

DEVELOPMENT OF INDIVIDUAL BASED MODELS IN MARINE FISHERIES RESEARCH

J. Jayasankar, Tarun Joseph and Shruthy AbrahamFishery Resources Assessment Division
ICAR-Central Marine Fisheries Research Institute**Setting**

Fish population dynamics describe how a stock or a combination of them changes over time as a function of growth, recruitment, mortality, immigration and emigration (Quinn & Deriso, 1999). It is the basis for understanding fish populations and associated fisheries and is the central component of any effort to assess the population dynamics so as to provide quantitative advice for fishery management (Hilborn & Walters, 1992).

Modern fisheries stock assessment models are evolving towards increasing complexity (Maunder & Punt, 2013), with capabilities to assimilate a diverse suite of data and incorporate spatial structure (Cadrin & Secor, 2009) and the influence of environmental factors. As the number of such efforts increase, the behavior and performance of these complex models need to be tested to assure a scientific basis for fishery management. These efforts to test the plethora of models have resulted in extensive simulation studies. These have been conducted to examine the robustness of the models and incorporate various process and measurement errors, including data quality and quantity (Chen *et al.*, 2003), mis-specifications of life history parameters (Deroba & Schueller, 2013; Punt, 2003), fishery characteristics (Cope & Punt, 2011), and violations of model assumptions (Guan, Cao, Chen, & Cieri, 2013).

Amongst these approaches one stream was oriented towards focussing on the habitat and ecosystem wherein the entire blend of biological dynamics are seen in action and models were built to suit them, leading to the ecosystem based models. Several approaches have been developed at the ecosystem level, motivated by the observation of some recurrent patterns of marine ecosystems, suggesting that interactions within the ecosystem are important structuring factors (Dickie and Kerr, 1982). For example, a widespread observation is the stability of the production of many marine ecosystems compared to that of individual species (e.g. Sutcliffe *et al.*, 1977; May *et al.*, 1979; Murawski *et al.*, 1991). The maximum sustainable yield (*MSY*) is extended to a set of exploited species that are considered to form a single stock (Brown *et al.*, 1976; FAO, 1978): the equilibrium production of the multispecies assemblage would then be a parabolic function of fishing effort and the *MSY* would correspond to the exploitation of half the virgin biomass of the whole assemblage. More recently, Polovina (1984) and Christensen and Pauly (1992) developed the ecosystem model ECOPATH, which is widely used among fisheries scientists. In this model, species are



aggregated into functional groups, which are related by fluxes of matter. Forming the basis of the model are two equations of mass conservation, describing the production and the consumption at equilibrium for each group of species.

This leads to the most important aspect of modelling, testing the sensitivity of assessment models for mis-specifications requires an operating model to predict population dynamics with known or assumed population parameters. However, most operating models are formulated identically to the population dynamic component built into the assessment model (Cope & Punt, 2011; Deroba & Schueller, 2013; Guan *et al.*, 2013; Punt, 2003), which implicitly assumes that the dynamic processes of the population are fully understood. To avoid this problem and test the assessment rigorously, an alternatively structured operating model is necessary to simulate the population dynamics.

