Supplementary information: Ecologically Sustainable Exploitation Rates – A multispecies approach for fisheries management

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Table of contents

SUPPLEMENTARY TEXT

Baltic Sea Application

Data description

The biomass index time series (for 1988-2014) for cod (Catch per unit effort, CPUE, kg/h trawling) were assembled from trawl surveys (ICES subdivisions 25-28) and retrieved from the ICES DATRAS database (www.ices.dk). Biomass time series for sprat and herring (ICES subdivisions 25-29) were assembled from hydro-acoustic surveys (years 1988-2014). Total biomass of the fish populations only included fishes > 30 cm (i.e. spawning fish) for cod and fishes above one year of age for sprat and herring (i.e. excluding recruits). Time series for sprat and herring were based on surveys from quarter 4 whereas the time series for cod was composed of data from quarter 4 where available (years 1998-2014), and back calculated from quarter 1 for the beginning of the time series (years 1988-1997). The back calculated data was based on predictions from a linear regression analysis for 1998-2014 (n=17) ($Cod\ biomass_{\ q4\ year\ t} = \gamma + \varphi * Cod\ biomass_{q1\ year\ t}$), showing that quarter 1 and quarter 4 cod data are strongly correlated ($\gamma = 55.64$; $\varphi = 0.72$).

Exploitation rate was modeled in a similar way as other studies (Bell, Fogarty, & Collie, 2014; Langangen et al., 2017; Lindegren, Andersen, Casini, & Neuenfeldt, 2014), i.e. total landings divided by survey data from the same year. The exploitation rate data was standardized to a mean of zero and unity variance, and species biomasses were ln-transformed and centered prior to model fitting. This centering of variables infer that the MAR-model is centered on zero mean, otherwise model intercepts need to be fitted.

Critical biomass limits

Critical biomass levels for the fish stocks in the Baltic Sea are the Blim-values for spawning stock biomass, which have been used in stock assessments. These points refer to the biomass levels below which there may be reduced recruitment (ICES, 2015). To be applicable, Blim-values from stock assessments (Cod=63000 tons, Sprat=410000 tons, Herring=430000 tons; ICES, 2014), were rescaled to the magnitude of survey data by relating the mean of stock assessment data, from the same years as the survey data, to Blim-values. This results in Blims on a ln-transformed and centered scale (cod=-0.71, sprat=-0.98, herring=-0.50).

Model fitting and model selection

MAR-models with covariates can be fitted to time series of species abundances using for example ordinary least square (Ives, Dennis, Cottingham, & Carpenter, 2003), generalized least square (Lütkepohl, 2007), maximum likelihood (Ives, Dennis, Cottingham, & Carpenter, 2003) or Bayesian approaches (e.g. Langangen et al., 2017). We used generalized least square implemented in the MTS-package in R (Tsay, 2015). The benefits of using the generalized least square method includes its computational speed, asymptotic normal properties and more precise estimate than ordinary least square for constrained models (Lütkepohl, 2007), i.e. for models with certain parameters set to zero. For normal distributed data generalized least square further gives the same estimates as the maximum likelihood approach (Lütkepohl, 2007).

A true exhaustive search was implemented to find the final model (the model with the lowest AICc). Two restrictions on potential model structures were made: (i) the diagonal of the **B** matrix was always included in the model fitting because intraspecific competition for food resources tend to be important for both the clupeid fish populations (Casini, Cardinale, & Hjelm, 2006) and cod in the Baltic Sea (Casini et al., 2016); (ii) exploitation rate was also always included since the main objective of this study was to investigate the effect of altered exploitation rate on species biomasses.

An Akaikes information criterion intended for constrained multivariate models fitted to small sample sizes (AICc) (eq. 7.91 in Burnham & Anderson, 2002), was used to find the final model structure:

$$\mathrm{AICc} = T * \ln\left(\left|\widehat{\textstyle\sum}_{\boldsymbol{E}}\right|\right) + 2n_{par} + 2n_{par}(n_{par} + v)/(\mathrm{T} * \mathrm{S} - n_{par} - v), \qquad \text{(S1)}$$

where the first term, T*ln($|\widehat{\sum}_{\boldsymbol{E}}|$), defined as T times the natural logarithm of the determinant of the estimated process error covariance matrix, measures goodness of fit and the other terms penalizes for the number of parameters, n_{par}. T is the length of the time series, v is the number of estimated parameters in the process error covariance matrix, which are also included in the total number of parameters, and S is the number of rows in the (SxT) time series matrix of observed data.

R^2-values refer to conditional R^2, i.e. the proportion of the variance in ln(biomass) change between subsequent years that is explained by the model (Ives, Dennis, Cottingham, & Carpenter, 2003).

In order to investigate the effect of model complexity on ESERs we additionally fitted two model structures: one model assuming that species are decoupled, i.e. do not affect each other (Single species model), and one model assuming that all species affect each other (Full model).

Final model

To exemplify the approach we fit MAR-models to survey data for the three commercially most important fish populations in the Baltic Sea: cod (*Gadus morhua*), sprat (*Sprattus*

sprattus) and herring (*Clupea harengus*). The final model (Tab. S1), following model selection (see "Model fitting and model selection" above), gives a good fit to the observed time series (Fig. 2). This model includes three parameters related to interspecific trophic interactions (Tab. S1): mutual negative effects between sprat and herring, and a negative net effect of sprat on cod. The negative effects between sprat and herring are expected as they compete for food (Casini, Cardinale, & Hjelm, 2006), and the somewhat counterintuitive negative net effect between sprat and cod could result from competition between sprat and cod larvae for zooplankton, or sprat predation on cod eggs (Köster et al., 2005; but see Gårdmark et al., 2015). Residual plots do not indicate any strong violations of model assumptions (Fig. S3 & S4) and the model is stationary (max (λ_B) = 0.78[0.59 0.87]), making it suitable for estimating ESERs.

It is further interesting to note that after model selection we end up with a completely different MAR-model of the three dominating fish stocks in the Baltic than what was found in an earlier study using MAR-models (Lindegren, Möllmann, Nielsen, & Stenseth, 2009). Here we have used survey data from 1988-2014, whereas the previous MAR-model (Lindegren, Möllmann, Nielsen, & Stenseth, 2009) used model output from a Multispecies Virtual Population Analysis from 1974-2005. Moreover, since the Baltic Sea fish community has undergone a regime shift during the end of 1980:s (Möllmann et al., 2009), our estimated model reflects the current regime, whereas the previous Baltic MAR-model (Lindegren, Möllmann, Nielsen, & Stenseth, 2009) reflects a time span covering also the transition period. This is probably a major reason for the more stable dynamics of the current model (max (λ_B) = 0.78[0.59 0.87]), compared to the previous Baltic MAR-model (Lindegren, Möllmann, Nielsen, & Stenseth, 2009) (max (λ_B) =0.93).

