VI. Application 3: Recruitment Prediction

Contributors: S. Sarah Hinckley, Bernard Megrey, Thomas Miller

Definition

What do we mean by recruitment prediction? The first thing to consider in defining this term is the time horizon of the prediction. Short-term predictions mean the use of individual-based, coupled physical biological models (ICPBMs) of fish early life history to predict annual recruitment, most likely to aid managers of a fish stock. These predictions may be made via indices or other measures of prerecruitment or recruitment, derived from ICPBM output, that correlate well with other independent reasonable predictors of recruitment (derived from stock assessment models, juvenile or pre-recruit surveys conducted with acoustic or trawl or other net-based survey methods). These may be used alone or in conjunction with other predictors such as spawning stock biomass. Actual numerical estimates (of the correct magnitude) derived from ICPBMs may be possible, but only if certain conditions are met (e.g. the super-individual method, proportionality indices or other methods to relate model indices to real population numbers are used, spawning biomass, or egg production estimates as initial conditions are included, etc.). A benefit of these indices would be that they would serve as a replacement for expensive juvenile surveys.

Under this definition, the forecast window for recruitment predictions would be limited to the number of years from spawning to recruitment for each species of interest. This is due to the fundamental lack of predictability of the regional and small scale ocean physics. This prediction window will be different for each species due to differences in the unique aspects of a species life history.

Longer-term recruitment predictions that are likely under different future scenarios of climate, fishing, ocean-variability, etc. may also be derived from ICPBMs through the use of the models to gain a mechanistic understanding of the important bio-physical processes underlying recruitment variability. This knowledge may, for example, help us understand simple correlations between bio-physical factors and recruitment, and when such correlations may or may not hold up.

In order to develop recruitment predictors from ICPBMs, we also need to carefully consider what we mean by the term “recruitment”. There are many ways of defining recruitment. The operational definition depends on the purpose or goal of the prediction. Are we predicting recruitment for management purposes? If this is the case, then recruitment is often defined as the number of fish entering the exploited segment of the population, where the meaning of “exploited segment” depends on the distinctive attributes of each fishery (i.e. gear type, time and space scales). If examining life history characteristics or gaining ecological understanding is the goal, recruitment could be defined as the number of fish reaching a juvenile nursery area, the number maturing or the number reaching a particular age.

Objectives of recruitment prediction

There can be several different objectives for recruitment prediction, and these will affect not only how we select a predictive index from the model, but how the ICPBM itself is constructed and its relevant physical and biological details. Recruitment prediction may be undertaken to test our understanding of the processes that affect recruitment. ICPBMs may be developed to clarify mechanistic processes underlying correlations between physical or biological factors and recruitment. Recruitment prediction may be applied or pragmatic, for example, to aid in the reduction of the number of recruitment scenarios that must be performed in the stock assessment modelling process.

Who are the clients/consumers of the forecasts? To maximize the usefulness of recruitment forecasts, they need to be tailored to the "clients" who will use them. The needs of scientific researchers, resource managers, and commercial fishery concerns may be different. For example, a forecast prepared for a scientist might be used as a null hypothesis to demonstrate whether (or not) the forecast embodies sufficient understanding of the processes and mechanisms that cause good and bad year classes. In contrast, commercial fishery business decision-makers may require a forecast only to base future buying decisions regarding capital expenditures for equipment or ship improvements. Their emphasis is not so much on perfect understanding. For example, if a forecast tells them they can expect several years of good recruitment, then they might decide to purchase automatic fish filleting equipment optimized for small fish sizes. If recruitment is not expected to be good, then they can conclude they will be exploiting older individuals from the population and they should opt to purchase filleting machines optimized for larger fish sizes. In either case their goal is to maximize product recovery, and having the right equipment for the correct circumstances plays a large role in attaining their goal.

Indices of recruitment from ICPBMs

When using ICPBMs to aid in the prediction of recruitment, an index that appears to correlate well with recruitment can be used. Often, these indices relate to some underlying theory about recruitment success. Some examples of recruitment or prerecruitment indices that have been or could be derived from ICPBMs are (1) the number of larvae or juveniles that reach a specified nursery area weighted by their residence time there (Parada *et al.*, in review), (2) the number that reach a nursery area by a particular date, size or age (Baumann *et al.*, 2006; Bartsch *et al.*, 2004), (3) indices of larval drift or retention, such as the number going in a predefined direction (Wildebuer *et al.*, 2002; Wespestad *et al.*, 2000; Stockhausen, AFSC, pers. comm.), or that experience different levels of bottom depth anomalies (Baumann *et al.*, 2006) or a survival rate after a certain number of days of drift (Allain *et al.*, in Review, (4) indices of overlap of larvae with their prey (Hinrichsen *et al.*, 2005), or (5) indices of juvenile particle density at the end of a simulation to look for density-dependent processes related to recruitment (Baumann *et al.*, 2006).