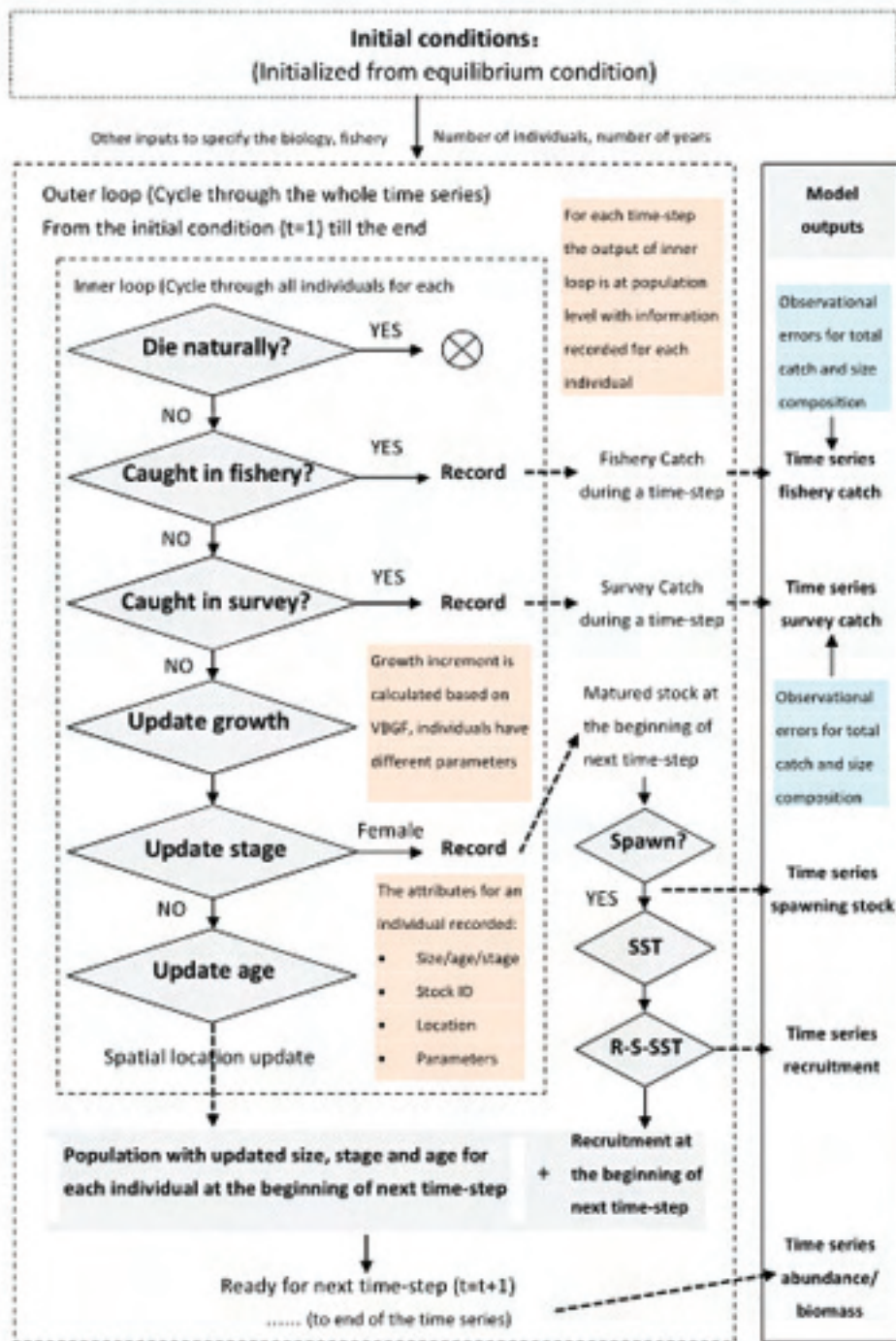
Individual-based models (IBM), which consider each individual of a population as an independent entity, have been widely used in ecology (Grimm & Railsback, 2005). The events (e.g., birth, death and predation) that occur within the simulation are at an individual rather than population level and the overall population dynamics that emerged is the sum of the individual interactions and behaviours.

The majority of individual-based models in fisheries science are developed to investigating fish behavior and fleet dynamics. They have been used to simulate the behavior of individual fish or fishermen with rules that determine their movement (Tyler & Rose, 1994; Wilson & Yan, 2009). Spatial heterogeneities in individuals and/or their environment have been added to develop spatially explicit individual-based models (Werner, Quinlan, Lough, & Lynch, 2001). However, only a few of these models have been developed for simulating fishery population dynamics. Kanaiwa, Chen, and Wilson (2008) developed an individual-based lobster simulator to simulate seasonal, sex-specific population dynamics for the American lobsters to evaluate the assessment model for that species. Further, the models that have been developed are either species-specific or focused on one particular aspect of fish life history (Kanaiwa *et al.*, 2008).