Out-of-sample test of the final model

We tested the prediction accuracy of the final model on out-of-sample data. The time series (n=27) was divided into training (n=17) and test data sets (n=10). The matrix-structure of the final model (Final model Tab. S1) was fitted to training data and thereafter used for prediction. Two tests were performed: a test of the models mean prediction accuracy (i.e. eq. 2 in Methods) and a true forward prediction. The model gives a decent forward prediction for cod (Fig. S2b), and out of phase predictions for sprat and herring (Fig. S2c-d). Further, observed means are within the 95% prediction bounds of the model (i.e. eq. 3 in Method section), but the predictions are very uncertain (Fig. S2a). This points to a very important aspect with this modelling approach, that is, uncertainty in parameter estimates should be accounted for when estimating ESERs; as with any type of assessment model (Link et al., 2012; Thorpe, Le Quesne, Luxford, Collie, & Jennings, 2015).

Assumptions and future directions of the ESER approach

MAR-model assumptions

A critical assumption of the ESER approach, if using MAR-models, is that long-term changes in exploitation rate affect species' biomass linearly on a ln-scale. The fitted model should thus be scrutinized in terms of potential non-linearities. In our example, residual plots do not indicate any strong non-linearities within the ranges of observed data (Fig. S3). Ideally, the functional form of relationships between all variables should be known beforehand and estimated using a mechanistically complex model; but such a model requires a large number of parameters (but see e.g. Ye et al., 2015), some of which are preset before fitting multispecies fisheries models (Plagányi et al., 2014). Further, with an increasing number of parameters, the risk of overfitting increases; that is, the model might describe random errors rather than the underlying mechanistic relationships. A MAR-model could thus, due to its simplicity and entirely statistically fitted parameters, be referred to as a model of intermediate complexity for ecosystem assessment (Plagányi et al., 2014). Moreover, linear stochastic models often give good approximations of non-linear stochastic models (Ives, Dennis, Cottingham & Carpenter, 2003; Ripa & Ives, 2003), and tend to describe the general dynamical features of many ecological systems (Ripa & Ives, 2003). For long-term effects caused by changes in covariates, as implemented in the current study, one study has also shown a fitted MAR-model to have greater prediction accuracy than a non-linear model fitted to data simulated by the same non-linear model (Ives, 1995). Thus, the prediction accuracy of a linear stochastic model might outperform the prediction accuracy of a non-linear model fitted to time series; but this result is contingent on the specific way the non-linear model was fitted (Ives, 1995). Further, MAR-models have also given reasonable predictions of plankton abundances to long term changes in covariates (Beisiner, Ives, & Carpenter, 2003; Ives, Carpenter, & Dennis, 1999). Yet, it should be noted that strong non-linear signals, which set in when large changes in exogenous variable are induced in non-linear models, are not well captured by MAR-models (Certain, Barraquand, & Gårdmark, 2018).

The analytical approach of estimating ESERs relies on the stationary distribution of MAR-models (Note, however, that ESERs can be derived based on any statistical multispecies model, using extensive computer simulations). Two important assumptions inherent in MAR-models are that process errors should be normally distributed and temporarily uncorrelated. Thus, when applying the analytical ESER approach, a biologically plausible MAR-model should be built, and model residuals should be checked for normality and autocorrelation. This can be done using either statistical tests or graphical methods (in our example, we used partial autocorrelation functions and normal probability plots to assess temporal correlation and normality of model residuals, respectively). If the assumption of normally distributed process errors is not met, the multivariate normal formulation of the stationary distribution will not hold and the analytical approach is unfeasible. Further, if the second assumption, i.e. that process errors are temporarily uncorrelated, is not met, the variance of the stationary distribution will be underestimated (Ripa & Ives, 2003). Neglecting this assumption would thus lead to overestimated ranges of ESERs, i.e. that particular exploitation rates would be reckoned as ecologically sustainable, while they are in fact not, due to omission of the process error assumption.

When fitting a MAR-model there is another type of uncertainty that can be acknowledged, that is, observation error. If this is explicitly acknowledged, a state-space approach can be used to separate process and observation errors when fitting a MAR-model (Holmes, Ward, & Wills, 2013). Now, since the variance-covariance of the stationary distribution of the states is proportional to the variance-covariance of the multivariate normal process errors, a state-space approach would probably decrease the variance-covariance of the stationary distribution of the states, compared to the case when a state-space model is not fitted. In effect, this would decrease the ranges of ESERs. However, whether such an approach would overall decrease the ranges of ESERs also depends on parameter uncertainty. Since the number of fitted parameters for a specific model structure would increase when separating observation from process errors, such an approach would potentially lead to an increased parameter uncertainty. The overall ranges of ESERs might thus be similar using the two approaches, but qualitative differences are likely since these approaches tend to give qualitative different parameter estimates, at least for univariate models (Knape & de Valpine, 2012).

Before fitting a MAR-model, stationarity of time series should be assessed in order to reduce the risk of so called spurious regression, i.e. reduce the risk that erroneous relationships emerge only due to non-stationarity in the data set. To this end, there are a handful of different statistical tests that can used to test for stationarity. These tests have seldom been used in ecology, yet in other fields, such as econometrics, they are the norm (Tsay, 2014). Here, we used two of the most well-known tests, the Dickey-Fuller test (Dickey & Fuller, 1979) and the Phillips-Perron test (Phillips & Perron, 1988), to test the null hypothesis that a given time series follows a random walk process (i.e. that $\rho = 1$ in $y_t = \rho y_{t-1} + u_t$). We used the most basic version of the tests, i.e. assuming no deterministic trend or random drift, and found that we can reject the null-hypothesis (Tab. S2). Yet, it should be noted that these tests are sensitive to the choice of test type, time series length and how close a time series is to non-stationarity (Elliot, Rothenberg, & Stock, 1996).

Future directions

Future research should specifically seek alternative ways of modelling exploitation rate. Here we have modelled exploitation rate as landings at time t/survey data at time t. Exploitation rates should preferably be estimated from independent data sets, e.g. effort data combined with survey data not used as observations of the biomass variables of the model. Notably, previous MAR-models for marine fish communities have either used a similar approach as in the current study (Bell, Fogarty, & Collie, 2014; Langangen et al., 2017; Lindegren, Andersen, Casini, & Neuenfeldt, 2014) or fitted MAR-models to exploitation rates estimated in other models (Lindegren, Möllmann, Nielsen, & Stenseth, 2009).