Indices may be compared to data, for example surveys of prerecruits or recruits. Indices may also be compared to stock assessment model estimates of recruitment. In this case, caution is needed. The same data may be used in the ICPBM and the stock assessment model (for example, spawning stock biomass); therefore, the indices produced by them may not be independent.

The proper choice of recruitment indices will depend on the objectives of the work, on the life history of the species, and on theories of what processes are critical to recruitment variability. The development of a conceptual model (see below) can aid in the choice of indices.

The need for a conceptual model

Development of a conceptual model of the processes controlling recruitment for each species and area is key to the use of ICPBMs in recruitment prediction and to the choice of the proper indices derived from the models. Development of a conceptual model is a way to organize thinking about what is important, how important a role particular processes play, and what life stages are affected. If this is neglected, important factors or processes may be missed in the ICBPM.

To develop a conceptual model, it is necessary to identify:

(1) the life stages, and their duration,
(2) the variation in mortality at each stage,
(3) biological and physical factors affecting each stage, and the "intensity" of the effect,
(4) processes important within each stage.

It may be necessary to develop different conceptual models for the same species in different areas, if different processes at different life stages are thought to be important. For example, Gulf of Alaska (http://www.pmel.noaa.gov/foci/forecast/mgt.html, Figure 1) and Bering Sea (http://www.pmel.noaa.gov/foci/sebscc/results/megrey/bs_concept.html, Figure 2) walleye pollock conceptual models below contain the same life stages and duration. But they differ with respect to which life stages experiences the most variability in mortality and the factors that influence mortality and survival. Therefore somewhat different ICPBMs have been developed, and different indices may be necessary to predict recruitment.

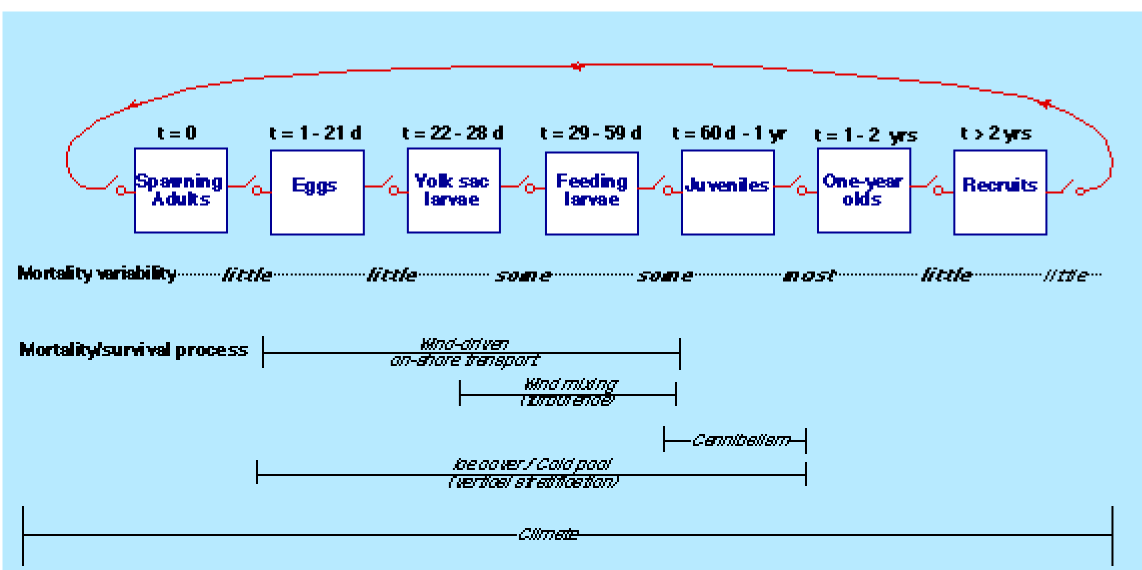

Figure 1. Gulf of Alaska walleye Pollock conceptual model (from Megrey *et al.*, 1996)