A typical IBM framework

Although many leads can be followed to formulate a framework under which IBMs could be modelled, the ringside view of the process can best be obtained from a simple depiction of an algorithm, one such being given below (Cao *et al.*, 2016).

The below figure depicts the steps and sequences alongside the checks and balances which create the sequences in a cogent way. Now the different life stages like, natural death, fishery mortality, growth, enhancement of age and stage, spawning and recruitment could have their own sub-conceptualisations of being either deterministic or probabilistic





and under either whichever established process presumed, thereby leading to a combination of options in the programming and software sense. A typical look at the possibilities could result in the following steps;

Stage	Model definition
Initial condition	Equilibrium; with an assumed period to attain that
Stock spatial structure	Multiple stocks each with unique biological identities
Stock recruitment relationship	Specified functional relationship between spawning stock and its recruitment rate; Beverton- Holt, Ricker <i>etc.</i> or even incorporation of environmental parameters like SST
Recruitment	Can be directly put or could be derived from the S/R relationship with random fluctuation added; must be adjusted as per the intra annual pattern expressed by the resource(s) modelled
Natural mortality	Could be randomness added to the base value defined based on length or age
Fishing mortality	Classic method of merging catchability, effort and selectivity; random threshold could be used to simulate fishing mortality
Growth	VBGF based depiction
Life stage	Number of stages and the mean size at each stage could be the core with random normal deviations completing simulated values
Survey	Modelled similar to Fishing mortality
Observational error	A lognormal based error term added to the catch figure aggregated over time, length and area
Multi-species	Parallel replication of these steps for as many resources as planned to be simulated/ studied

A broad-based IBM

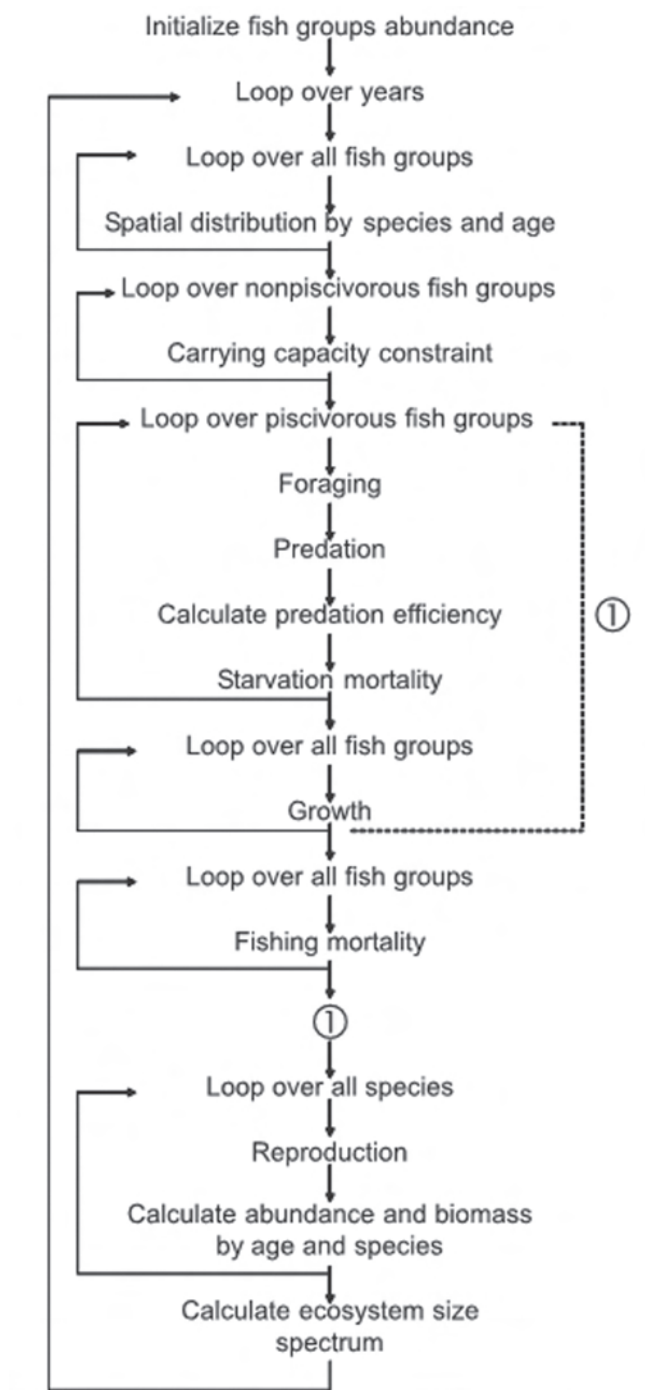
Another more holistic variant of this type of IBM could be one including much more broader habitat based components like availability of lower trophic level (LTL) biomass and the higher level foragers and their predators. The availability of food and the growth stage combination clearly heralding the status of larval mortality and the resultant niche based competitions between resources could also be included through IBM thereby scaling up to simulate regional ecosystems. One such comprehensive model is "Object oriented Simulator of Marine Ecosystem Exploitation (OSMOSE)" (Shin and Cury, 2001, 2004). Herein the criterion for the selection of prey by a predator was considered to be firmly based on body sizes with opportunism applied at individual level with a localization principle based on the vicinity coming into picture. A cohort or super individual was made as pivot and the bio-phological dynamics applied on that and replicated to the tune existing in the area and focus. Four



