

Postbus 68 | 1970 AB IJmuiden

Ministerie van Landbouw, Natuur en Voedselkwaliteit  
T.a.v.: Vincent van der Meij  
Bezuidenhoutseweg 73  
2594 AC Den Haag

Auteur(s): Iago Mosqueira, Morgane Amelot

The following report summarizes the work carried out in 2021 for further development and testing of the methodology used for management strategy evaluation for the exploited stocks in the IJsselmeer. The work was concentrated on methodological issues related to parts of the current analysis (Tien et al., 2020) that were considered less robust: improving the use of survey and market data in the conditioning of operating models, and refining the status indicators based on length samples in the catch.

For the later, an alternative method to the one currently applied (LB-SPR, Hordyk et al. 2014) was implemented into the FLR simulation platform and tested on both simulated and real data. The LIME method (Rudd and Thorston, 2017) was chosen as a possible replacement, as it is more adaptable to the particularities of the IJsselmeer fisheries (e.g. gear selectivity).

Regarding the conditioning of operating models, an algorithm based on Approximate Bayesian Computation (ABC, summarized by Sunnåker et al. 2013) was implemented and tested. The method is a natural extension of the one currently used, with more flexibility about the sources of data to be included and the manner in which they can be used.

Finally, a new harvest control rule was implemented and tested, based on one successfully applied to a commercially valuable fishery (Southern bluefin tuna, Hillary et al., 2016). This rule reacts to changes in stock status indicators, rather than distances to reference values, and has interesting properties that appear to be make it valuable for stocks in need of recovery.

## Evaluation of an alternative length-based status estimator

Management procedures require some indication of the changes in status of a stock to inform the rule that will decide on the next course of management action. In the 2020 MSE analysis, catch length frequency data, available through a sampling program, was used as input data to the LBSPR method (Length-based Spawning Potential Ratio, Hordyk et al (2014)) to provide an indicator of stock status. The method appeared to perform well when tested against a number of similar indicators, and was used in combination with a harvest control rule, in one of the management options tested in 2020 (Tien et al., 2020). LBSPR assumes that catch data is obtained from a fishery with selectivity that reaches a plateau (i.e. older/larger fish remain a target for the fishery), while the gillnet fleets operating in the IJsselmeer are known

DATUM  
3 January 2022

ONDERWERP  
briefrapportage

ONS KENMERK  
2200005.IM.mb

POSTADRES  
Postbus 68  
1970 AB IJmuiden

BEZOEKADRES  
Haringkade 1  
1976 CP IJmuiden

INTERNET  
[www.wur.nl/marine-research](http://www.wur.nl/marine-research)

KvK NUMMER  
09098104

CONTACTPERSOON  
Iago Mosqueira

TELEFOON  
+31 (0)317 488995

E-MAIL  
[marine-research@wur.nl](mailto:marine-research@wur.nl)

Wageningen Marine Research levert met kennis, onafhankelijk wetenschappelijk onderzoek en advies een wezenlijke bijdrage aan een duurzamer, zorgvuldiger beheer, gebruik en bescherming van de natuurlijke rijkdommen in zee-, kust- en zoetwatergebieden..

Wageningen Marine Research is onderdeel van Wageningen University & Research. Wageningen University & Research is het samenwerkingsverband tussen Wageningen University en Stichting Wageningen Research en heeft als missie: 'To explore the potential of nature to improve the quality of life'

to have a narrow selectivity pattern, with a sharp decrease for older ages. Although breaking this assumption did not appear to invalidate the use of this method, according to some tests we run, it did have an effect in the interpretation of the catch samples obtained in 2020.

All of this led to this exploration of alternative length-based estimators that could be set to incorporate a different selectivity curve. We identified the Length-based Integrated Mixed Effects (LIME) method of Ruud and Thorston (2017) as a possible candidate. This model works with different selectivity curves and was tested in comparison with other length-based method (Chong, et al, 2019).

The method was tested on simulated data, generated from the current pikeperch operating model, and on the actual samples obtained for that stock in the IJsselmeer fishery over the last few years.

### Methods

The LIME model is a mixed-effects model that can be applied to a single year of length frequency data from samples of landings, but, in contrast with LBSPR, can also be applied on time series, and also make use of survey indices (Rudd and Thorson, 2018). This model could potentially estimate random variations in recruitment, fishing mortality and other biological processes, as well as the magnitude (variance) of the random variations of each of those processes. Furthermore, LIME allows to set any functional form of selectivity, and might be able to estimate it if data is sufficiently informative. LIME and LB-SPR performances against logistic selectivity have already been compared in the past (Chong et al., 2020).

### Simulated data

A simulated dataset was generated to evaluate the estimates provided by LIME against the values present in the population. This simulation is based on the current operating model for IJsselmeer pikeperch, with a von Bertalanffy growth model being used to generate a number of correlated random length samples. Two OMs were generated with catch data being the result of the activity of fleets with either a flat-topped or a dome-shaped selectivity. This allowed evaluating the impact of the selectivity being mis-specified.

### Life history parameters

Values need to be given to this length-based method on a number of life-history and biological parameters. For these tests, the following values were used (Table 1), equal to those used in previous analysis for this stock.

