 2006), and (v) silhouettes (Rousseeuw 1987; Kauffman and Rousseeuw 1990). Generally, these diagnostics are variations on the theme of comparing distances or dissimilarities within and (or) between potential clusters.

Simulation testing of the MUE

Simulation testing offers a way to experimentally explore and manipulate complex biological systems that are unavailable for direct experimentation (Peck 2004). Although this approach is powerful, the challenge lies in how to traverse the huge landscape of potential scenarios to reach general conclusions. Particular to this study is devising a set of test stocks that differ enough to be relevant as management units

(e.g., having traits relevant and of concern to managing fisheries), but not so different that the results become self-evident. Given the above-mentioned theory on what a stock is in the first place, there is no natural or obvious way of manufacturing realistic stocks.

A group of three “true” test stocks (areas A–C, Fig. 2) was determined using a composite of real spatial abundance indices (adapted from Cope and Punt 2005) with several interesting traits: (i) all test stocks show a similar and general decline over time (a trend of concern for management), (ii) test stock C demonstrates a notable fluctuation from the mid-1980s to early 1990s (indicating a reaction to the environment different from the other stocks), and (iii) the indices for test stocks differ in their trend over the last 5 years (increasing: test stock A; stable: test stock B; and declining: test stock C; Fig. 2, normalized mean index). These are arbitrary characteristics (different or additional ones could be identified), but are arguably relevant for properly assigning separate management actions for each test stock.

The efficacy of the two-step clustering approach to identifying the true number of management units was challenged by constructing scenarios based on five factors: (1) number of areas sampled, (2) number of years in the abundance index, (3) the CV of the abundance indices (independent of year and area), (4) number of resamples used (U in Fig. 1), and (5) the cluster validity diagnostic used to identify k (Table 1). Each simulation involved 100 trials. This was sufficient to characterize relationships among scenarios, which were commonly established with <50 trials.

Scenario factors 1–3 explored issues related to data (Table 1). All of the simulations were based on there being 12 areas, but these were allocated to test stocks in two ways: (i) series 444 — 4 areas for each test stock and (ii) series 246 — 2, 4, and 6 areas for test stocks A, B, and C, respectively. Three time series lengths were explored (scenario 2, Table 1). In cases where only a subset of the 45-year time series was used, the years evaluated were either the last years (i.e., the last 25 or 5 years) or were selected randomly (e.g., 25 or 5 years selected randomly and nonconcurrently from the available 45 years). The CV of the abundance indices was also varied to assess sensitivity to the quality of data (scenario 3, Table 1).

Scenario factors 4 and 5 highlight issues involving method application (Table 1). The value of U was varied logarithmically to illustrate the effect of increasing the number of times simulated indices are clustered to capture the uncertainty in abundance indices and assignments to management units. Lastly, the effectiveness of the cluster diagnostics used to evaluate the estimated level of stock structure was evaluated by altering when (e.g., in the first or second clustering step) and which diagnostic was used. The success of particular cluster validity diagnostics varies (Estivill-Castro 2002), and in the present case, only two of them (silhouettes and Hubert's Γ) consistently performed well. Therefore, all further results use only these two diagnostics. The two-step approach to clustering areas allows multiple diagnostics to be used during a single application. One could use silhouettes for both the first (Fig. 1, step C-3) and second (Fig. 1, step F-3) clusterings, or one could switch to the Hubert's Γ statistic for the second clustering. All four combinations of the two cluster diagnostics are con-

sidered. An example of the two-step cluster approach using series 444 is illustrated in Figure 3.

Performance of the estimator is evaluated in a twofold manner: (i) tallying the number of trials that k is chosen correctly (the true number for k is 3 for all simulations) and (ii) assessing whether the stock assignments are correctly chosen when k is chosen correctly. This means that even if the final k chosen is 3, but the correct assignments are not made (e.g., areas belonging to test stocks A and B are grouped together), this is counted as a failure. A perfect score then, given 100 trials (T in Fig. 1), is 100.

Applied examples

Applying the MUE requires exploration over several iterations of two-step clusterings of simulated spatial indices (U in Fig. 1) under all combinations of the cluster validity diagnostics, followed by interpretation of the subsequent clusters. The estimated number of clusters is defined at the asymptotic k value as number of simulations increase. Ideally, the different validity diagnostic combinations should conclude the same k at the asymptote. Silhouette values (Rousseeuw 1987) were calculated for each area within each cluster and have maximum values of 1 (exact matching to a cluster) and a minimum of -1 (no relationship to members within the cluster). Silhouette plots (Kauffman and Rousseeuw 1990) were used to visualize and analyze management units and the strength of membership within each unit. A silhouette coefficient (SC, the maximum average silhouette value) >0.5 indicates significant overall structuring among clusters (Rousseeuw 1987). Within cluster average silhouette values >0.5 were interpreted as support of a strong management unit distinction, whereas silhouette values between 0.25 and 0.5 were taken as indicative of a weak but possibly meaningful distinction. Silhouette values <0.25 offered no support for management unit designation (Kauffman and Rousseeuw 1990).

The MUE was applied to data for four species: (i) Pacific halibut (*Hippoglossus stenolepis*), (ii) walleye pollock (*Theragra chalcogramma*), (iii) Pacific cod (*Gadus macrocephalus*), and (iv) cabezon (*Scorpaenichthys marmoratus*). These species provided contrast in data type and quality and life history characteristics and highlight important aspects and challenges to applying the MUE process.

Pacific halibut are assessed annually by the International Pacific Halibut Commission (IPHC) within several regulatory areas (Clark and Hare 2006; Fig. 4). Setline surveys within each regulatory area (Soderlund et al. 2007) provide fishery-independent measures of population abundance. Growth, morphometric, and dispersal data provided conflicting evidence of population structure, while recent research suggests complex movement among areas (Blaylock et al. 2003; Hauser et al. 2007; Loher and Seitz 2007). Ten years of survey indices and CVs for nine regulatory areas were used to investigate population structuring in Pacific halibut.

Walleye pollock and Pacific cod are two of the most important species taken in the eastern Bering Sea fishery. Both stocks are currently assessed and managed as one unit in this region (Thompson et al. 2007). Both species have a common distribution on the continental shelf and upper slope (~ 300 m), though walleye pollock are semipelagic and Pacific cod are demersal. The Alaska Fisheries Sci-

Fig. 2. An example (from left to right) of the sampling and normalizing procedure using one sampling ($U = 1$) for three different areas (i.e., test stocks). The middle columns of panels show the generation of the sampled index from the mean index values by area assuming a yearly coefficient of variation (CV) of 50%. The final panel shows the three normalized, sampled indices among areas; these are the values used in the primary cluster analysis (Fig. 1, step C) from which area cluster assignments are obtained. The above procedure with subsequent clustering is repeated U times (Fig. 1, step D).