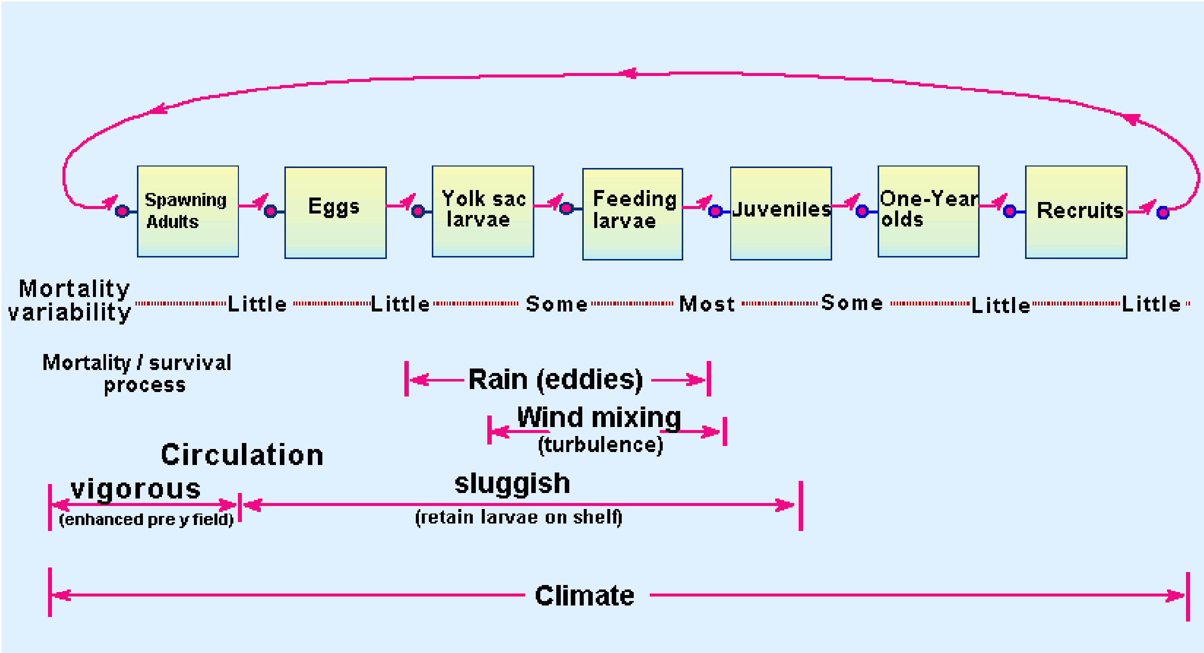

Figure 2. Eastern Bering Sea walleye pollock conceptual model (from Megrey and Wespestad, 1997)

Conceptual models are not stagnant. They evolve as new information and understanding become available. For example, the original GOA pollock conceptual model (Figure 1) has recently been modified to include the effects of regime scale climate impacts as well as predation and competition effects (species-to-species interactions) known to be important at the ecosystem level. (Bailey, 2000; Bailey *et al.*, 2005, Megrey and Macklin, unpublished).

Forecasting accuracy

How accurate do recruitment forecasts have to be before they become useful? This is a difficult yet relevant question that needs some immediate research attention. A recent paper by De Oliveira and Butterworth (2005) offer a concrete example of a possible approach. Their premise was that environmental indices that provide short-term predictions of recruitment have the potential to improve the average yield from highly productive resources that sustain recruit fisheries without an associated increase in risk (of resource 'collapse'). In this paper they asked, *How accurate does an environment-dependent spawner-recruit relationship have to be before they affect management decisions?* Specifically, what are the benefits of using environmental indices to set appropriate Total Allowable Catches (TACs)? Through a controlled simulation experiment, their conclusion was that an environmental index needs to explain roughly 50% or more of the total variation in recruitment ($r^2 \geq 0.5$) before the management procedure starts showing benefits in terms of the summary performance statistics for risk and average catch. Having similar quantitative information on recruitment forecasts from ICPBM models would help frame the circumstances in which they could prove to be of benefit.

If an index derived from an ICPBM is to be used for recruitment forecasting, it is critical to assess its accuracy and to build trust in its ability to forecast.

Techniques for forecasting

Forecasts can take many different forms. They can take the form of quantitative annual estimates of absolute abundance (e.g. there will be 5.5 billion recruits next year). We do not believe these are very useful and they are difficult to produce with any accuracy and precision. They can be qualitative. For example, the forecast could be given in terms of recruitment being in a particular state—below average, average, and above average (high, medium, and low) — with appropriate methods used to operationally define those states such as long terms averages, or quantiles (33%, 50%, or 66%) based on observed recruitment trends. Rothschild and Mullen (1985) give a good example of how recruitment information (from data or models) can be usefully described by non-parametric classification based on Markov chains. Finally, a recruitment forecast could be the result of an ensemble estimate from numerous stochastic forecast implementations. The forecast can be delivered as a probability statement—for example, the probability of achieving a given recruitment level or state given x conditions and y assumptions is 10%. The most appropriate form depends on many factors including many that have been discussed above, such as who the forecast is being prepared for, how it will be used, the required accuracy, and the required forecast horizon.