Table 1: Life history parameters employed in the estimator runs.

Parameter	Value
MK	1.5
Linf	96
CVLinf	0.2
L50	25
L95	42.89
Walpha	3.485257e-05
Wbeta	2.671735
Steepness	0.8
SL50	38
SL95	47

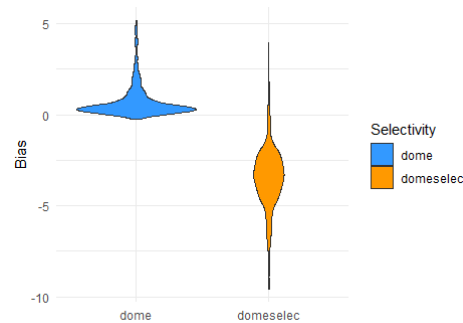
The performance of the LIME method was evaluated across a range of scenarios that considered alternative model options, data availability and assumptions. The model was tested using the length distribution in the catches, combined or not with a biomass index, generated from the survey. The method was tested on time series of different lengths (1, 5, or 10 or 25 years). Finally, the ability of the method to estimate selectivity was also investigated.

Bias refers here to the difference between the value of a metric as returned by LIME or LBSPR, and the value obtained from the assumed true population in the operating model. Two indicators are reported here, one related to exploitation level,  $F/F_{MSY}$  or the fishing mortality over the value at  $MSY$ , and a proxy of biomass status,  $SPR$ , the spawning potential ratio.

## Results

We report here only on the main results of this analysis, related to the bias (i.e. systematic error) in the two indicators obtained from LIME : the ratio of  $F$  to  $F_{MSY}$  ( $F/F_{MSY}$ ) and the Spawning Potential Ratio ( $SPR$ , measuring current spawning potential in comparison of that of the stock in absence of exploitation). The  $SPR$  estimate from the LBSPR method was also calculated for comparison.

### *Data available for 1 year*



*Figure 1: Distribution of the values for the bias ratio of the estimates of  $F/F_{MSY}$  from the LIME model against the OM real values, in runs where selectivity was set (blue) or estimated by the model (orange) using 1 year of length frequency data.*

Running LIME with a single year of data is similar to running the LBSPR estimator in the previous MSE (Tien et al, 2020). This choice could be considered as a suboptimal use of the LIME method, as the mixed-effects structure specifically designed to deal with data time series. The method appears to be sufficiently accurate at estimating a proxy for exploitation level ( $F/F_{MSY}$ ) if selectivity is set to the form used in the OM (bias close to 0), but not if required to also estimate the functional form of the selectivity curve (Figure 1).

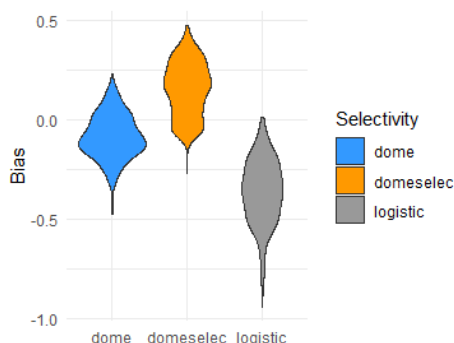


Figure 2:  
Distribution of the values for the bias ratio of the estimates of  $F/F_{MSY}$  from the LIME model against the OM real values, in runs where selectivity was set (blue), estimated by the model (orange) using 1 year of length frequency data.

A comparison was carried out between those two runs of LIME and LBSPR (Figure 2), in this case on the bias of their estimates for SPR, the stock status indicator employed in Tien et al (2020). The bias in LIME estimates is still better when run

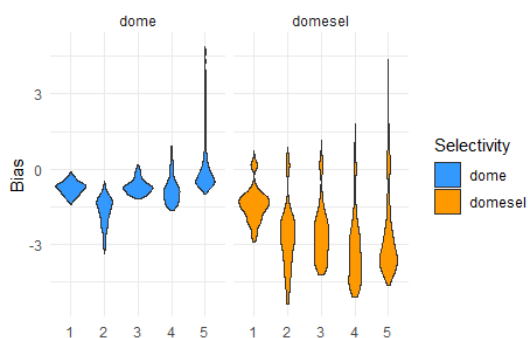


Figure 3: Bias ratio in  $F/F_{MSY}$  estimates for the LIME model, with selectivity set (blue), or estimated by the model (orange), and using 5 years of length frequency data.

with a set selectivity. LBSPR appears to underestimate SPR to a greater extent. Bias for SPR is lower than that obtained in the  $F/F_{MSY}$  calculation.

#### Data available for 5 years

While LBSPR can be run with multiple years of length data, the estimation is done independently for each year. In contrast, LIME is designed to be able to treat multiple years and types of data in an integrated manner to improve estimates of fishing mortality changes over time. We tested the performance of both methods using five years of catch data.

The bias in  $F/F_{MSY}$  estimates obtained with set or estimated selectivities are still clear (Figure 3). Bias over the five years is not stable. Simulated length frequencies are generated with the same variance every year, so this estimate variability reflects mostly the effect on the estimator of the changes in abundance it is meant to report on.