Here we assume that state variables represent the temporal variation in total biomass of fish populations exploitable in the fisheries, and thus that each ln(biomass) unit of a population (e.g. independent of fish size or age) is impacted by, and impacts, other populations to the same extent. However, size-dependent feeding is very common among marine fish populations (Barnes, Maxwell, Reuman, & Jennings, 2010) and may govern their structure and dynamics (de Roos & Persson, 2013; Gårdmark et al., 2015). It might thus be important to account for size structure among fish populations when estimating ESERs. In a MAR-model, size-dependent interactions could be introduced by treating the total biomass of size classes of the populations as state variables (similar to Lindegren, Andersen, Casini, & Neuenfeldt, 2014), or by implicitly and indirectly model size structure through the inclusion of time lags (i.e. fitting a VARX(p,s)-model). The framework of estimating ESERs can be adopted independent of which of the approaches that is taken (see Lütkepohl, 2007 for derivation of the stationary distribution of VAR(p)-models). Species interactions in a MAR-model are further assumed to be linear on a ln-scale. This assumption infers that strong non-linearities in interactions, such as those often involved in regime shifts (Gårdmark et al., 2015), cannot be accounted for by this model. As such, regime shifts often involve a complete reorganization of a system, with different states inferring different interactions among species and environmental forces (Gårdmark et al., 2015). Thus, under the potential existence of regime shifts in a system, the current approach of estimating ESERs would only be valid for models fitted to time series within regimes. Moreover, in order to avoid that a system switches from one state to another requires some prerequisite knowledge of points where changes in the biomass of one or a couple of species lead to a large overall change in the system. Such information is seldom available and extensive research is conducted on how to anticipate such critical transitions (Lindegren et al., 2012; Scheffer et al., 2012). However, for the Baltic Sea, recent research (Casini et al., 2009) actually indicates the existence of a critical population size of sprat, which separates two potential ecosystem configurations. Above this population size threshold sprat tend to control summer zooplankton dynamics, potentially hindering cod from recovery to its previous high biomass state due to food competition with cod larvae (but see Gårdmark et al., 2015). Now, assume that the Baltic Sea community was currently in a high cod state (in reality it is the opposite [Casini et al., 2009; Gårdmark et al., 2015]) and that the management objective was to keep the system in this state. Under such circumstances an upper critical biomass limit for sprat would, in addition to Blim's for all species, be incorporated in the multispecies objective (i.e. two critical biomass limits for sprat in Fig. 1). The estimated ESERs would then, theoretically, correspond to a low risk that a regime shift occurred or that any species in the system went below its Blim. Further, the multispecies objective could be changed to have a focus on just one or a couple of the investigated species, or include other type of species, such as grey seals or some bird species dependent on forage fish (Cury et al. 2011; Österblom, Casini, Olsson, & Bignert, 2006).

ESERs in specious systems

As described in the main text, an increasing number of species included in an ESER analysis will eventually lead to no support for ecologically sustainable exploitation. However, for a specious system, it may be more appropriate to divide species into functional groups, depending on their ecological role in a system; as for example, piscivorous and planktivorous fish. Based on such a grouping the multispecies objective could be extended in two ways by either: (i) defining that we are only willing to accept a maximum probability that any species in each functional group goes below its Blim; or (ii) defining that we are only willing to accept a certain probability that the total biomass of any functional group goes below a limit for its total biomass. In the first setting, the objective would be to derive exploitation rates associated with a low probability (lower than a predefined maximum acceptable probability) that any species in each functional group went below its Blim. Mathematically, this can be described as follows:

$$\varphi(\boldsymbol{\mu}_{\mathrm{F}}) = \min_{j\in\{1,\ldots,k\}}(\alpha - P_j(\boldsymbol{\mu}_{\mathrm{F}})) \qquad \text{(S2)}$$

where α is a constant giving the predefined maximum acceptable probability that any species in each function group, *j*, goes below its Blim, and $P_j(\boldsymbol{\mu}_{\mathrm{F}})$ is the probability that any species in functional group *j* goes below its Blim, given a vector of mean exploitation rates, $\boldsymbol{\mu}_{\mathrm{F}}$. Since $P_j(\boldsymbol{\mu}_{\mathrm{F}})$ gives the probability that any species in functional group *j* goes below its critical biomass limit, the overall multispecies objective, $\varphi(\boldsymbol{\mu}_{\mathrm{F}})$, is determined by the maximum probability, $P_j(\boldsymbol{\mu}_{\mathrm{F}})$, across all functional groups.

For the second scenario, new critical biomass limits for the total biomass of each functional group should first be defined. The stationary distribution of total biomasses could then be readily retrieved, since the multivariate normal formulation of the stationary distribution infers that any linear combination of the distribution is still normal. The stationary distribution of the total biomass of functional groups, $\mathbf{Y}_\infty(\boldsymbol{\mu}_{\mathrm{F}})$, can therefore be described by the following equation:

$$\boldsymbol{\mu}_{\mathrm{Y}} = \mathbf{e}_{\mathrm{Y}}\boldsymbol{\mu}_{\mathrm{X}} \qquad \text{(S3)}$$

$$\mathbf{V}_{\mathrm{Y}} = \mathbf{e}_{\mathrm{Y}}\mathbf{V}_{\mathrm{X}}\mathbf{e}_{\mathrm{Y}}^{\mathrm{T}},$$

where $\boldsymbol{\mu}_{\mathrm{Y}}$ is the (*n x 1*) mean vector of total biomasses of functional groups given a vector of mean exploitation rates $\boldsymbol{\mu}_{\mathrm{F}}$; $\boldsymbol{\mu}_{\mathrm{X}}$ is the (*m x 1*) mean vector of species biomasses given a vector of mean exploitation rates $\boldsymbol{\mu}_{\mathrm{F}}$; $\mathbf{e}_{\mathrm{Y}}$ is a (*n x m*) zero matrix with ones in position (*i,j*) mapping species *j* to functional group *i*; $\mathbf{V}_{\mathrm{Y}}$ is the (*n x n*) covariance matrix of the stationary distribution of the total biomass of functional groups; and $\mathbf{V}_{\mathrm{X}}$ is the (*m x m*) covariance matrix of the stationary distribution of the species biomass.

Similar to the case where conservation of each species is of concern (eq. 4 Methods), the multispecies objective would now read:

$$\varphi(\boldsymbol{\mu}'_{\mathrm{F}}) = \alpha - P_Y(\boldsymbol{\mu}_{\mathrm{F}}), \qquad \text{(S4)}$$

where α is the predefined maximum acceptable probability and $P_Y(\boldsymbol{\mu}_{\mathrm{F}})$ is the probability that the total biomass of any functional group goes below its limit of total biomass.