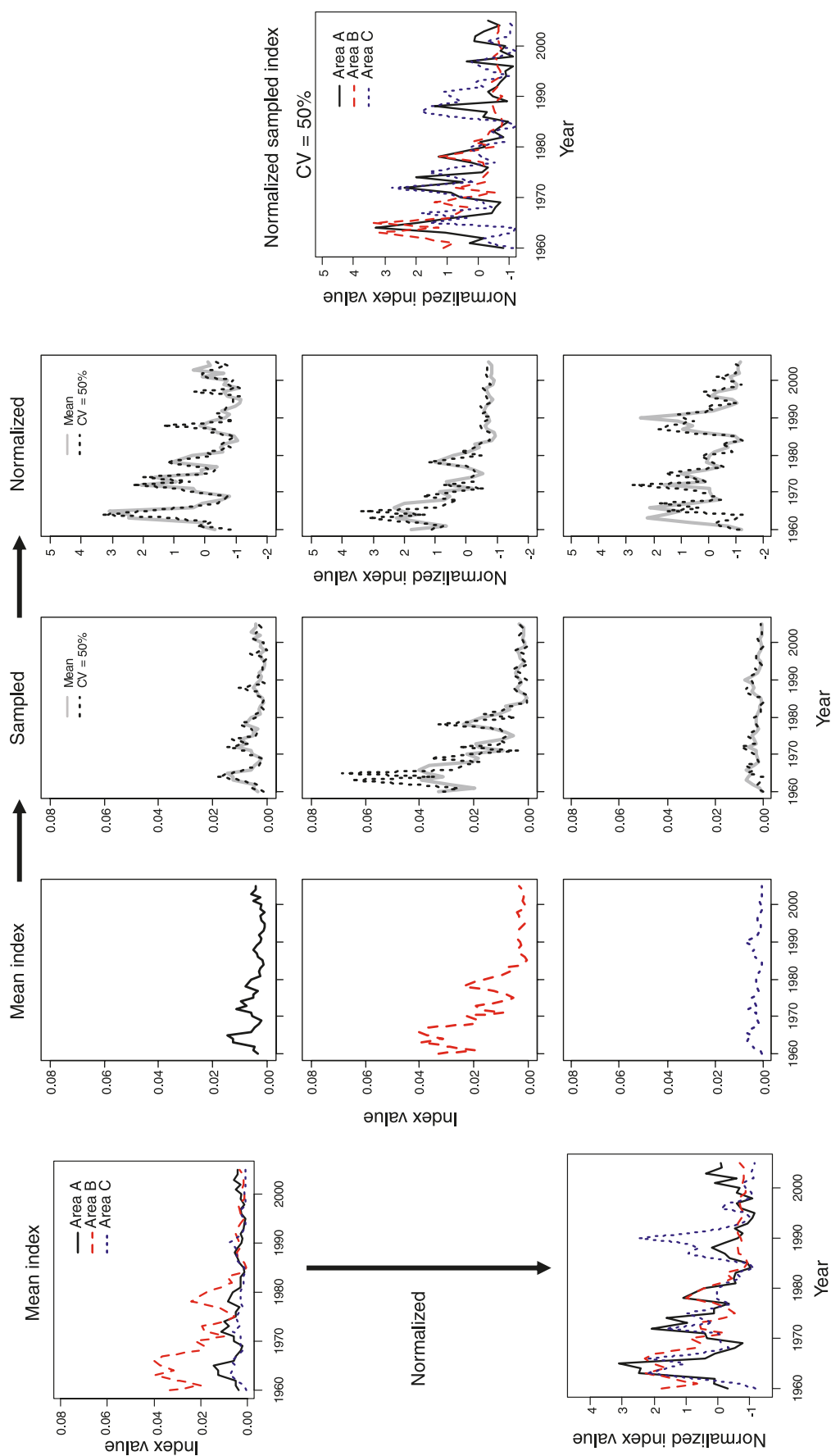


Table 1. Description of the scenarios and variable dimensions for simulation testing of the management unit estimator.

Scenario	Variable
(1) No. of areas	Series 444: 4 A, 4 B, 4 C Series 246: 2 A, 4 B, 6 C
(2) No. of years	45, 25*, or 5*
(3) No. of simulations	1, 10, 100, 1000
(4) Coefficients of variation (CVs)	25%, 50%, 75%, 100%
(5) Cluster validity pairings [†]	Hg ^{Hg} , Hg ^{Sil} , Sil ^{Sil} , Sil ^{Hg}

*Years used were either randomly chosen from the time series (random) or the last consecutive years in the time series (last).

[†]Superscripts indicate the cluster validity diagnostic used during the simulation stage (step 1 cluster); normal script indicates the diagnostic used for the final trial cluster (step 2 cluster). Sil, silhouettes; Hg, Hubert's Γ .

ence Center (NOAA Fisheries) performs annual fisheries-independent abundance surveys of the eastern Bering Sea continental shelf for several species, including walleye pollock and Pacific cod (Acuna and Kotwicki 2006). The trawl tows are designated into six substrata (Fig. 4), and 22 continuous years of data were used for both species to identify management units.

Cabezon are found in nearshore waters generally less than 100 m from Baja California to Alaska (Love et al. 2005) and offers an example of high data resolution and quantity (e.g., many areas and long time series), but poor quality (e.g., fishery-dependent indices with high CVs) in an emerging commercial fishery. Along with the recently developed commercial fishery, cabezon have long been prized by recreational fishers. The first assessment (Cope et al. 2004) considered fish in California waters as one stock, but the subsequent assessment (Cope and Punt 2005) considered two California stocks. As in many data-limited fisheries, there is no long-term fisheries-independent data set available for cabezon, so for the estimation of management units, the historical California Commercial Passenger Fishing Vessel data set (Hill and Schneider 1999) was used to construct a time series of CPUE. Data were collected in statistical blocks about 100 nautical miles² (1 nautical mile = 1.852 km) in area (see Hill and Schneider 1999 for specific details). Eighteen locations were defined by the nearest port, with adjacent blocks attributed to each port. Each location therefore represents a potential cabezon population. Blocks with no cabezon catch and those for which a modified index of relative importance (IRI; Cortes 1999; Pinkas et al. 1971), based on CPUE and frequency of occurrence, was less than that expected if all blocks contributed equally to the overall IRI value ($1/(\text{total number of blocks})$) were omitted. These restrictions eliminated blocks with inconsistent and low catches of cabezon. The abundance indices for each location were computed by standardizing the raw catch and effort data using the delta-log-normal approach (Vignaux 1994; Maunder and Punt 2004), with 100 bootstraps used to estimate the uncertainty about the indices (e.g., CVs). This analysis resulted in 18 indices of abundance with up to 45 years of data and year-specific CVs.