## Discussion

The initial results on the application of LIME appear encouraging, and the estimates it provides for the two indicators,  $F/FMSY$  and  $SPR$ , are sufficiently unbiased. However, the variance in mean bias observed when applied over a number of years could be problematic. Bias in the abundance estimator can generally be compensated during the tuning process which would return values for the HCR parameters that take that bias into account. Changes over time in the strength of that bias, or more worryingly in its sign, would result in over-conservative exploitation levels.

During this study, contact was made with the authors of LIME to enquire about some convergence issues in a limited number of model runs. They indicated that they were now aware of certain problems with the method, yet to be reported, that lead them to generally recommend that it should not be used in its current formulation.

A final decision will have to be made on whether the use of any of these estimators (LBSPR, LIME) is to be pursued further. An ongoing project for the United Nations Food and Agriculture Organization (FAO) evaluating these estimators, and comparing them with simpler length-based indicators for certain data-limited fisheries (Kell et al, pers. Com.) has found that most simple indicators are able to perform as well as the estimators, when applied to harvest control rules driven by trends rather than comparing estimates of abundance with reference values.

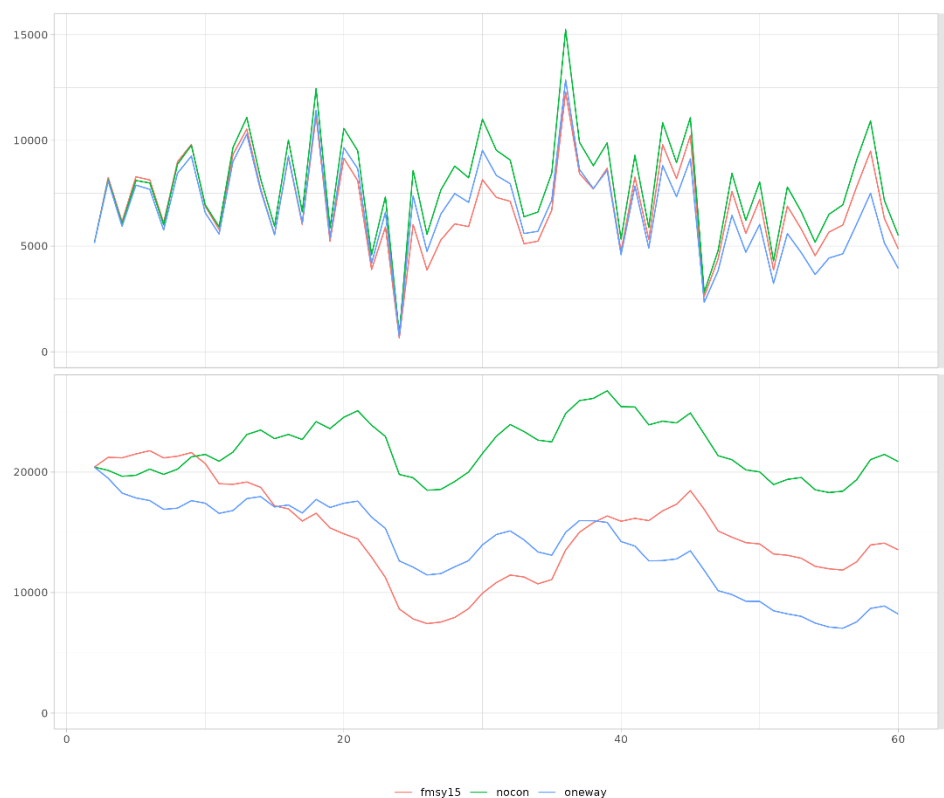
### **Conditioning of OMs using Approximate Bayesian Computation.**

The operating model (OM) is the part of the MSE tool that represents the biological stock, and incorporates both the uncertainty on the stocks characteristics and the various natural sources of variability in its dynamics (recruitment, growth, mortality). Conditioning of OMs is an essential step in the development of an MSE analysis. The past and future dynamics of the stock, but also the uncertainty around them, need to be well specified to allow simulations to compare robustly the expected performance of alternative MPs (Punt and Donovan, 2007). The MSE carried out in 2020 for IJsselmeer stocks applied a relatively simple but robust approach. A series of *feasible trajectories* (Bentley and Langley, 2012) were generated from prior distributions on key populations parameters, and their ability to explain various sources of data was used to decide on their validity as possible models for the population.

This approach is relatively simple to apply, and can be quickly tailored to the differences in data availability and quality between different stocks, as was the case for those in the IJsselmeer. Approximate Bayesian Computation (ABC) formalizes this simulation-based mechanism by applying the ideas behind Markov chain Monte Carlo (MCMC) algorithms to the process. MCMC is a method commonly used in Bayesian statistics to obtain samples for a complex distribution by randomly proposing parameter values from prior distributions, computing the quality of model to data when using those parameters, and then accepting or rejecting them based on the combined likelihood. The method ensures that the most likely area of the model likelihood is sufficiently explored. See for example Sunnaker et al (2013) for a good overview of the logic and methods behind ABC.