model classes, which represent particular ecological entities, are used: the class "system", the class "species", the class "age class", and the class "fish group" (Shin and Cury, 2001). From each class, which is characterized by attributes and functions (e.g., growth, predation), a number of objects are created that are part of the simulated system. The architecture of OSMOSE is hierarchical, because a fish group belongs to an age class, which in turn belongs to a species. This structure enables the investigation of some key variables at different levels of aggregation, in particular the size spectrum of fish assemblages.

The process of implementation of OSMOSE can best be explained using the flow-chart given here:

As can be seen from the figure, the dynamics associated with growth, mortality, reproduction (spawning) etc. could be modelled using the conceptualisation described in the previous case. But the new broadbased habitat and trophism based components need some elaboration. The parameterization of the components is presented in the following table.





Stage/ Component	Model Definition
Foraging	This is to be planned in such a way that the movement probabilities to the nearest spatial cell is highest and the availability of suitable prey/ LTL leading to feeding / starvation otherwise; It is a function of biomass and vicinity
Predation	This is functioned based on the spatio temporal co-occurrence of prey- predator and the size of both; The prey- predator size ratio was subjected to a literature (Fishbase) based threshold and the subsequent dynamics planned thereafter.
Starvation mortality	This is depicted as a function of density dependent issue dependent on intra specific competition and is built upon predation efficiency as defined by Beverton and Holt (1957)

With these cardinal principles in place OSMOSE is rolled out to simulate regions under study but with two very important safeguards, first being the localised calibration and the second the sensitivity analysis. These are computationally intensive procedures leading to thousands of trial runs with various combinations of input parameters including crucial ones like larval mortality and plankton availability, whose sensitivity have been historically be recorded as delicate and hence crucial. Once validated with a decent strip of time step these calibrated tweaked models can be put to great use in estimating, simulating and forecasting marine fishery resources.

Conclusion

Though IBMs offer a very robust modelling crucible for complex marine ecosystems, their success rate is severely dependent on the local tuning and sensitivity testing. Further as these are trophic level flow based, proper input on the LTL front using feeder models like Nutrient Phytoplankton Zooplankton Detritus(NPZD)- Regional Ocean Modeling systems(ROMs) may have to be coupled with the OSMOSE runs for more efficient forecast/ simulation. As such for systems where good coverage on the crucial biogeochemical and productivity parameters coupled with regular sample surveys on resource biology is undertaken these type of IBMs could turn out to be real boon.



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