There are three notable attributes of this data set relative to the others: (i) many more areas to consider, (ii) longer time series, but not continuous in all areas, and (iii) high CVs for most years and locations. The third item is directly

addressed via the two-step cluster approach, but the first two items need additional attention. Deciding which locations and years to include in an analysis is not always straightforward. The cabezon example highlights a situation wherein there is a trade-off between using the highest special resolution (e.g., number of locations) and the longest time series for clustering. To evaluate which years and locations should be included in the analysis (the analysis requires each area to have a common time series), it is instructive to plot the number of years all locations have in common versus the number of locations. The steepest portion of the curve, which may include several year–location combinations, indicates the biggest gain in locations given the number of common years. The year–location combinations within this portion of the graph are the recommended subset of data to use with the MUE. Multiple combinations of years and locations are then considered in turn and compared for consistency in identifying management units.

Results

Simulation testing of the MUE

Incorporating uncertainty and the two-step cluster approach

Using the two-step clustering approach clearly leads to improved estimates of the true number of stocks k (Fig. 5). The one- and two-step approaches are equivalent and poor at estimating the correct number of management units as uncertainty increases when there is only one simulation. Correct estimation of the management units is drastically improved using the two-step method as the number of simulated data sets (U) is increased from 1 to 1000, even when uncertainty is very high (CVs of 100%).

To determine whether the MUE approach creates structure when none is there, additional null tests were performed wherein 12 areas from the same test stock were clustered under each scenario of U and CV. As expected, no population structure was supported in any scenario or test stock.

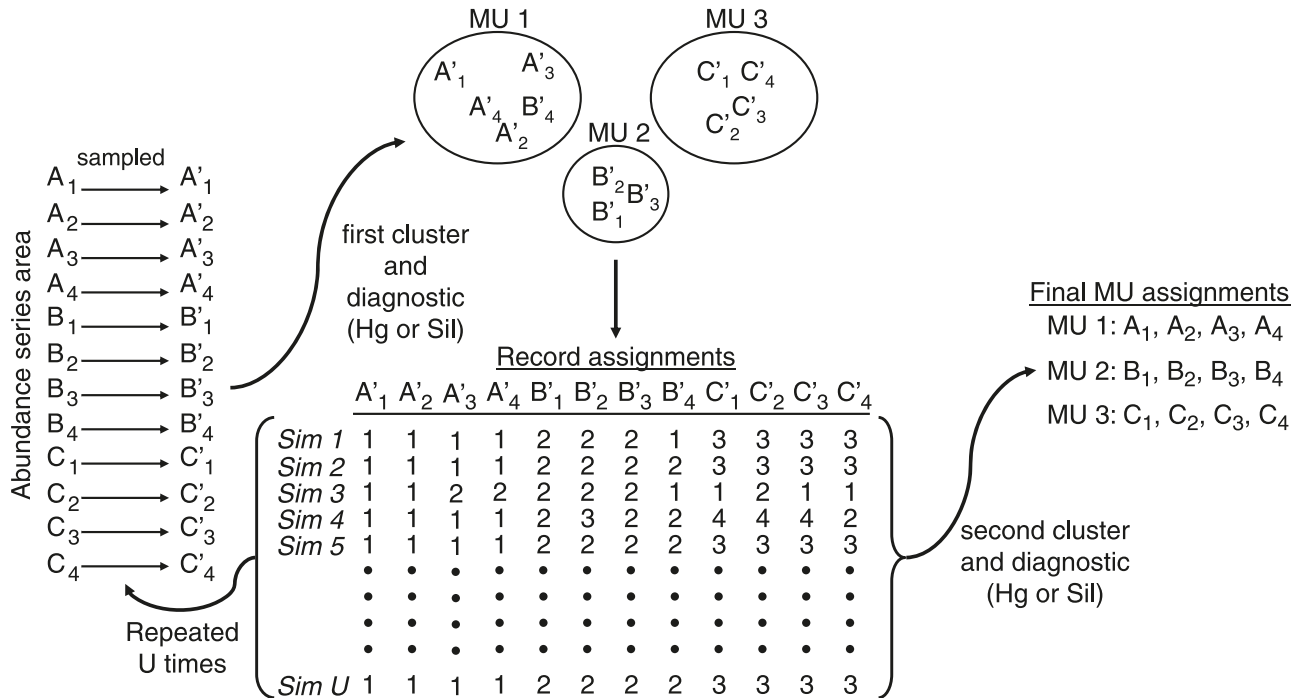
Estimator performance

Results for the estimator performance using 1000 simulations across differing time series lengths, CVs, and cluster validity diagnostics are provided (Table 2). Generally, the relative performance of the estimator under this example deteriorated when CVs increased, the number of years with data was shorter, the years were not consecutive years, and the number of areas per management unit was unbalanced. Overall, the estimator was likely to recover the correct number of management units and cluster assignments even when there was only five consecutive years of data with CVs = 0.5. A more detailed look into failed simulations under scenarios with high CVs revealed that most of them either correctly identified the number of true management units, but misassigned one of the areas, or were off by one management unit (Table 3), thus suggesting that the two-step MUE provides valuable insight into management units even under very poor data quality and quantity.

Choice of cluster validity diagnostic

The performance of the estimator depended on the choice of cluster validity diagnostic applied to each clustering step

Fig. 3. An example of the two-step cluster method using series 444 as an example. Each area time series is sampled based on the yearly coefficient of variation (CV) value. The areas are then clustered, the most data-supportive number of clusters (k) is chosen using the highest cluster diagnostic value for each k , and areas are assigned membership to a management unit (MU) based on their normalized yearly values. These assignments are then recorded, and the whole process is repeated U times. Note how assignments and number of MUs may vary among simulations. Once all simulations are complete, a final nominal clustering on the simulation assignments is made to produce the final estimate of MUs, again based on k with the highest cluster diagnostic value. Sil, silhouette cluster diagnostic; Hg, Hubert's Γ cluster diagnostic.



(Table 2). The results were most sensitive to the diagnostic used in the second cluster step; when misestimates were made, using silhouettes led to underestimating the true number of management units, while using Hubert's Γ had the opposite effect (Table 3). The Hg^{Sil} pairing (using Hubert's Γ in the first step, silhouettes for the second step) had the best overall performance, while performance was poorest using Sil^{Sil}. Nevertheless, the difference between best and worse is sufficiently small not to reject any diagnostic combination, and applications should therefore consider all four diagnostic combinations.