In practical terms, the use of ABC for the OM conditioning allows to consider multiple sources of data, and in multiple forms, when evaluating simulated populations. The algorithm applied in this test is that of Wilkinson (2013). The code makes use of the forecasting and simulation tools in the FLR toolset (Kell et al, 2007).

The objective of the work was to test the current ABC algorithm on the data available for the pikeperch and perch stocks, and identify any extensions or modifications that might be necessary.



## Methods

In essence, the ABC algorithm extends the methods used in the past for conditioning operating models for the IJsselmeer stocks (Tien et al., 2020), based on Bentley and Langley's (2012) *feasible trajectories*, and where priors for carrying capacity ( $K$ ) and initial depletion level ( $d$ ) were drawn to generate possible initial populations that are then projected for the reported total catch. ABC formalizes further the evaluation of the quality of the simulation run by (1) assessing how well the simulated population explains the totality of the survey data, and (2) by employing probability distributions to compute the likelihood of a population with the drawn parameters being able to generate the data, both catch and survey.

Development tests for the algorithm were based on an operating model generated from life history, with values chosen to mimic the biology of pikeperch in the IJsselmeer. Three alternative histories of exploitation were applied to the initial stock: a one way trip with catches linearly increasing, a flat trajectory of catches at a mostly constant level, and one where the stock was overexploited to 1.5 times the fishing mortality at MSY and later brought down to MSY levels (Figure 4). All runs were started with populations with  $K = 23,000$  t and initial total biomass at 75% of that value ( $d = 0.25$ ).

The algorithm was run for 1000 iterations. Different values for the variances of the proposal distributions, those used to propose a new value from the previous one in a Markov chain, were applied until an acceptance rate of between 30 and 35% was obtained, a value generally deemed as indication of good mixing of the chain (Gelman and Rubin, 1992). The algorithm was given the actual total catch from each

*Figure 4. Simulated population trajectories employed in the simulation testing exercise. Recruitment in thousands of individuals and total biomass ('B') in tonnes.*

OM, to which a 10% CV lognormal error was added (to represent measurement

error), and the abundances at age obtained from a survey with fixed selectivity, also with a 10% CV lognormal observation error.

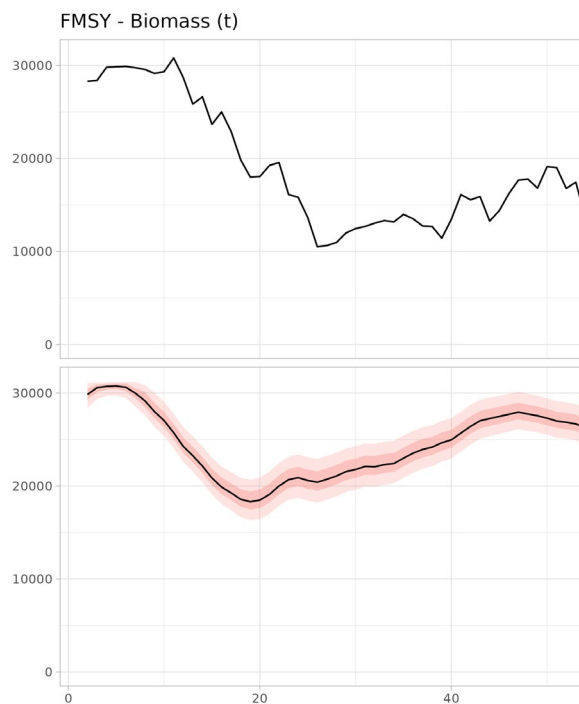
Runs were then conducted for both pikeperch and perch in the IJsselmeer using the catch data and surveys used in the previous OM (Tien et al, 2020) In the case of pikeperch, survey information was used in the algorithm only for ages 1 to 3, while age 0 abundances were used to provide information on the deviances from the assumed stock-recruit relationship.

## Results

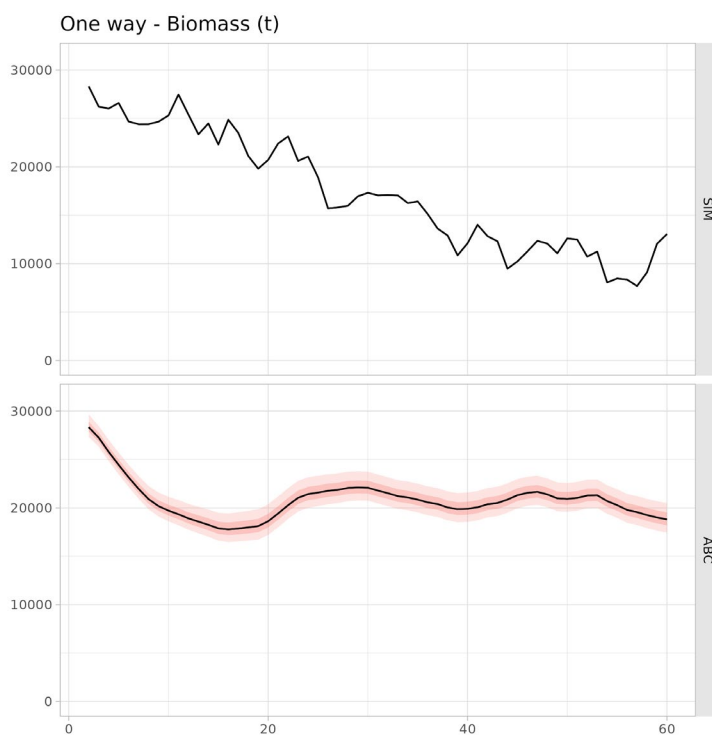
Test runs of the algorithm for these three trajectories showcase its ability to explain the trajectories of the biomasses for the various OMs (Figures 5, 6 and 7). The observed differences in uncertainty reflect the expected amounts of information about stock productivity contained on each trajectory. A stock that has been over-exploited and recovered, like the FMSY case here, is bound to provide us with data that can be used to define its carrying capacity more precisely.