An additional challenge in estimating ESERs in specious systems is model fitting, since models of highly diverse systems may include a large number of parameters, and thus lead to high parameter uncertainty. A high parameter uncertainty would in general lead to a low probability of attaining the multispecies objective, and thus a decreased range of ESERs. However, whether there is straightforward relationship between the number of species and the number of parameters in a model is not clear-cut as model selection may favor less complex models (Burnham & Anderson, 2002).

SUPPLEMENTARY FIGURES

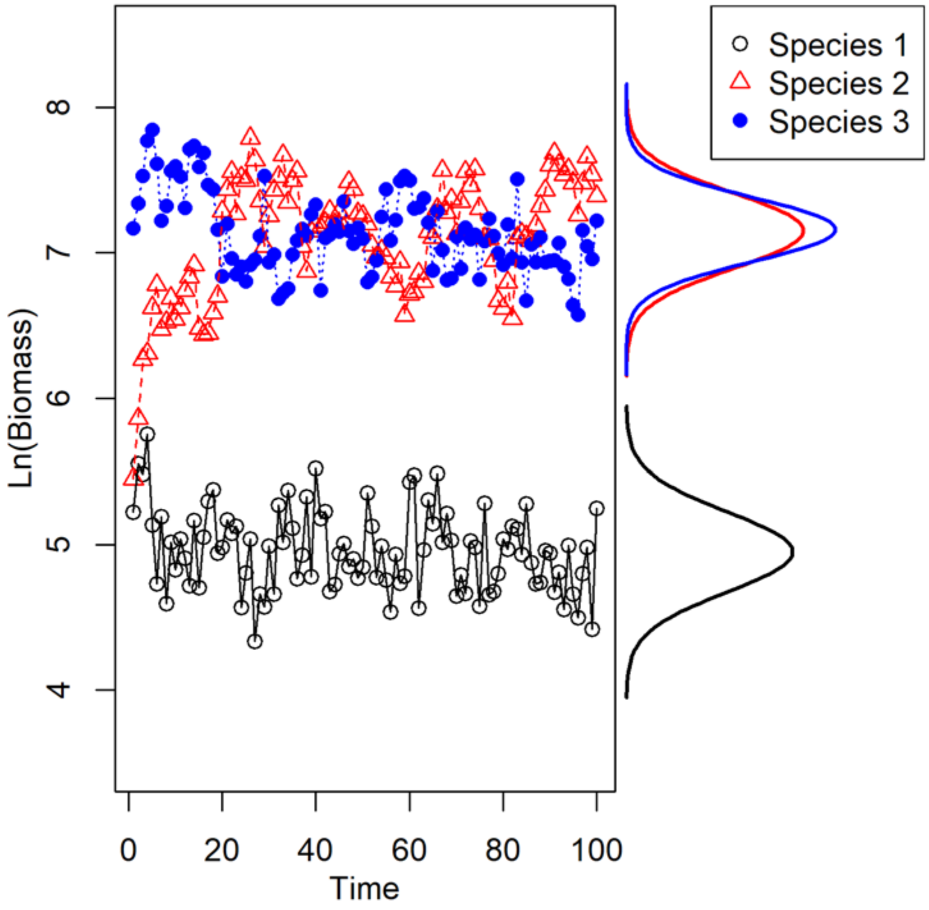

Fig. S1. Stationary distribution of a MAR-model with covariates. The figure illustrates a time projection of a MAR-model with covariates held at fixed values. The distributions to the right illustrate the stationary distribution, i.e. the distribution of ln(biomass) abundances that would accumulate if the MAR-model was simulated over infinite time.

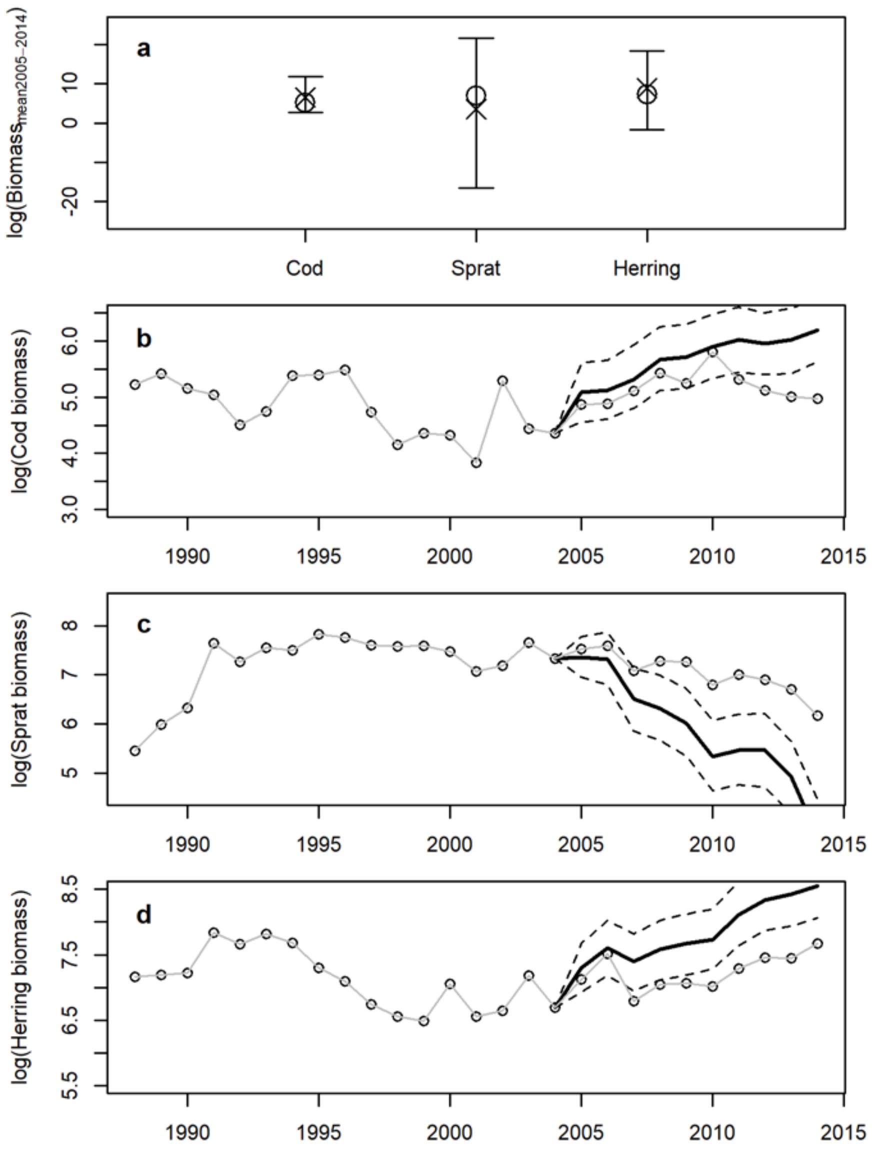

Fig. S2. Model evaluation of the final model in our example of applying ESERs. The final model is first fitted to 1988-2004 data and thereafter used for prediction. (**a**) Mean ln(biomass) for 2005-2014 data. Observed data is shown by small circles and predictions, which are based on observed mean exploitation rates, are shown as small crosses. Confidence intervals for model predictions are based on 2.5 and 97.5 quantiles of 500 bootstrapped parameter sets. The bottom panels show true forward predictions for cod (**b**), sprat (**c**) and herring (**d**). Grey lines with small circles show observed data and black thick lines with striped confidence bounds show true forward conditional forecasts. Forecasts are conditional on time series of exploitation rate.