Applied examples

Pacific halibut

The Pacific halibut data strongly support at least two management units (average silhouette values (SC) = 0.58; Fig. 6a). All four cluster diagnostic pairings supported the same two management units: (i) Bering Sea – Aleutian Islands (subareas 4E–4D–4B–4A–3B) and (ii) Gulf of Alaska – western Alaska – British Columbia (3A–2C–2B) (see Fig. 4a for subareas). The subarea off Washington and Oregon (2A) was only weakly associated with the Bering Sea – Aleutian Islands cluster. The Gulf of Alaska area (3A) was only weakly associated with the western Alaska – British Columbia cluster and could be treated as its own cluster.

Walleye pollock and Pacific cod

The Bering Sea trawl data did not support any stock

structure for walleye pollock (SC = 0.26; Fig. 6b), but did strongly support at least two management units for Pacific cod (SC = 0.52; Fig. 6c). There was a distinct onshore (subareas 1 and 2) – offshore (subareas 5 and 6) grouping of management units for Pacific cod. The midregion (subareas 3 and 4) for Pacific cod was completely unresolved, neither its own management unit, nor affiliated strongly with either of the other management units.

Cabazon

The large number of years, locations, and missing data points required further initial analysis before clustering. Two versions of the data series provided a range in the trade-off between the number of years in the time series and locations (Fig. 7a): (i) 36 years with 15 locations and (ii) 29 years and 18 locations. The former suggested six management units, while the latter suggested five to eight (Fig. 7b). Both data series were explored for consistency in clustering of management units.

Two management units were strongly supported by both data sets: one in southern California (Oceanside–Dana Point – Huntington/Newport) and another in south-central California (Morro Bay – San Simeon; Figs. 7c and 7d). In addition, a management unit in central California (Monterey – Santa Cruz) was supported by both data series. One could also argue for a nonadjacent Ventura/Oxnard – Bodega Bay management unit as indicated in the 29-year time series, though this cluster is based on members with large CVs (Fig. 7e) and is an unstable cluster as the number of years and loca-



Fig. 5. Estimates of the number of management units (k) using either the one- or two-step cluster management unit estimator with increasing simulation numbers: (a) 1 simulation, (b) 10 simulations, (c) 100 simulations, (d) 1000 simulations. The true value of k is 3, and the simulations presented are based on series 444 with 45 years of data. Hubert's Γ for both clustering diagnostics was used for this example.

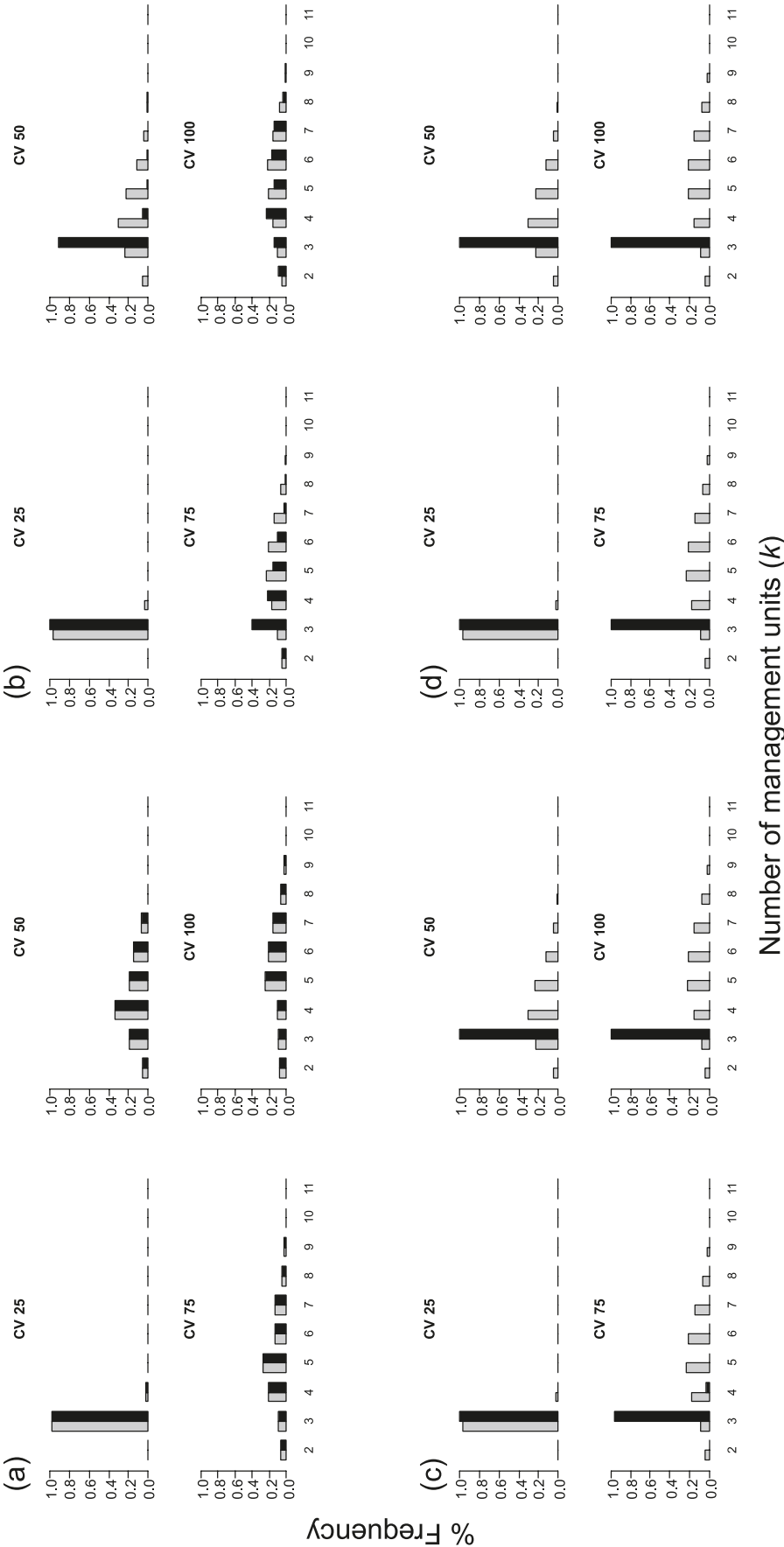


Table 2. Percentage of correctly identified management units for the different series types and number of years and composition of data (either randomly chosen or last consecutive years), coefficients of variation (CVs), and cluster diagnostic pairings.