The distributions of the prior and posterior distributions for both parameters (carrying capacity,  $K$ , and initial depletion,  $d$ ), together with the actual initial biomass (defined as  $K * d$ ), are summarized in Figure 8. The algorithm is clearly updating the estimates of initial biomass, and in all cases, posterior distributions are very distant from the real value (red line). With relatively uninformative priors for both parameters, as in these tests, the algorithm cannot separate depletion and virgin biomass, and only the combination of both is brought to values close to real.

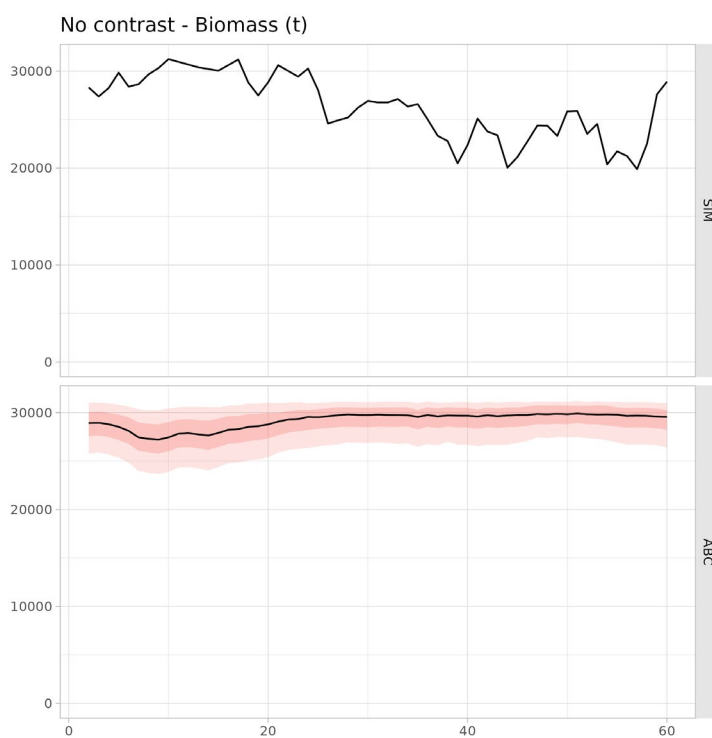
Runs of the algorithm with real IJsselmeer data for pikeperch (Figure 9) and perch have been up to his point less successful than expected. Acceptance rates are very low and the algorithm is unable to move away from a very narrow combination of values for both parameters.



*Figure 5: Example run of the ABC algorithm for the FMSY OM trajectory. Top panel shows the OM biomass while the bottom panel shows the inference made by ABC.*

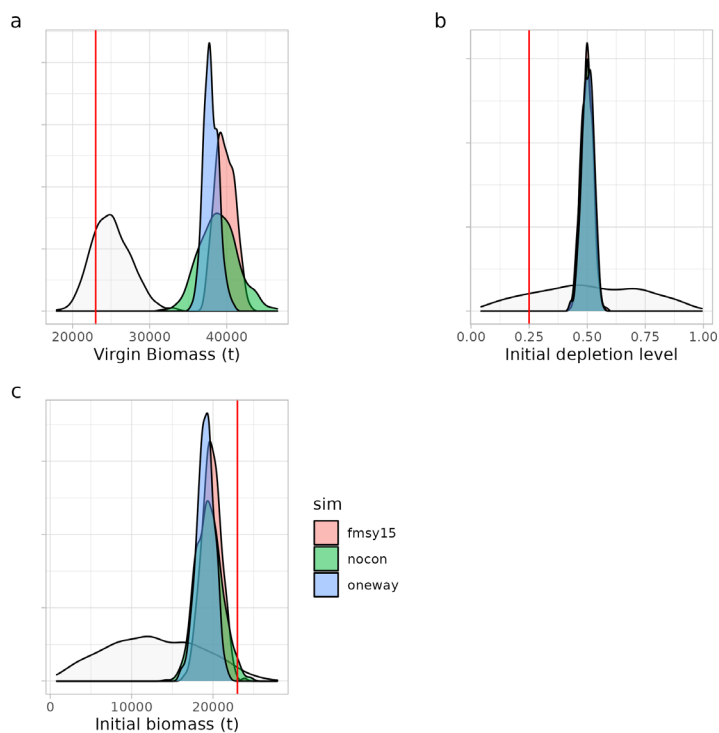


*Figure 6: Example run of the ABC algorithm for the one-way OM trajectory. Top panel shows the OM biomass while the bottom panel shows the inference made by ABC.*