A caution should be offered regarding the use of recruitment estimates from stock assessment models to calculate metrics as described above. Changes/updates in annual stock assessment/cohort analysis models and resulting recruitment estimates make the most recent estimates of "recruitment" somewhat of a moving target. Stock assessment models estimate recruitment by summing up all of fishes from a cohort (all individuals with the same birthday) that have died due to the fishery (i.e. the catches) and then make adjustments for the ones that have died from natural causes. In other words, the recruitment estimate is the population that had to have existed in order to generate the catches we have observed. The data point of most interest is usually the current year. If a cohort is still contributing to the catch, then in next year's assessment an additional year of catches and losses from natural mortality will increase the recruitment estimate relative to the current year. The recruitment estimate will gradually increase through time and finally will stabilize once the cohort is completely fished out (i.e. no more individuals of the cohort survive to add to the catches).

Philosophy of modelling

Approaches to understanding mechanisms that regulate recruitment in fish have increasingly taken an individual-based approach. This approach can be justified on two general grounds. Field research into recruitment processes in fish has demonstrated that the individuals that survive early life often possess a unique suite of genotypic or phenotype traits that are not simply a random draw from the distribution present at spawning. For example, numerous studies involving otolith microstructure have demonstrated that survivors are selected from a narrow window of the original distribution of birthdates. Other research has shown selection based on growth rate, size at settlement, spawning location and maternal source. Together, these studies highlighted that we would likely not understand mechanisms regulating recruitment by measuring mean rates; rather, we needed to characterize the sources, patterns and consequences of variation among individuals in early-life traits and understand why the unique subset of traits possessed by recruits conferred a survival advantage. The second justification for individual-based approaches invokes the importance of spatial processes in regulating recruitment. Sinclair and Iles (ref) proposed a Member-Vagrant hypothesis in which population persistence relied upon the existence of closed trajectories that allowed surviving larvae to complete their life cycle. Those larvae that "followed" appropriate trajectories became members of the reproductive population; individuals that "followed" inappropriate trajectories were lost to the reproductive population. This hypothesis built on the existing understanding of the importance of population structure within a species, to emphasize the importance of the spatial location of larvae at different points in development on their subsequent survival.

Coupled physical biological models addressing questions involving fish early-life histories typically have adopted an individual-based approach. The majority of such models have used a grid-based hydrodynamic model to predict currents at nodes on the grid, which are then used in a LaGrangian particle-tracking algorithm to move particles that represent the early life stages around the model domain. For example, in one of the earliest applications of such models, Bartsch and colleagues (ref) considered the trajectories of herring larvae in the North Sea. The model results indicated the importance of a retentive area off of the east coast of Scotland. Subsequently, ICPBMs have become more sophisticated in both the representation of the current fields, and the biological representation of individual fish. Such models have been used to quantify the contribution of different spawning locations to recruits, the role of physical processes in regulating feeding, and the influence of mortality on spatial distributions.

However, it is vital to assess and separate the biological motivations for individual-based approaches to study fish populations from the computational motivation. Computationally, individual-based approaches are attractive because they combine elegantly the grid-based, spatially-specific predictions of hydrodynamic models with biological processes. In so doing, such models create individuals that differ with respect to their trajectories and thus their exposures to environmental forcing. To ease computational demands, population-level predictions are derived by expanding the predictions for a single particle by a multiplier to represent the contribution to the population. This approach implicitly assumes that all variability in early-life history is spatially-determined. Simply stated, this approach assumes that all variability arises because of difference among the trajectories followed by individuals, and not by inherent biological inter-individual variability. The approach emphasizes the importance of Member-Vagrant type ideas at the expense of phenotypic variability among individuals. Not all models make this assumption. A few do include and sample from distributions of traits. For example, in their detailed model of feeding Fiksen and Mackenzie (ref) sample from distributions of reactive distances to estimate feeding incidence. However, ICPBMs of the entire early life history that incorporate inherent inter-individual variability have yet to be developed. Whether the development of such models is important depends entirely on how total phenotypic variability is partitioned between spatially-derived sources and inherent inter-individual differences. This partitioning is, as yet, unexplored and unquantified.

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