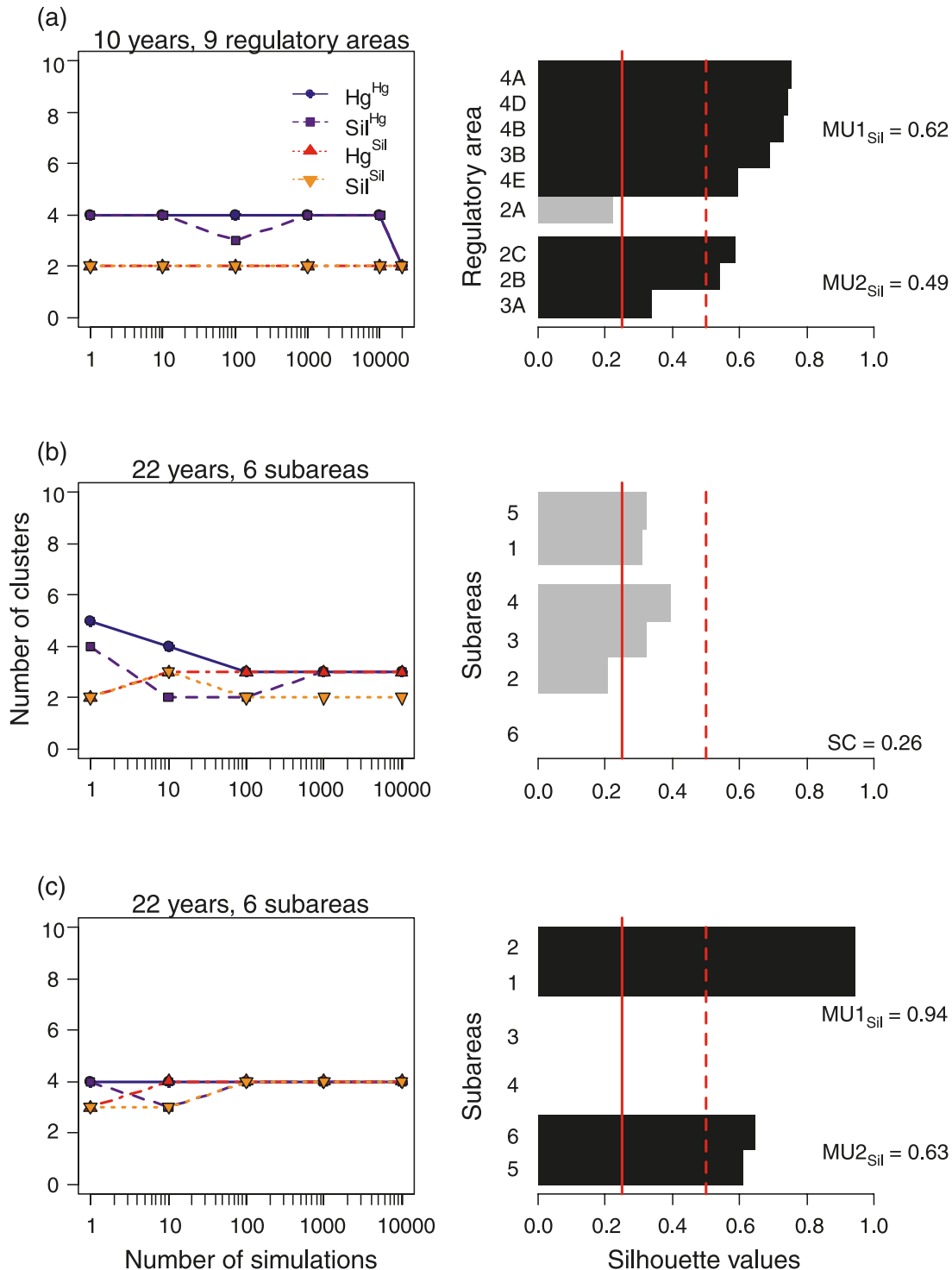
			Step 2 cluster validity diagnostic							
			Silhouette				Hubert's Γ			
Step 1 cluster validity diagnostic	Time series	Order	25	50	75	100	25	50	75	100
Series 444										
Silhouette	45	Last	90	100	100	100	100	100	100	100
	25	Random	100	89	82	76	94	85	81	77
	25	Last	60	100	100	100	100	100	100	100
	5	Random	44	20	14	13	34	15	7	6
	5	Last	100	100	45	40	100	100	54	20
Hubert's Γ	45	Last	100	100	100	100	100	100	100	100
	25	Random	99	93	85	77	94	86	74	64
	25	Last	100	100	100	100	100	100	100	91
	5	Random	40	17	12	10	27	9	4	3
	5	Last	100	72	14	10	100	91	39	9
Series 246										
Silhouette	45	Last	98	100	79	2	100	100	84	62
	25	Random	100	90	80	74	94	86	80	78
	25	Last	64	100	100	100	100	100	100	100
	5	Random	43	16	15	12	35	17	8	6
	5	Last	100	0	0	17	100	100	76	64
Hubert's Γ	45	Last	100	100	100	100	100	100	100	100
	25	Random	98	93	83	73	93	87	77	66
	25	Last	100	100	100	100	100	100	61	37
	5	Random	40	18	11	9	28	9	6	4
	5	Last	100	0	6	16	100	50	47	44

Table 3. Example of detailed results for the final assignment of clusters for the scenario using the last 5 consecutive years under 1000 simulations.

		Final cluster value k										
Cluster diagnostics	CV	2	3	4	5	6	7	8	9	10	11	True
Series 444												
Si ^{Si}	75	55	45	0	0	0	0	0	0	0	0	45
	100	40	60	0	0	0	0	0	0	0	0	40
Si ^{Hg}	75	86	14	0	0	0	0	0	0	0	0	14
	100	81	19	0	0	0	0	0	0	0	0	10
Hg ^{Si}	75	1	54	31	14	0	0	0	0	0	0	54
	100	0	20	20	20	40	0	0	0	0	0	20
Hg ^{Hg}	75	12	39	39	10	0	0	0	0	0	0	39
	100	18	9	28	36	0	9	0	0	0	0	9
Series 246												
Si ^{Si}	75	100	0	0	0	0	0	0	0	0	0	0
	100	83	17	0	0	0	0	0	0	0	0	17
Si ^{Hg}	75	94	6	0	0	0	0	0	0	0	0	6
	100	84	16	0	0	0	0	0	0	0	0	16
Hg ^{Si}	75	0	76	24	0	0	0	0	0	0	0	76
	100	0	64	30	6	0	0	0	0	0	0	64
Hg ^{Hg}	75	0	47	53	0	0	0	0	0	0	0	47
	100	0	44	40	12	4	0	0	0	0	0	44

Note: The true value of k is 3. The "True" column refers to the total number of $k = 3$ clusters that currently assign the 12 areas to each of the three clusters. Sil, silhouette cluster diagnostic; Hg, Hubert's Γ cluster diagnostic.