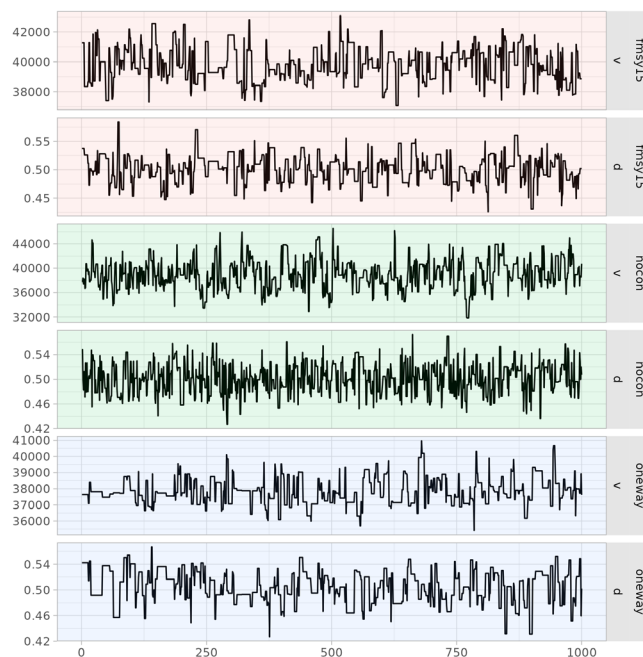


*Figure 7: Example run of the ABC algorithm for the no contrast OM trajectory. Top panel shows the OM biomass while the bottom panel shows the inference made by ABC.*





*Figure 8: Prior (in grey) and posterior (colored) distributions for virgin biomass, initial depletion level, and the combination of the two, the initial population biomass. Red lines indicate the values from the simulated population, equal across all trajectories.*



*Figure 9: MCMC chains for virgin biomass ( $v$ ) and depletion level ( $d$ ) for ABC runs on the three simulated populations.,*

## Discussion

The potential of the ABC algorithm has been well demonstrated when applied to simulated data. Unfortunately, its ability to generate viable OMs for pikeperch and perch in IJsselmeer is still not complete. When the algorithm was applied to real data, the proposal acceptance rate was very low, less than 10%, even after changes to the proposal distribution variances. Inspection of the MCMC chains appear to indicate that only a very narrow range of prior values is able to explain both catch and survey. Two possible avenues of work are now open. The first is to fully explore the effect of proposal and distance metrics variances, and consider options in which survey data is given a larger weight than the catch data, or viceversa. The second is to use a narrower prior distribution for the depletion level, or rather than attempting to condition a single model, create a reduced number of OMs with alternative values for depletion. MPs would then have to show their performance across levels of initial depletion before being deemed as robust.

The first of these options will be investigated early next year through a large simulation exercise that will explore the precise effect of each of the algorithm configurations on its performance with these datasets. This will help us adapting it to the particular features of these datasets. The second will be tested by exploring a narrow range of possible values for initial depletion and quantify the effect on the algorithm behaviour. A later step would require constructing appropriate priors for this quantity, a process that would ideally be based on an agreement around the table from multiple parties with knowledge and views on the status of these stocks. Other changes already planned to be carried out in 2021 to the OMs could also help the algorithm performance. The OM will be set to run from March to April, so as to better cover both the biology and the management cycles. This could diminish the apparent conflict between catch and survey data, by separating catches as obtained from different cohorts.

## Development of trend-based Harvest Control Rules

Reliable estimates of stock status are often difficult to obtain, and specially in data-limited situations. The performance of an MP is likely to be affected if the estimator or indicator informing it is not robust enough to variations in sample size, information content of the data, or random variability in the system. This is likely to be of greater concern if an MP is set to achieve management objectives measures in the tails of a probability distribution. For example, aiming at a 5% probability of the stock being below some limit reference point is bound to be more of an unstable target than a 50% probability of the stock being over the target level.

In either case, an alternative to an unstable status indicator is to track trends rather than actual values, and react according to the direction and strength of that trend, computed over an appropriate period. This was the basis for the CPUE-based MP explored during the 2020 IJsselmeer MSE. Here we present some exploratory runs of a similar HCR, one with a proven good dynamic behaviour (Hillary et al, 2016). The rule allows for assymetric responses to increases and declines, which can be tuned to obtain faster stock recovery, for example, or a very low risk of depleting the stock.

### Methods

A set of MP runs was conducted to test the behaviour of the trend-based HCR. The rule was either informed by a perfect observation of stock abundance or an indicator based on mean length in the catch.

