

A bayesian model for European hake with priors based on life history invariants

Authors: Santiago Cerviño(1), Margarita Rincón (2), Samu Mäntyniemi (3), José Castro (1) and Javier Ruiz (2)

(1) Instituto Español de Oceanografía (IEO), CO de Vigo, Spain; (2) Instituto de Ciencias Marinas de Andalucía, Consejo Superior de Investigaciones Científicas (ICMAN-CSIC), Spain; (3) Fisheries and Environmental Management Group, University of Helsinki, Finland;

Presenter contact details: santiago.cervino@vi.ieo.es, Phone +34 986492111

Summary

European hake is a main target fish for the fleet operating in Atlantic waters, although there are many biological unknowns that compromise the quality of the current assessment and scientific advice. Growth, natural mortality and reproduction are main biological processes required to develop population dynamic models for assessment purposes. Currently, the parameters defining these processes such Von Bertalanffy asymptotic length, M , L 50% of maturity or Beverton-Holt steepness are estimated outside the model and set as constants. Population dynamic bayesian models provide a suitable platform to develop solutions to this kind of problems since Bayesian models allow using additional knowledge from similar species in the form of the priors. Informative priors for biological key parameters have been developed based on available data for Northern hake combined with information from other hake species all over the world. This information is analyzed on the light of ecological theory for life history invariants (LHI) to produce the required priors. LHI figures are relatively constant among similar species. Information from other hakes may help to fill the gap in assessment and management of European hake. The pros and cons of using these informative priors to improve hake assessment are finally discussed.

Introduction

ECOKNOWS (Effective use of ecosystem and biological knowledge in fisheries) is a FP7-KBBE project on the topic of "improving fisheries assessment methods by integrating new sources of biological knowledge". The main aim of the project is to develop models that use biological information which is likely to be useful for the management of specific stocks in a bayesian statistical context. Bayesian statistics uses "prior" knowledge that we already have before starting to analyze new data. If the new data include more information about the parameters, then the Bayesian calculus combines the prior information with the new information in a process that can be called scientific learning. Northern hake has been one of the selected case studies to prove the value of this biological information improving assessment models. This work, still in course, is being performed throughout two main tasks: (1) the development of a bayesian model in JAGS (Plummer, 2013) similar than the current hake assessment model (ICES, 2012) and (2) the development of priors based on life history invariants (LHI) (Beverton, 1992 and Charnov, 1993) using biological information from different hake species all over the world. The progress in these tasks is presented here for discussion.

Material and Methods

The first stage of this work is the development of general population dynamic model (GPDM). The goal of this work is to develop a Bayesian model for Northern hake able to deal with the biological process. In this first stage our aim is that the model presented reproduces as much as possible the structure and main assumptions of the current ICES model in a Bayesian framework. This means that no informative priors are used in this stage. A full model description with their structure and main assumptions has already been presented in Rincon *et al.* (2013).

In parallel with the first stage we have developed biological priors based on existing information from other hakes and also based on life history theory. These priors consider

biological parameters for maturity, growth and natural mortality, but also for the interactions among these parameters. Information from other hakes was taken from FishBase (www.fishbase.org) and also from a grey literature revision. LHI theory predicts that the relationship between some life history parameters is relatively constant. Based on this theory, biological priors might be built based on the expected value of these parameters and their variability estimated from other hake information. Charnov and Berrigan (1991) present 3 invariant patterns in life history: (1) L_m/L_{inf} is relatively constant among similar taxa; (2) k and L_{inf} are negatively correlated; and (3) k/M tends to be relatively constant in similar taxa (where L_m is length at maturity; L_{inf} and k are the VonBertalanffy asymptotic length and growth rate and M is the natural mortality). Starting with the available information for length at maturity for Northern hake and with the LHI figures from hake literature we have built priors for L_{inf} , k and M and also priors for the interaction among them.

Results and Discussion

The Bayesian model is near to be complete and all the main processes (biological, fishing fleets and surveys) needed to reproduce the current ICES model have already been implemented. However, the convergence level needs to be improved. This task is progressing reducing the model complexity in term of length, time and fleets aggregation. Although it is necessary to keep a minimum level of model complexity to answer the required questions; for instance, some critical parameters (e.g. growth parameters) can only be estimated accurately if the length groups are detailed enough to follow the length distributions along the time.

Regarding the LHI analysis, the results show their usefulness to develop biological priors for L_{inf} , k and M presenting some specific behaviour for hake. For instance, whether for most fish the value of the LHI L_{inf}/L_m is around 1.5, in the case of hake this is near 2.5. This means that hake continues growing after maturity much more than most fish, which is an important feature in hake productivity. Other important finding is that maturity, growth and mortality are processes that can not vary independently and the consideration of the correlations among these parameters might improve the accuracy of the biological parameters estimated inside an assessment model.

References

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