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Eco-evolutionary impacts on survey data and consequences for fisheries management

Eco-evolutionary drivers of survey bias and consequences for fisheries stock assessment

Eco-evolutionary forces conspire to bias fisheries survey data

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# Abstract

Surveys of managed populations are the result of many factors: biological, ecological, genetic, and statistical (observation); these play out in space. We show that some/all/none of these factors is the most influential in terms of the uncertainty in survey data and quantify the impacts on the resultant management outcomes (via error in SSB/depletion). This finding does/does not hold up when the underlying environmental driver is/is not included in the assessment. This finding does/does not hold up when the model used to perform the assessment is very complex (e.g., includes age comps)/depends wholly on the index. These findings did/did not vary by species life history, with those that are more sensitive to ecological forcings and/or fast-living showing greater bias than those who don’t.

These results indicate that survey designs should carefully consider the genetic and ecological aspects of surveyed species when optimizing spatial survey designs, and stock assessors should also think about this when at-will inputting environmental drivers into the assessment.

* What did you find? [core results – say something useful – no motherhood statements or deference to the main text!]
* What does this mean? [interpretation in context]
* What is it good for? [application]

No one will bother to download and read your full paper (or cite it) if they are not interested by the abstract.

# Introduction

Ecological and evolutionary factors interact with fishing activity to induce dynamic variability in marine resources. **Genes environment growth reproduction movement prey availability chaos what is chicken and egg – AND fishing pressure can impact this – what is important to model? Climate change makes it more complicated.** Surveys of animal populations underpin the scientific management of living natural resources. In the fisheries management context, the survey often comprises some of the most important data streams: for data-rich fisheries, the biomass time series as well as compositional data can inform population structure and recruitment. In data limited fisheries, a survey is sometimes the only data input present aside from catches. These pieces in the estimation framework (the assessment) result in the management quantities that impact livelihoods (harvest rates) and the conservation/perpetuation of the stock and fishery.

An observation of species abundance, often in terms of biomass, is the result of all the eco-evolutionary complexity mentioned above, as well as the timing, gear type, sampling design and expansion (standardization) method of the survey used to make the observation. Much attention has been given in recent years to the value of considering spatio-temporal factors when standardizing surveys (Thorson and friends), optimizing multi-species survey designs (Oyafuso 2021, 2023), with the recognition that the dynamism within the marine system that will impact fisheries management occurs in a special theatre. It has long been assumed that population that is non-homogenous through space can induce bias in a survey (**cite**).This can occur because homogenous fish are patchily spaced out, hetereogenous phenotypes are present (and perhaps differentially encountered by gear, etc), or a mix of the two.

The ideal survey captures both the scale and trajectory of a population through time, and has associated sampling error that does not preclude the estimation of management quantities. Population processes such as allele frequency matters most in this context when it impacts demographic rates (growth, mortality, reproduction, and movement) as these can all impact the precision and accuracy of the survey. In turn, demographic rates might

**It is unusual to model the entire system in an assessment so we typically hope our survey is doing a good job of capturing the variability.**

**Clarify that the genetic variation matters most when it impacts demographic rates (growth, mortality, reproduction). Growth particulary improptant because it can impact contact selex, and also maturity schedules.** Given that many regions are revisiting their survey designs, AND we are using spatio-temporal standardizers, AND we know climate change-fishing pressure is causing species to move and evolve, it’s useful to disentangle which of these forcings are most influential. Specifically, if we find that it “all comes out in the wash”, that’s reassuring. There might be certain genotypes or life histories that render stocks more susceptible to undesireable outcomes in this management framework. It’s also important to know whether our assessment methods, if any, are capable of handling this problem. So the big-picture is we want to break down “things fisheries managers should consider” when it comes to evolutionary/life history factors (genetics), climate-change susceptibility (o2/temp issues), potential predator-prey dynamics, how this plays out in space, how this plays out in your survey design, and how it plays with your assessment. The hypothesis is that any degree of patchiness induces bias in a survey (we know this from earlier work). I think that morphometric variation will exaggerate the patchiness effect, and perhaps induce undesireable bias even in non-patchy populations. Those that are fast living/evolve quickly (degenerate to patchy) have the highest risks of becoming...

This study uses Ev-OSMOSE, an ecosystem model that captures [**summary, cite Morell]. Briefly describe validation.** This enables us to investigate how ecosystem and evolutionary dynamics contribute to bias in a) survey observations of biomass and age composition data, and b) management quantities estimated from stock assessment models of variant complexity. We hypothesize that the performance of the assessment model is better predicted by the individual species’ eco-evolutionary response profile – how it reacts to a warming and deoxygenating ocean – than the complexity of the assessment, or whether or not the assessment includes an environmental index. These results can illustrate which eco-evolutionary characteristics might bias data collection for a managed species, and the trade-offs in assessment methods for such populations.