The decision rule is defined as

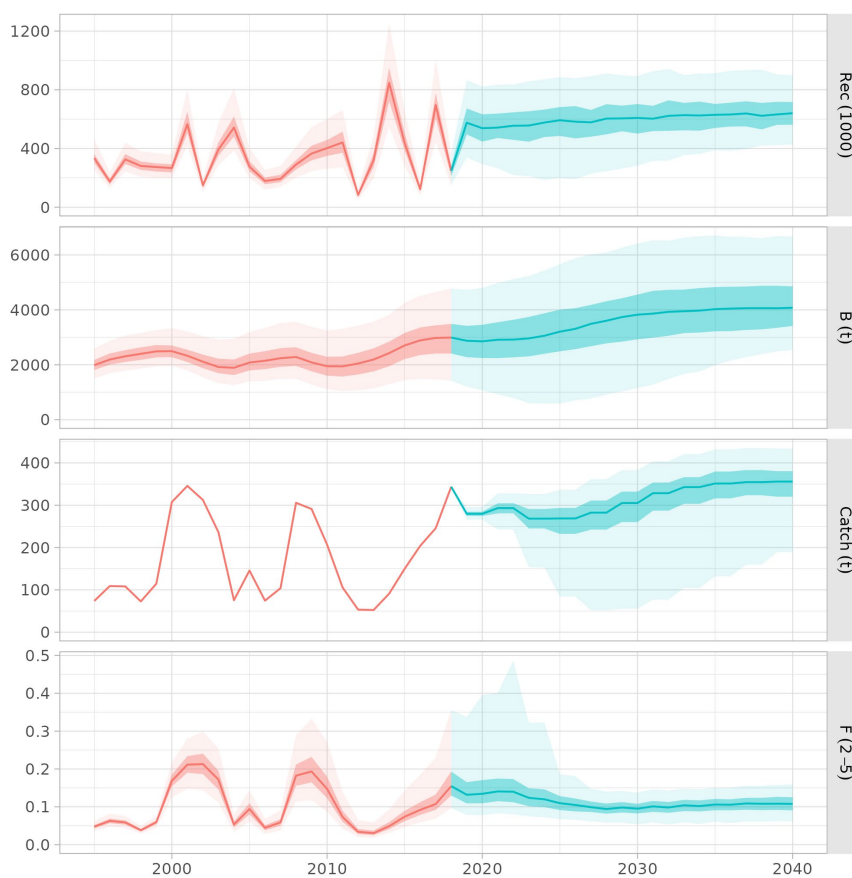
$$TAC_{y+1} = TAC_y \times \begin{cases} 1 - k_1 \lambda^\gamma; \lambda < 0 \\ 1 + k_2 \lambda; \lambda \leq 0 \end{cases}$$

where  $\lambda$  is the slope in the regression of the employed metric (e.g. SSB) in log space for the last five years,  $k_1$  and  $k_2$  are gain parameters and  $\gamma$  is an asymmetry parameter that permits stronger or weaker action for negative biomass trends.

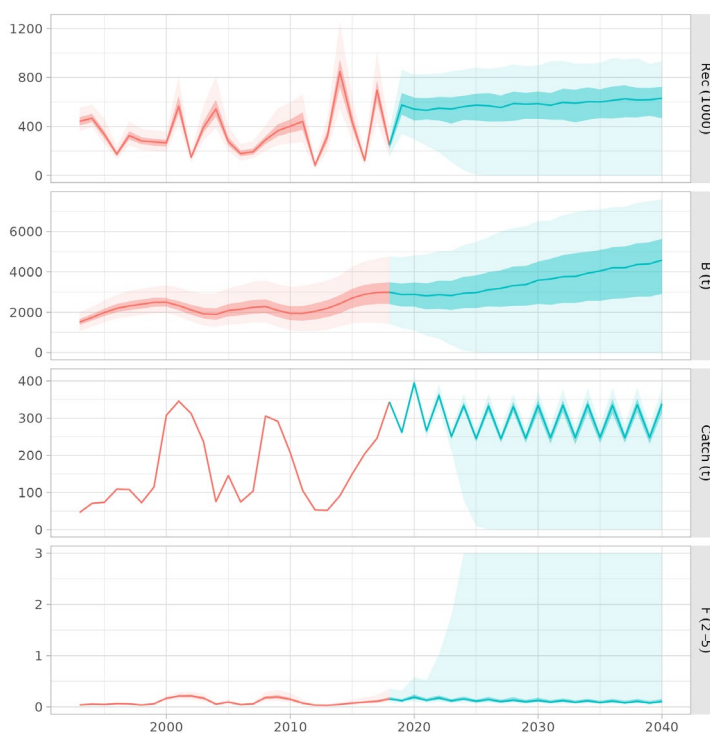
The runs presented here had as their sole purpose the development and testing of the approach, including the extension of the MSE framework so that the HCR could be applied to either estimates of stock abundance or any kind of equivalent metric, like simple indicators based on length data. No attempt was made to tune the HCR parameters to achieve any of management objective, and they were left at values assumed to be reasonable for testing purposes.

### Results

Initial runs confirmed that this rule has a good potential to be employed to drive management decisions based on total allowable catches and recover a stock, if sufficient time is given (Figure 10). Its performance on real-world situations is likely to be limited by factors not included in this analysis, such as the available time-span for recovery, the variability of recruitment, or probability of low recruitment events. The initial performance of the rule when applied using a length-based indicator (mean length in the catch) cannot be stated from this limited exercise (Figure 11), again solely intended to provide a proof of concept. Catch oscillations, for example, are larger than expected, and the impact of sampling sizes on the MLC estimator will have to be investigated. The assymetry of the rule, as defined by the relative values of the  $k_1$  and  $k_2$  arguments, will require further correction, so as to decrease the probability of the stock falling below the agreed limit reference points.