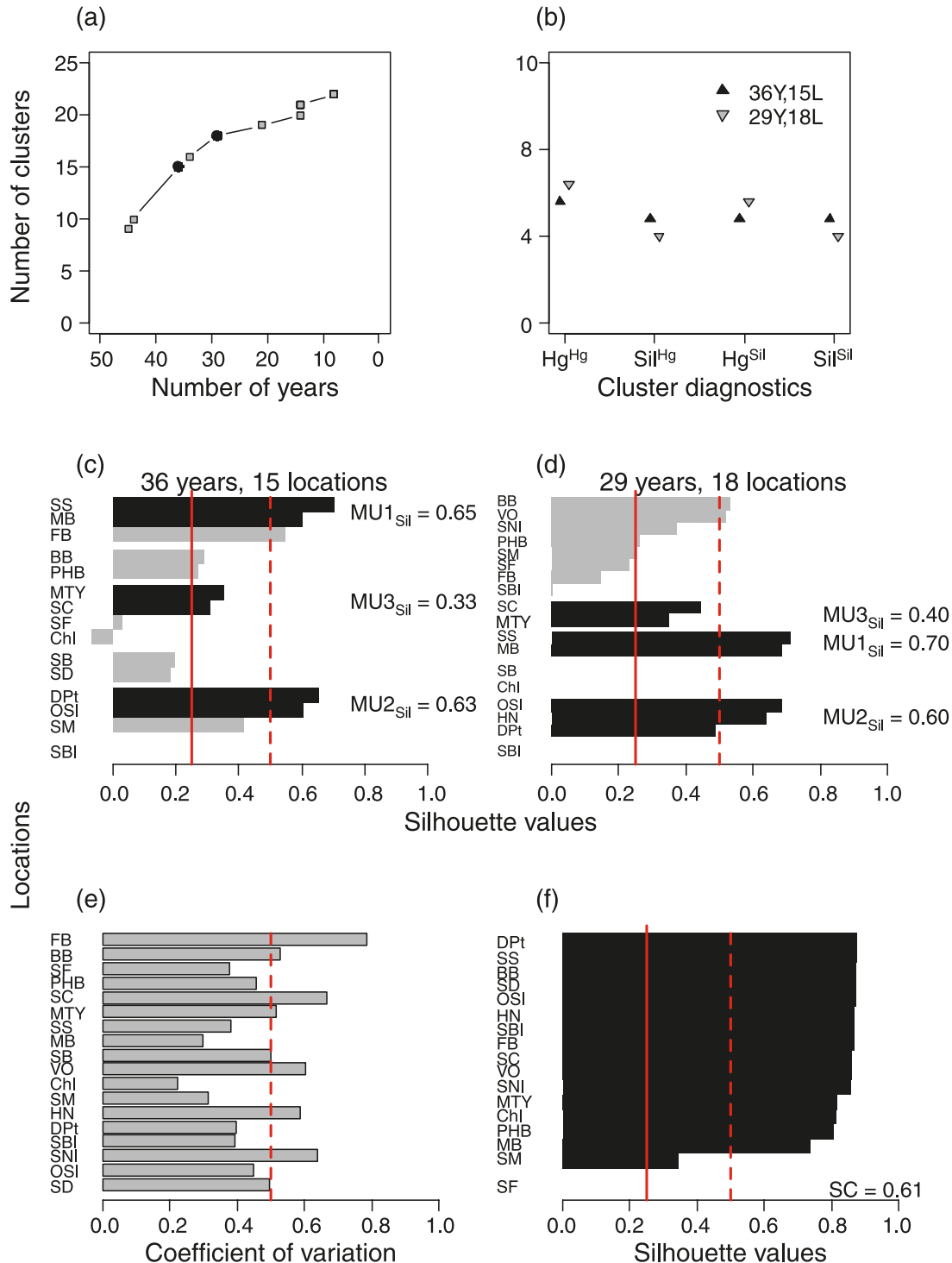
Fig. 6. Left-side figures: plots of final cluster number chosen by each cluster diagnostic pairing for increasing simulations runs. Asymptotic behavior as simulation number increases demonstrates convergence to a final cluster value. Right-side figures: silhouette plots of the clustering groups best supported by the data. Solid and broken vertical lines indicate silhouette values of 0.25 and 0.5, respectively. Black bars indicate strong members of a management unit. Gray bars indicate weakly affiliated members of a cluster. MU_{xSil} refers to the management unit average silhouette value, where x is the management unit number. SC, silhouette coefficient.



tions are changed. In fact, as locations are increased and years are decreased, the overall average CV for all locations increases dramatically, and all but the two strongest clusters remain weakly intact. This trend highlights how the informa-

tion content of the cabezon data decreases, and results of the MUE become less reliable as the number of common years decrease (unlike the Pacific halibut data that had fewer, but better measured yearly values).

Fig. 7. (a) Plot of years in time series vs. number of locations to determine which years and locations to use in the cluster analysis for cabezon. The solid circles represent the two time series analyzed. (b) Number of clusters chosen for each cluster diagnostic pairing after 20 000 simulations for each time series used. (c and d) Silhouette plots for each of the time series. Solid and broken vertical lines indicate silhouette values of 0.25 and 0.5, respectively. Black bars indicate strong members of a management unit. Gray bars indicate weakly affiliated members of a cluster. MU_{xSil} refers to the management unit silhouette value, where x is the management unit number. (e) Coefficients of variation (CVs) for each location in the cabezon fishery. The broken line indicates a CV of 50%. (f) Cluster analysis on cabezon effort data. SC, silhouette coefficient. Refer to Fig. 4c for location abbreviations.



Given the fishery-dependent nature of the cabezon data, the influence of effort on the final clustering was also considered (Fig. 7f). Effort did not show any structure among

areas and thus did not seem to influence any aforementioned designation of management units based on the CPUE relative abundance.

Discussion

Defining management units: the MUE

The observation that populations respond differentially to environmental and exploitation variation throughout a species range has been recognized for well over a century (Sinclair 1988; Smith 1994). Basic biological sampling has revealed differences in migration patterns, growth rates, and reproduction schedules. These differences translated observably into fluctuating catches, but less straightforwardly into population regulation. Although many tools have since been used to draw lines around population units of concern for fisheries management, it seems apparent the unit itself should be as flexible as the population dynamics underlying it. This new approach to clustering abundance indices is a direct attempt at finding those natural, fluctuating units.