# Methods

**Overview**

There are three components to our simulation study: 1) the operating model (OM), which simulates an **ecosystem with many species** under a set of assumptions about the genetic, ecological, and demographic structure and the behavior of a singular fishery fleet; 2) the sampling model, which surveys the population(s) within the OM and generates a time series of biomass and compositional data; and 3) the assessment model, which takes the catch and survey data and generates estimates of management quantities for a single species. Our analysis involves four focal species, selected for their how their unique eco-evolutionary characteristics manifest as spatial responses to a climate change scenario. We perform single-species stock assessments on the data sampled from these populations using a small set of assessment models, corresponding to methods that do/do not account for age structure of the stock, and do or do not incorporate environmental information.

**Operating Model**

We simulated populations using the Ev-OSMOSE model, which incorporates genes and projected environmental conditions onto a model spatial system (**northern barents sea**). **Describe model features, including spatial extent, point to scenarios below; do they all use the same climate change assumption?** **Explain that we are getting single-species time series from each scenario for X focal species, chosen for their distinct expected response to climate change over the next Y years (details belwo)..** Variation among operating models was determined by RecDevs. Number of years. Treatment of early/post years (eg is there a burn-in)? Species we examined (3 max, maybe life history related). Runtimes.

**Data Generation**

We extended the previously-published model to include a sampling regime that generates an index of relative abundance, uncertainty thereof, and compositional data for the surveyed species. The sampling routine assumes that all ages and lengths of all species are equally likely to be sampled (e.g., no age- nor length-based survey selectivity is assumed). We assume that the catchability of all species is 1 and this does not vary spatially (but see Gruss et al 2023). The survey follows a simple random design with 100 stations (unique cells in the OM domain) operating over six weeks during the Boreal summer (mid-June to early-August; results of a sensitivity analysis to a higher and lower number of stations are provided in the Appendix). For each replicate of the OM, the 100 survey stations are randomly selected at the beginning of each year, and a ‘track’ through the stations from south to north is generated such that all 100 stations are visited over six weeks with minimal total transit distance. The estimate of biomass for the entire region for species *s* in year *y* and its associated variance is calculated by expanding the average biomass across all stations for the entire region, based on the area *A* of each spatial cell. **Equation**. Age compositional data are obtained by multinomial sampling of the numbers-at-age in each surveyed cell. **Equation. Compare to existent survey study designs.**

**Estimation Model (stock assessment)**

This study is concerned not only with the degree of bias that genetic and ecological factors can induce in survey data, but also the robustness of commonly-used assessment frameworks to that bias. Therefore, we constructed four assessment model frameworks along two axes: model complexity and consideration of environmental impacts (Figure X).

The first axis, model complexity, is addressed by whether or not age structure is considered in the model. These are represented by JABBA and WHAM. **Describe JABBA and emphasize use in many fisheries, data inputs. Describe SS or WHAM.** Both model types use the catch and survey biomass data; the WHAM model also uses the age-compositional data. **Describe what both assessment approaches produce. Reference appendix for how these models were parameterized.**

**Experimental Design**

*Simulating morphometric and spatial patchiness via four focal species*

In the real world, morphometric diversity arises via a combo of eco-evoluationary forcings, as well as fishing pressure. This can covary with space due to habitat/fishing behavior, or not (particularly for mate-selecting individuals like POP). Because this study works with real/representative species, we selected those that are expected to manifest distinct responses to a singular climate change scenario. **In the model, morphometric diversity and spatial patchiness co-arise via the following:** This occurs in the model thru the functional relationship between o2/temp/growth. For the focal species, this means that when temp is X, growth is Y. this is published as a realistic. The spatial “layer” of o2/temp means that individuals residing in areas Y will be larger. **Species x will become like scenario 1 because y; detail other two. Detail life history distinctions among them.**

To investigate the relative impacts of spatial patchiness and morphometric diversity, we selected four focal species that represent distinct responses across these axes (Figure X). The first focal species is Sole, which the population is genetically homogenous and spatially uniform (low morphometric diversity, low patchiness). The second two species, Cod and Dab, exhibit gradient-style responses. These are distributed evenly through space but exhibits genetic/phenotypic diversity **of relevance to the survey (high morpho diversity, low patchiness, POP example).** The fourth and final scenario is Herring where both measures are high: the species exhibits high morphometric diversity and is spatially patchy, such that the survey might encounter a single unit of genetically ‘unique’, and morphologically unique individuals who are similar to one another but distinct from those found in other patches (**this is like a big haul example). Mention food availablilty etc.** All four of these case study species are dealing with eco-evoluationary forcings that impat their spatial distribution of biomass and age structure for various reasons, and this can only be captured by the ecosystem model.