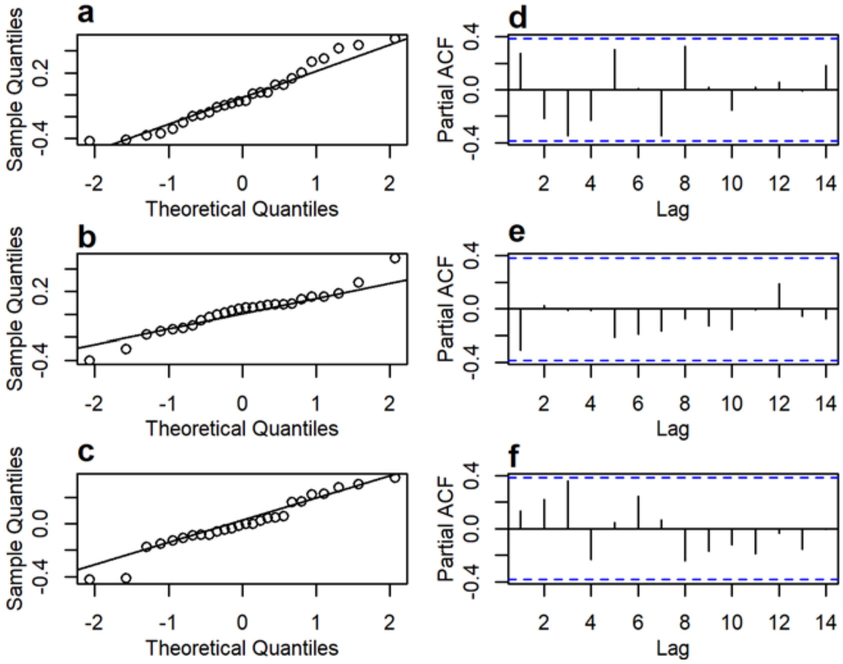

Fig. S3. Model adequacy for the final model in our example of applying ESERs. Left panels show normal probability plots for cod (**a**), sprat (**b**) and herring(**c**). Right panels show partial autocorrelation functions for cod (**d**), sprat (**e**) and herring (**f**).

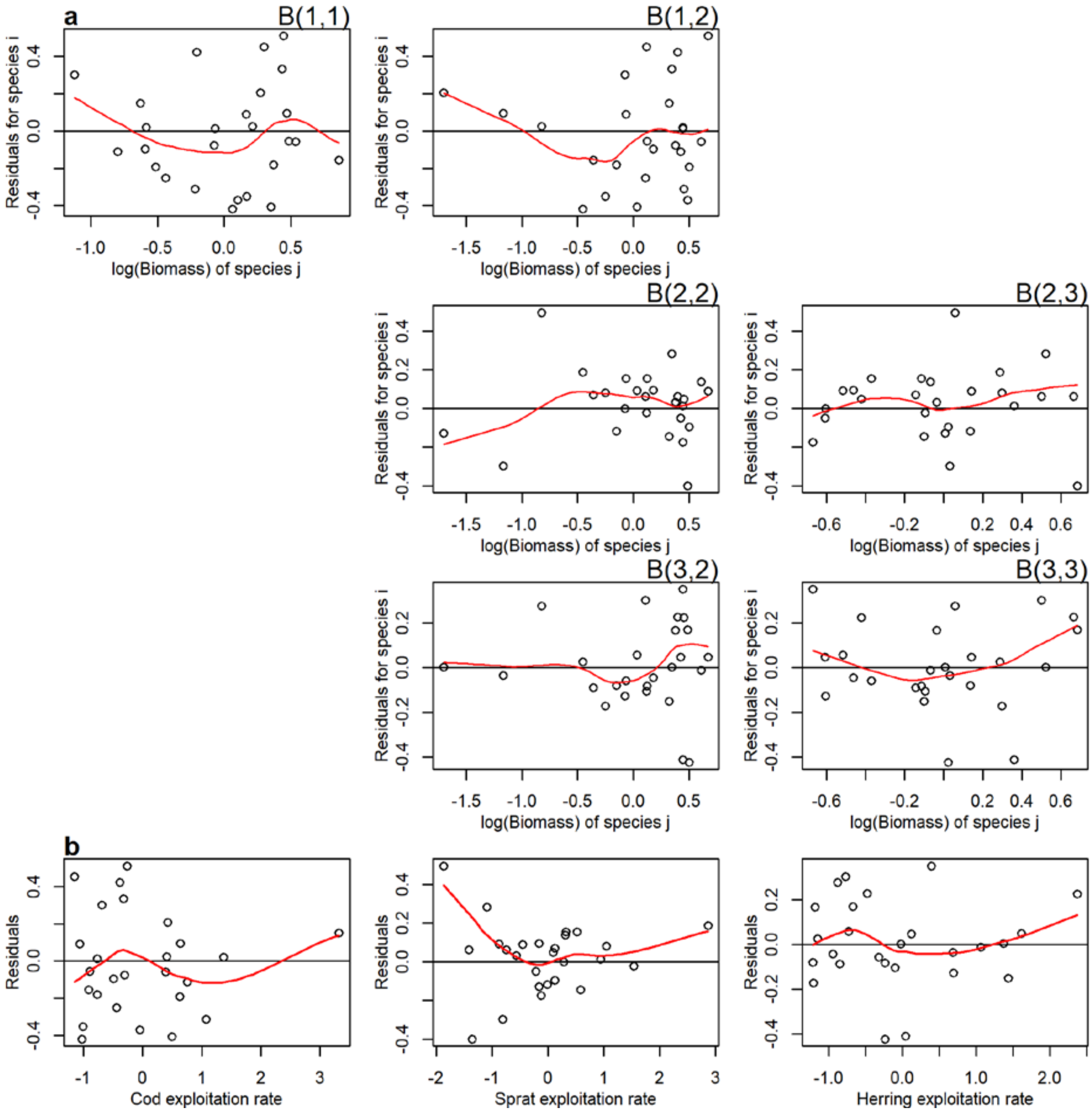

Fig. S4. Partial residual plots for the final model in our example of applying ESERs. **a)** Model residuals as a function of observed ln(biomasses). The panels show the potential existence of non-linear interactions among species. Subpanels are structured in the same way as the **B**-matrix, thus showing potential non-linear net effects (‘interactions’) between species in column *j* and row *i*. The x-axis corresponds to observed ln(biomass) of species *j* in year *t-1*, and the y-axis shows model residuals for species *i* at time *t*. Cod is represented by index (1), sprat is represented by index (2) and herring is represented by index (3). **b)** Model residuals for each species as a function of each species’ observed exploitation rate. The exploitation rates are shown as anomalies, i.e. with a mean of zero and unity variance. Red lines show the fit of local polynomial smoothers, with curved relationships indicating non-linear effects.