Rothschild (2007) made an important step in this direction by considering abundance trends among nominal cod stocks in the Atlantic. He proposed that abundance trends were an appropriate way to identify stock units and used correlations among the indices to identify five cod stocks that differed from the putative stocks on which management was based. Similarly, Holmes et al. (2008) compared adult biomass trends of North Sea cod in different regions and concluded there was asynchrony in population dynamics, arguing such structure needs consideration in assessment and management of the species.

The present study takes such work a step forward by offering a framework based on the theoretical underpinnings of partitioning analysis and cluster diagnostics while simultaneously accounting for abundance index uncertainty. This latter is particularly important because sampling error in abundance estimates can be large. Ignoring this uncertainty may lead to erroneous conclusions regarding population structure, as shown in the simulation analyses. The approach of this paper performed well even when the CVs for the abundance indices were so large as to generally be uninformative in assessments that fit models to abundance indices. Therefore, even when abundance data is too uncertain for assessing stock status, the MUE may still offer insight into spatial patterns in abundance to focus management and further data collection.

It was not possible to consider all possible scenarios during the simulation testing (this would have been computationally impossible). The results should, however, be generally applicable. The method performed well in the simulation experiment, only failing badly when there were few data that were separated in time. Four pairings of cluster diagnostics were suggested to aid in interpreting the correct cluster assignments, but each had strengths and weaknesses. Overall, using Hubert's Γ during the step 2 clustering led to the most reliable results. Using silhouettes for both steps resulted in the most misestimates of management units, but still preformed generally well. When incorrect, cluster assignments based on Hubert's Γ tended to overestimate the number of true clusters, while silhouettes tended to over-clump. These observations may explain why the Hg^{Sil} pairing (silhouettes and Hubert's Γ for the step 1 and step 2 clusterings, respectively), and thus a combination of the two diagnostics, performed most reliably. The tendency for over- or under-clumping is an important consideration when ap-

plying these approaches to real data. Depending upon the philosophy of each management situation, one may choose the cluster diagnostic pairing to match the willingness to over- or under-estimate the number of management units, though as in the applied cases presented here, diagnostic pairings often converge on the same management units.

Interpreting management units: applied examples

Each of the applications highlighted issues relating to the applicability and challenges of applying the MUE to elucidating natural population groupings and effective management units.

Pacific halibut: gaining insight

Pacific halibut is an example of how using the MUE approach with population trends can offer greater insight into population structure. The management units for Pacific halibut have changed throughout the fishery's history. Anatomical and growth differences and movement argued for at least three management units (Bering Sea – Aleutian Islands, Gulf of Alaska, and southeast Alaska) during the early part of the fishery (Skud 1977; Blaylock et al. 2003). Subsequent tagging experiments and early genetic evidence indicated one genetic stock of Pacific halibut in the Northeast Pacific (Skud 1977; Grant et al. 1984). However, preliminary work on more sensitive genetic markers indicate possible genetic structuring (Hauser et al. 2006; Hauser et al. 2007), while parasitic markers also revealed population structure among the northern Bering Sea, central Bering Sea, and southern British Columbia (Blaylock et al. 2003). Stock assessments based on the IPHC regulatory areas and under the assumption of no movement among areas have been conducted for several years, even though Pacific halibut are considered one spawning stock (Clark and Hare 2006, 2007). The use of multiple management units has recently been reconsidered in light of inconsistencies between abundance data and closed area assessment abundance estimates, and tagging data indicating substantial movement of adults from west to east (Webster and Clark 2007), lending credence to one coast-wide assessment (Clark and Hare 2007). Whether these changes in perceived population connectivity are static and only become clearer with better population sampling or have changed through time is unknown.

Applying the MUE to the last 10 years of abundance data indicate that two management units separating the Bering Sea – Aleutian Islands from the other areas is supported. This is not inconsistent with the information found in each of the studies discussed above and is supported further by the dramatic increase of catches in the Bering Sea – Aleutian Islands during the past 10 years (Clark and Hare 2006). Such a sudden increase in catch could alter population dynamics even when areas are highly connected. Additionally, the weak clustering of the Gulf of Alaska area (3A) may more appropriately indicate a transition zone between the Bering Sea – Aleutian Islands stock and the western Alaska – British Columbia stock and should thus be treated instead as its own stock. These proposed management units do not suggest Pacific halibut constitute isolated populations, but rather intermixing populations with different population trajectories and thus in need of different management attention. It also supports the continued collection of abundance estimates at

the resolution of each regulatory area to monitor whether these putative management units change over time, something much more difficult to determine with other measures of stock relatedness.

Walleye pollock and Pacific cod: traversing subtleties

Bering Sea walleye pollock and Pacific cod are both gadoids and are wide ranging with major migratory behavior. However, the results were markedly different and are a good study in contrast, demonstrating that the MUE is not compelled to find stock structure and, when structure is found, how such population structure may or may not be relevant to management. The schooling, semipelagic nature of walleye pollock tends to result in spatially homogenous populations (Kotwicki et al. 2005), whereas the gregarious but mainly demersal Pacific cod have shown inshore–offshore and basin-specific population structuring similar to the Atlantic cod (Hutchings 1996; Ruzzante et al. 1998; Rothschild 2007). Both walleye pollock and Pacific cod exhibit population structure within the North Pacific (Olsen et al. 2002; Cunningham 2007), but no studies have looked among sites within the Bering Sea. Currently, both stocks are assumed as one management unit within the Bering Sea (Thompson et al. 2007).

The MUE revealed no apparent structuring, and thus one management unit, for Bering Sea walleye pollock, but identified at least two management units for Pacific cod. These management units for Pacific cod are not conventional stocks because they represent spatially structured life history stages. This example demonstrates how the MUE will indicate differences among areas regardless of the biological mechanism. Such differences need then be explored by the analyst to determine how such differences in abundance relate to management goals.

Specifically, the results for Pacific cod highlight the need to consider the MUE results carefully because the two management units were depth-segregated (one management unit shallower than 50 m and the other deeper than 100 m). A closer look at the biological information from putative management unit reveals generally smaller individuals being taken in the inshore areas versus offshore (Acuna and Kotwicki 2006; Lauth and Acuna 2007). Whether this indicates a true nursery grounds or sustained population structuring is unclear. The unresolved nature of the two middle subareas is sensible given the movement history of individuals into and out of subarea 3 (Shimada and Kimura 1994). Additional clustering attempts to explore relative relationships when either subareas 5 and 6 or 1 and 2 were removed (advisable when strong grouping may obscure finer relationships; Rousseeuw 1987) revealed a moderate alignment of subarea 3 with subareas 5 and 6. Given the complicated movement patterns, yet distinct population dynamics among subareas, three interpretations are reasonable. One approach to assigning management units is to recognize the combined subareas 1 and 2 as a nursery ground, but assign one management unit for the whole area. Alternatively, subareas 1 and 2 could be considered a separate management unit from the other subareas and be subject to different management goals. Thirdly, a more liberal assignment of management units suggests the following four groups: subareas 1 and 2; subarea 3; subarea 4; subareas 5 and 6.