Each of these four focal species represents four eco-evoluationary scnarios, from which survey data are sampled **time dimensions.** These data sets are then passed to all of the four stock assessment frameworks described above, for a total of sixteen experimental scenarios (four eco-evoluationary paradigms and four assessment methods). Each assessment method was fit to **1000** replicates of the operating model, with variation induced by Y (see above). Because the operating model represents the entire ecosystem (all species), the same 1000 replicates were used for each of the sixteen experiments.

**Performance Metrics**

We evaluate the performance of each experimental scenario through several lenses. The foremost is the comparison between the reference points and time series of estimated biomass from the stock assessment to the true population (the operating model). We quantify this relationship by calculating the mean average relative error (MARE) across experimental replicates for each species, year and scenario. The MARE scores indicates the bias induced in the management system as a result of the eco-evolutionary forces specified in the OM and modeling decisions made for the assessment. A secondary, metric is a visual and quantitative comparison of the compositional data, biomass and variance thereof in the true population and from the survey, and the model-estimated fits to the observed survey data for each scenario. The quantitative comparison among these data sources is again the MARE of either the observed data and

This metric illustrates how eco-evolutionary forces may induce discrepancies between the population and survey observations, and how well various assessment models might respond to these data.

**Assessment model diagnostics**

We applied two modern diagnostic tools designed to detect systematically poor fits to survey data. Though our study is not a management strategy evaluation, it is useful to know whether the scenarios presented here result in mis-fits sufficient enough to be flagged by such an algorithm (as, in practice, an assessment author won’t know which scenario they are in). A run’s test (Carvalho et al., 2021) was conducted on the fits to the biomass time series data, and an examination of one-step-ahead residuals (Trijoulet et al.) was done for the fits to the survey age compositions. For each scenario, we calculated the p value for the run’s test given by XX, YY is failure; one-step-ahead residuals were visually examined for cohort patterns and for outlying values greater than 4.

# Results

# Discussion

Limitations:

* we didn’t built an optimum survey design, just used what was similar to what’s already done. Cite Zack and say there are ways to optimize for variance, but we still are revealing how those assumptions might be violated.
* We similarly aren’t going to go insane on the selectivity/estimation regime.
* The movement module is fairly crude with two layers: a binomial “habitat” layer that indicates whether or not habitat is suitable, and then random diffusion among suitable cells. This means that we lose the nuance as temperatures slowly increase, fish don’t slowly follow the gradient of desireable habitat; instead the binomial layer for suitable habitat changes abruptly.The focus of this study was on how these dynamics impact survey bias and determining thresholds.
* We had to pick certain values for the morpho-patchiness setup. There’s possibly intermediate cases but we wanted to show where the effect could be picked up.
* We also didn’t do a full MSE – e.g., respond to the (biased) assessment each year and change catches accordingly. This would’ve modulated the fishing pressure: for example, those with lower estimates of biomass would’ve been fished less hard, possibly reducing the impact of evolution. The fishing pressure versus evolution wasn’t the main angle.
* We didn’t use an STRS algorithm for designing the survey. These typically result in a multispp cv lower than the SRS cv (but higher than a single species survey cv). This is a ton of work must be tuned for a given system.
* There’s obviously more gradient than SPM vs WHAM but kept it simple. Mention how an ASPM might deal.
* The environmental treatment in each model type isn’t equal, but that’s the nature of what’s possible/what’s normally done. OM assumes panmictic reproduction which might not be the case in patchiness.

# References

# Tables

Table 1. Overview of experimental design .Description of four focal species

# Figures

Figure 1. First column: average biomass during projection period. Second column: Time series true (black points) and observed (blue points) survey biomass, with 95% quantiles (vertical bars), and fits to these data from the four assessment models (colored lines). Third column: MARE in spawning biomass for four assessment models fit to 1000 OM replicates (positive values indicate estimates greater than the OM). Fourth column: MARE in [SOME REFERENCE POINT] assessment models fit to 1000 OM replicates (positive values indicate estimates greater than the OM). Rows correspond to species.

Appendix: biomass x year x species. Survey tracks x year x species.

Potential Oms PRO/CONS

|  |  |  |
| --- | --- | --- |
| Model | Pros | Cons |
| Ev-OSMOSE | Built, parameterized  Genetics/habitat/climate are explicit  Is IBM so NAA for sure in there | I might not be able to run it  Unclear mod level  Need to build sampling module  Might be stuck with specific species |
| John’s Julia simulator | Built, in Julia | Hard for me to run  Would need to build sampling and climate module  I don’t think it’s numbers-at-age  Would need to deal with john |
| MixFishSim | Has catch and survey modules  Open source r package | I don’t think it has climate but it does have movement  Delay-diff model only tracks biomass, not NAA – so it’s impossible to do comps  Might need to re-write this model in TMB and with age structure. If not, limited to just doing JABBA-select with env covariate  Uses outdate packages (randomfields and mixfishsim) |
| AEP’s matrix code | Started in R, simple  Easy to manipulate life history | Definitely needs add ons for climate and sampling |