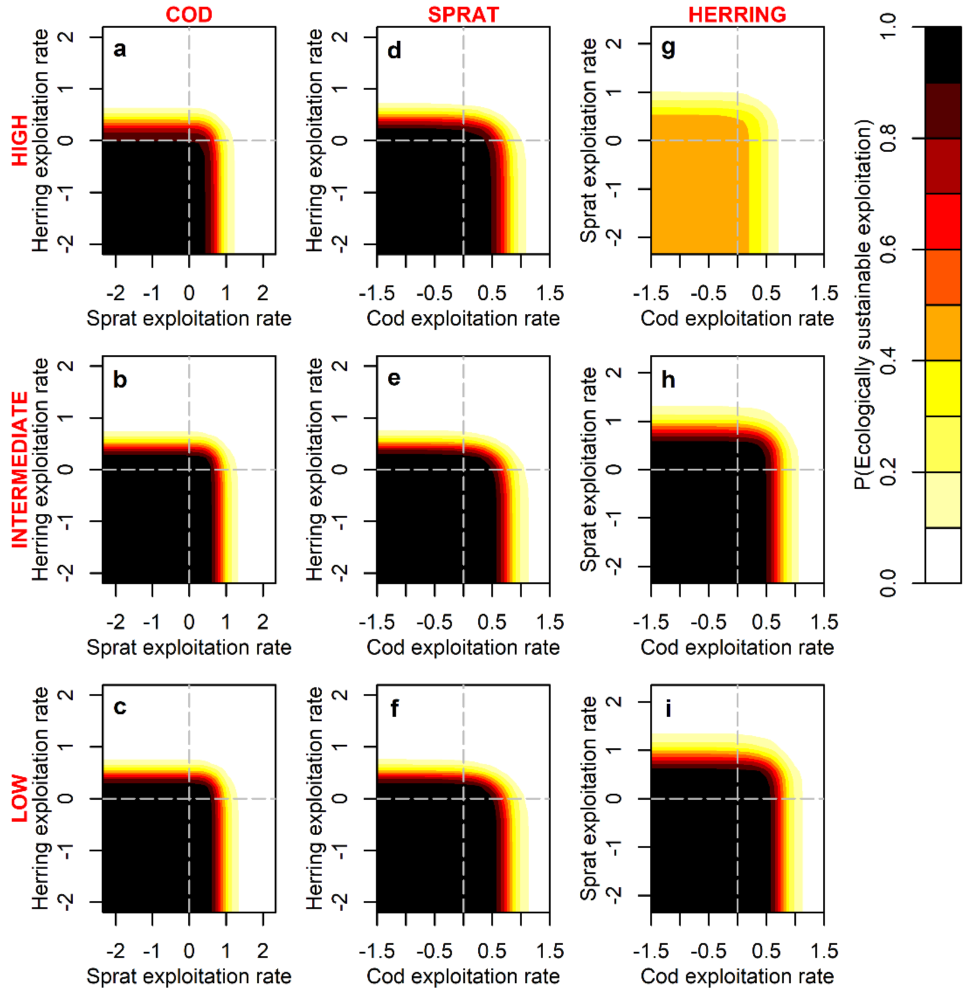

Fig. S5. Ranges of ecologically sustainable exploitation in the single species model. This figure shows the probability of ecologically sustainable exploitation as a function of exploitation rates, in a community of three non-interacting fish stocks. The probabilities are numerically found by evaluating if a specific exploitation rate combination is associated with a low probability (lower than a predefined maximum acceptable probability) that any interacting species in a community goes below its Blim, across 500 bootstrapped parameter sets. Top panels: (**a**), (**d**) and (**g**); middle panels: (**b**), (**e**) and (**h**); and bottom panels: (**c**), (**f**) and (**i**) show cases where exploitation rate of the species represented in each column (left: cod, middle: sprat, right: herring) is held at a fixed high (0.5), intermediate (0) or low (-0.5) level, respectively. Exploitation rates are represented as anomalies, i.e. as the number of standard deviations above or below mean historical levels (for 1988-2014). Dashed grey lines represent mean historical exploitation rates.