Additional consideration of the management unit is advisable when structuring of population dynamics may indicate a convergence of life history stages. For example, one area may include wide-ranging adults coupled with sedentary juveniles, as may be the case with Pacific cod. Including such biological interpretations of the resultant area groupings allows further insight into designating management units that match management needs.

Cabazon: fuzzy but informative

Cabazon proved a challenging example of interpreting management units with high quantity but low quality information. Such a situation is typical for fishery resources in data-limited situations that rely on fishery-dependent data. When detailed spatial data are available (e.g., statistical blocks in Fig. 4c), it is first necessary to identify the spatial scale at which the abundance indices will be developed. The finest scale of resolution is not always the best, because if there are too many poorly sampled areas with many data gaps, noise will swamp signal (Rousseeuw 1987; Bezdek et al. 1997). Prudence suggests combining spatial areas until data sufficient for broad exploration is obtained and spatial units are relevant to the management at hand (in this case, ports instead of blocks were chosen). Even at coarser spatial resolutions, data gaps may persist and one must decide between using more locations (clustering units) or more years (clustering data). This is not a trivial decision given all clustering is context-specific and often sensitive to outliers (Rousseeuw 1987; Bezdek et al. 1997; Stein et al. 2003). Figure 7a offers a simple way to visualize the space–time clustering dimension to maximize the value of clustering units and data.

Furthermore, as for Pacific cod data, if the difference between just one clustering unit and all others is large, relevant structure within the remaining clustering units may be obscured (Rousseeuw 1987). In some cases, this effect may be more pronounced when CVs are high. The cabazon example illustrates the importance of identifying strong, consistent groupings across various data combinations. Such consistency helps recognize and diagnose transient, context-specific clustering behavior. A jackknifed approach to exploring such sensitivity to area combinations may provide further insight, though documenting how available years change with area combinations would need attention.

The present results suggest at least two strongly resolved management units for cabazon: one above Point Conception and one below. This is consistent with the current stock assessment (Cope and Punt 2005), but an additional important management unit is also emerging north of Monterey Bay. Substantial population structuring and limited connectivity in nearshore populations is not unexpected (Cope 2004; Miller and Shanks 2004; Buonaccorsi et al. 2005) and is a strong driver for localizing management (Francis et al. 2007). Preliminary findings based on genetics support a notably similar designation of cabazon management units (Vilablanc and Nakamura 2007).

General remarks

The above method and applied examples argue for a more fluid definition of management unit to integrate biological, environmental, and stochastic elements as manifested in

population characteristics. It does not require static or hard barriers to interactions (e.g., movement into and out of an area is not considered substantial unless it homogenizes the dynamics of mixing subpopulations) or years of reproductive isolation, but rather supports continual reevaluation of how individuals within areas are interacting as manifested via area-specific population dynamics. This method is simple, cost effective to implement, and produces management units consistent with those applicable to standard statistical catch-at-age models (Methot 1990). It also argues for continual collection of spatially resolved data to characterize spatial relationships through time, even when present conditions suggest only one management unit.

The MUE method is constrained by the spatial resolution of the abundance data available. An "area", therefore, may in fact be composed of several distinct management units, but left untested because of the available data resolution. Testable areas may also straddle two underlying management units, thus creating ambiguous or uncertain groupings. Grouping of areas into a management unit is not, then, hard evidence that no additional structure exists within that group, but rather no information in the data is present to explore further management units. These examples highlight the importance of finding the right balance between data resolution and data information content. The higher the spatial resolution of data, the more population structure is potentially detectable. But if data quality is sacrificed for data resolution (i.e., more areas), the power to detect differences will decrease. We recommend a minimum spatial resolution in MUE analyses consistent with the simulation testing presented here: no less than 5 comparable years and CVs on average less than 100.

Although the examples given here all used some form of abundance measure, this two-step clustering approach could also apply to length and age compositions, weights, maturity, or other pertinent population traits (Crone 2001; Langley 2006; Gerritsen and McGrath 2007). The MUE could further be extended to cluster interspecific abundance trends for identifying multispecies aggregates and (or) biogeographic boundaries (Williams and Ralston 2002; Francis et al. 2007). Simulation testing of the above extended applications that use nonabundance index information is still needed to understand performance under varying data conditions.

There are two distinct advantages of using the two-step cluster approach with abundance data compared with other commonly used methods of stock identification: (i) it is based on the dynamics of the population and (ii) cost-effectiveness. Measuring dispersal and movement is often a major focus of research because it defines the explicit relationship of individuals in space (Cowen et al. 2006). Direct measurement of larval dispersal is difficult and expensive, while tagging studies of juveniles and adults may be misleading (Bolle et al. 2005) and (or) cost-prohibitive. Genetic measures often distill lifetime movements into a convenient measure of population differentiation, though this generally reflects historical connectivity that may differ from current connectivity (Waples and Gaggiotti 2006). In addition, it is difficult to maintain genetic sampling and analysis on a basis frequent enough to monitor relevant population changes on ecological scales. Likewise, advances in microchemistry have added a new and impressive technique

to recover individual spatial trajectories (Campana et al. 1994; Miller et al. 2005), but its effectiveness varies among taxa and time, it coarsely measures connectivity patterns, and it suffers the similar analytic and funding challenges as genetics. Such constraints to data collection can be particularly acute in emerging or data-limited fisheries.

Fishery-independent or -dependent sources of relative abundance measures are commonly available and are directly used in stock assessments, thus incurring no additional cost and maintaining consistency of population dynamics information (e.g., abundance indices) within the stock assessment process. As abundance trends accumulate through time, the relationships within management units may change, offering managers the ability to adapt appropriately to changing resource dynamics. Even when the uncertainty around the abundance index exceeds its usefulness as an informative source of population abundance within a stock assessment, the MUE can still offer insights into what scale the resource should be managed.

This approach does not invalidate other methods of detecting and defining population structure and management units. For instance, knowing the genetic composition of populations, the biological resiliency, or the actual mechanism behind dispersal and movement is invaluable for conservation and management decisions. This approach is instead an additional and practical tool for establishing management units at resolutions important to resources managers and useful under resource-limited circumstances.

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