*Figure 10: Test run of the trend-based HCR on the pikeperch OM with a shortcut stock assessment (perfect information on abundance).*



*Figure 11: Test run of the trend-based HCR on the pikeperch OM with the mean-length-in-catch estimator.*

## Discussion

The problems encountered with the LIME length-based estimator led to this initial research on the feasibility of using simpler length-based indicators to drive a trend-based HCR, rather than rely on estimates of stock status based on the proxies that either LIME or LBSPR can provide. HCR employing trends, rather than estimates compared to some reference value, have the ability to be useful when those estimates and references are difficult to obtain.

This trend-based HCR was originally developed for the Southern bluefin tuna, *Thunnus maccoyii*, stock. Its current application has another feature that could be applied to some IJsselmeer stocks. The proposals for TAC obtained from indicators coming from two sources of information (which in this case would be catch and survey) are combined for a final proposal. Trends in both length information in the catch, and abundance on biomass of the main age groups from the trawl survey, could both inform management. A full exploration of this approach, including an analysis of the quantity and timing of the information that can be expected to be obtained from each of them, would be an interesting contribution to the development of a new MP for these stocks. Data quality on each of those two sources, likely to vary for each stock, could be considered when combining their individual recommendations.

Finally, moving from a system where a biomass target sets a clear objective for the fishery, to one where management only responds to changes, will require sufficient communication among the various stakeholders.

## References

Bentley, N., & Langley, A. (2012). Feasible stock trajectories: a flexible and efficient sequential estimator for use in fisheries management procedures. *Canadian Journal of Fisheries and Aquatic Sciences*, 69(1), 161–177.

Chong, L., Mildenerger, T., Rudd, M., Taylor, M., Cope, J., Branch, T., Wolff, M., & Stäbler, M. (2019). Performance evaluation of data-limited, length-based stock assessment methods. *ICES Journal of Marine Science*, *77*(1), 97-108.

Gelman, A. and Rubin, D.B. (1992). "Inference from Iterative Simulation using Multiple Sequences". *Statistical Science*, *7*, p. 457--511.

Hillary, R.M., Preece, A.L., Davies, C.R., Kurota, H., Sakai, O., Itoh, T., Parma, A.M., Butterworth, D.S., Ianelli, J. and Branch, T.A. (2016), A scientific alternative to moratoria for rebuilding depleted international tuna stocks. *Fish Fish*, *17*: 469-482.

Hordyk, A., Ono, K., Valencia, S., Loneragan, N., & Prince, J. (2014). A novel length-based empirical estimation method of spawning potential ratio (SPR), and tests of its performance, for small-scale, data-poor fisheries. *ICES Journal of Marine Science*, *72*(1), 217-231.

Kell, L., Mosqueira, I., Grosjean, P., Fromentin, J.M., Garcia, D., Hillary, R., Jardim, E., Mardle, S., Pastoors, M., Poos, J., Scott, F., & Scott, R. (2007). FLR: an open-source framework for the evaluation and development of management strategies. *ICES Journal of Marine Science*, *64*(4), 640-646.

Punt, A., & Donovan, G. (2007). Developing management procedures that are robust to uncertainty: lessons from the International Whaling Commission. *ICES Journal of Marine Science*, *64*(4), 603-612.

Rudd, M.B., Thorson, J.T. (2017). Accounting for variable recruitment and fishing mortality in length-based stock assessments for data-limited fisheries. *Canadian Journal of Fisheries and Aquatic Sciences*. *75*(7): 1019-1035.  
<https://doi.org/10.1139/cjfas-2017-0143>

Sunnåker, M., Busetto, A., Numminen, E., Corander, J., Foll, M., & Dessimoz, C. (2013). Approximate Bayesian Computation. *PLoS Computational Biology*, *9*(1), e1002803.

Tien, N., Mosqueira, I., Brunel, T., van der Hammen, T, Molla Gazi K, van Donk S, Foekema E, de Bruijn P, de Leeuw JB. 2020. Bestandsoverzicht van snoekbaars, baars, blankvoorn en brasem en de evaluatie van potentiële oogstregels voor snoekbaars en baars in het IJssel-/Markermeer. Wageningen Marine Research rapport: projectnummer BO-43.18-100-283.00.

Wilkinson, R. (2013). Approximate Bayesian computation (ABC) gives exact results under the assumption of model error. *Statistical Applications in Genetics and Molecular Biology*, *12*(2).

Verantwoording

Projectnummer: 4318100283

Dit rapport is met grote zorgvuldigheid tot stand gekomen. De wetenschappelijke kwaliteit is intern getoetst door een collega-onderzoeker en het betreffende, verantwoordelijk MT-lid/director van Wageningen Marine Research.

DATUM  
3 January 2022

ONS KENMERK  
2200005.IM.mb

PAGINA  
15 van 15

Akkoord: Thomas Brunel

Handtekening:



Datum: 3/01/2022

Akkoord: Tammo Bult

Handtekening:



Datum: 3/01/2022