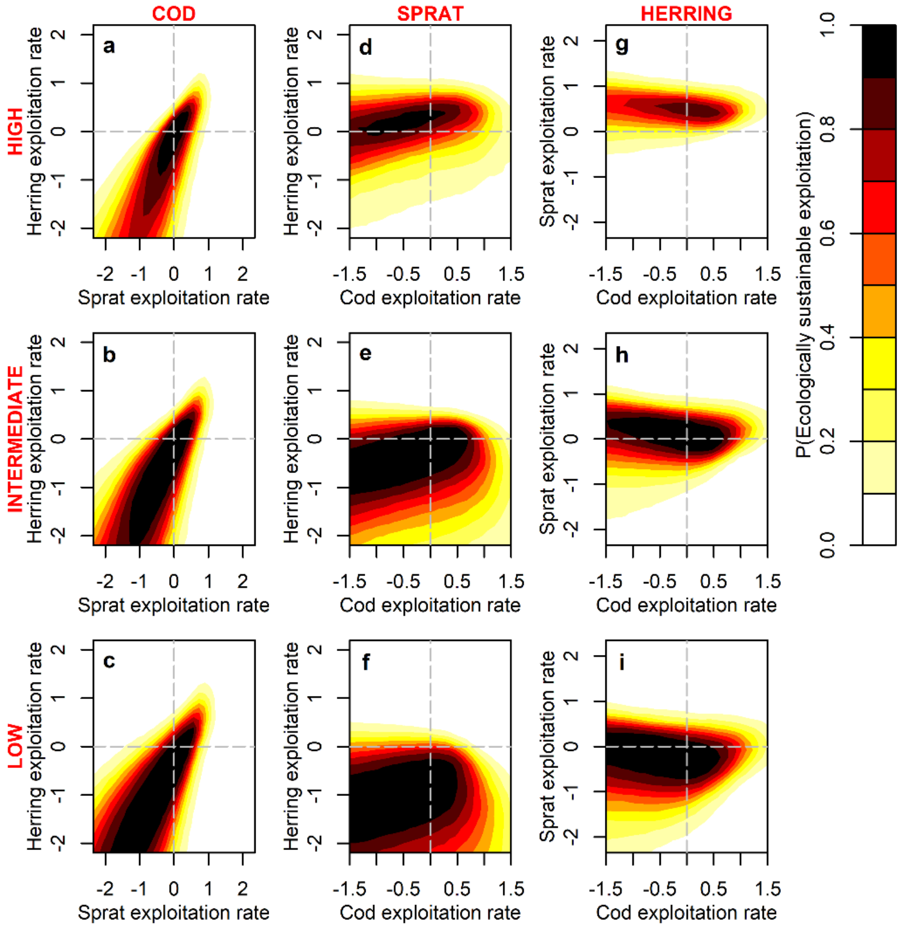

Fig. S6. Ranges of ecologically sustainable exploitation in the full model. This figure shows the probability of ecologically sustainable exploitation as a function of exploitation rates, in a community of three interacting fish stocks. The probabilities are numerically found by evaluating if a specific exploitation rate combination is associated with a low probability (lower than a predefined maximum acceptable probability) that any interacting species in a community goes below its Blim, across 500 bootstrapped parameter sets. Top panels: (**a**), (**d**) and (**g**); middle panels: (**b**), (**e**) and (**h**); and bottom panels: (**c**), (**f**) and (**i**) show cases where exploitation rate of the species represented in each column (left: cod, middle: sprat, right: herring) is held at a fixed high (0.5), intermediate (0) or low (-0.5) level, respectively. Exploitation rates are represented as anomalies, i.e. as the number of standard deviations above or below mean historical levels (for 1988-2014). Dashed grey lines represent mean historical exploitation rates.

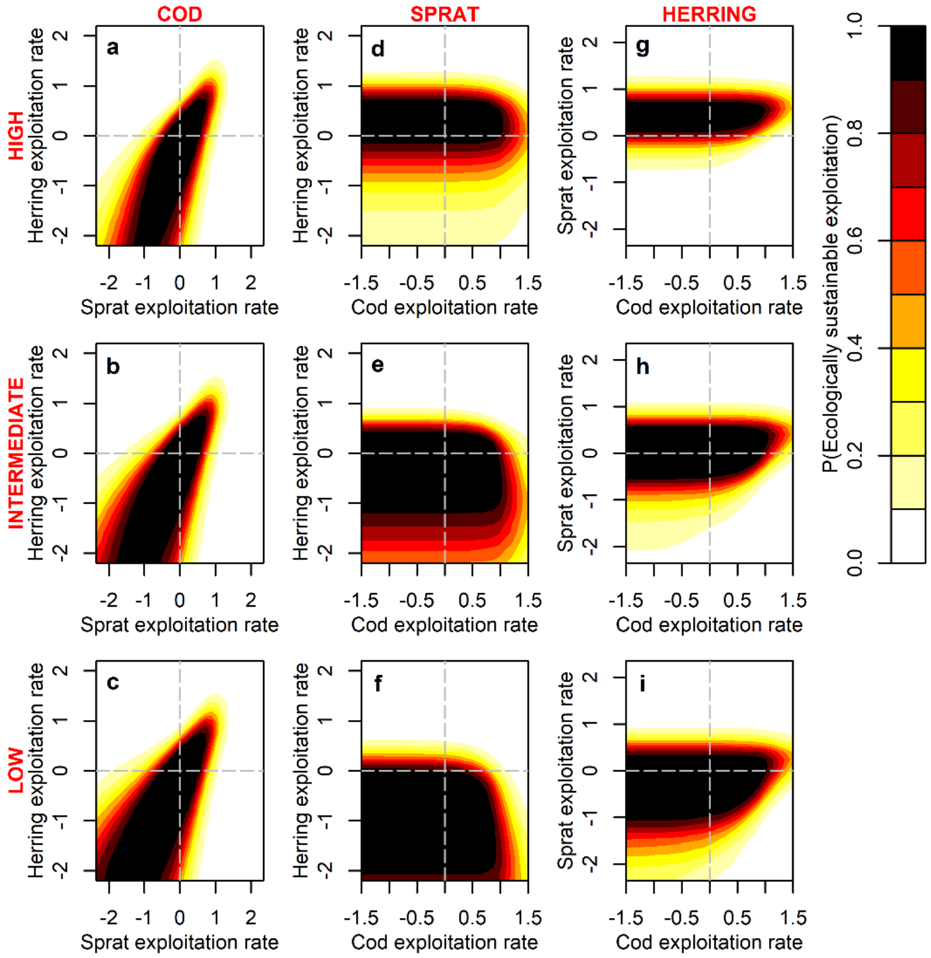

Fig. S7. Ranges of ecologically sustainable exploitation in the final model for the case where a high maximum probability that any species goes below its critical biomass limit is assumed ($\alpha = 0.2$). This figure shows the probability of ecologically sustainable exploitation as a function of exploitation rates, in a community of three interacting fish stocks. The probabilities are numerically found by evaluating if a specific exploitation rate combination is associated with a low probability (lower than a predefined maximum acceptable probability) that any interacting species in a community goes below its Blim, across 500 bootstrapped parameter sets. Top panels: (**a**), (**d**) and (**g**); middle panels: (**b**), (**e**) and (**h**); and bottom panels: (**c**), (**f**) and (**i**) show cases where exploitation rate of the species represented in each column (left: cod, middle: sprat, right: herring) is held at a fixed high (0.5), intermediate (0) or low (-0.5) level, respectively. Exploitation rates are represented as anomalies, i.e. as the number of standard deviations above or below mean historical levels (for 1988-2014). Dashed grey lines represent mean historical exploitation rates.

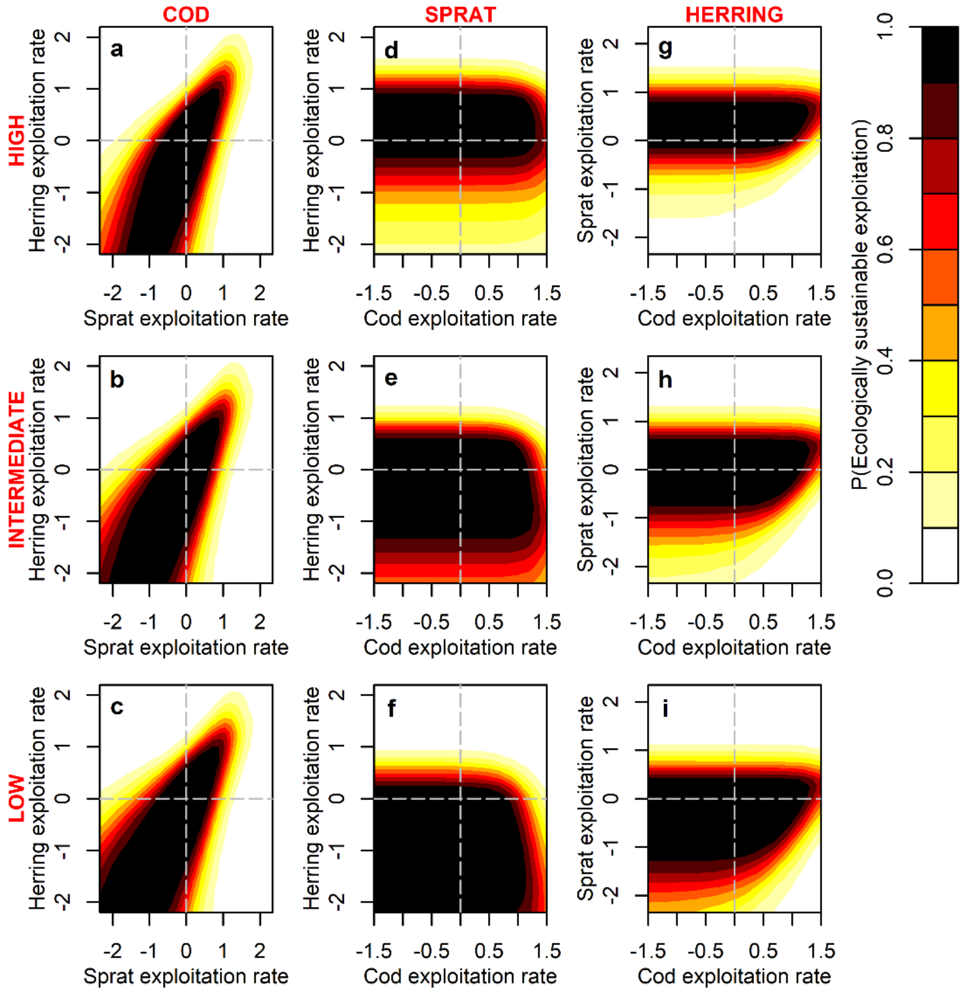

Fig. S8. Ranges of ecologically sustainable exploitation in the final model for the case where critical biomass limits are assumed to be 20 % lower than species' Blims;s. This figure shows the probability of ecologically sustainable exploitation as a function of exploitation rates, in a community of three interacting fish stocks. The probabilities are numerically found by evaluating if a specific exploitation rate combination is associated with a low probability (lower than a predefined maximum acceptable probability) that any interacting species in a community goes below its Blim, across 500 bootstrapped parameter sets. Top panels: (**a**), (**d**) and (**g**); middle panels: (**b**), (**e**) and (**h**); and bottom panels: (**c**), (**f**) and (**i**) show cases where exploitation rate of the species represented in each column (left: cod, middle: sprat, right: herring) is held at a fixed high (0.5), intermediate (0) or low (-0.5) level, respectively. Exploitation rates are represented as anomalies, i.e. as the number of standard deviations above or below mean historical levels (for 1988-2014). Dashed grey lines represent mean historical exploitation rates.

SUPPLEMENTARY TABLES

Table S1. MAR-model parameter estimates in our example of applying ESERs.

Final model

	B			D		
	Cod	**Sprat**	**Herring**	**D.Cod**	**D.Sprat**	**D.Herring**
Cod	0.17[-0.11;0.39]	-0.21[-0.42;-0.01]	-	-0.33[-0.45;-0.22]	-	-
Sprat	-	0.64[0.44;0.76]	-0.27[-0.47;-0.1]	-	-0.28[-0.37;-0.21]	-
Herring	-	-0.21[-0.38;-0.07]	0.39[0.08;0.57]	-	-	-0.24[-0.36;-0.16]

Single species model

	B			D		
	Cod	**Sprat**	**Herring**	**D.Cod**	**D.Sprat**	**D.Herring**
Cod	0.25[-0.04;0.48]	-	-	-0.33[-0.45;-0.22]	-	-
Sprat	-	0.64[0.38;0.78]	-	-	-0.27[-0.36;-0.2]	-
Herring	-	-	0.39[0.11;0.61]	-	-	-0.25[-0.36;-0.16]

Full model

	B			D		
	Cod	**Sprat**	**Herring**	**D.Cod**	**D.Sprat**	**D.Herring**
Cod	0.17[-0.17;0.37]	-0.21[-0.44;0]	0.03[-0.27;0.41]	-0.33[-0.45;-0.19]	-	-
Sprat	0.1[-0.11;0.28]	0.66[0.46;0.78]	-0.31[-0.54;-0.07]	-	-0.28[-0.37;-0.22]	-
Herring	-0.02[-0.2;0.21]	-0.21[-0.38;-0.05]	0.4[0.07;0.59]	-	-	-0.24[-0.36;-0.16]

[§] Final model refers to the model found through model selection based on AICc; single species refers to a model fitted assuming no interspecific interactions, i.e. assuming a diagonal **B**-matrix; and full model refers to a model fitted assuming that all species interact with each other. Predictors are arranged in columns and variates are order in rows. The **B**-matrix consist of species net effects on each other (‘interactions’) and the **D**-matrix exploitation rate parameters. Values within square brackets are 95% confidence intervals based on 500 bootstrapped data sets.

Table S2. Dickey-Fuller and Phillip-Perrons stationarity tests for our example of applying ESERs.

	Biomass			Exploitation rate		
	Cod	Sprat	Herring	Cod	Sprat	Herring
Dickey-Fuller test statistic	-13.12	-9.63	-8.7	-12.19	-9.2	-8.06
P-value	0.01	0.02	0.03	0.01	0.03	0.04
Phillips-Perron test statistic	-2.97	-3.04	-2.23	-2.93	-1.69	-2.12
P-value	0.01	0.01	0.03	0.01	0.09	0.04

[§] This table shows test statistics and p-values for the biomass and exploitation rate time series used in building the final MAR-model. These tests test if the null hypothesis, that is, that the time series are produced by a random walk process, can be rejected.

Table S3. Upper and lower limits of Ecologically Sustainable Exploitation Rates with 95% confidence intervals.

Model	**Upper limit Cod**	**Lower limit Cod**	**Upper limit Sprat**	**Lower limit Sprat**	**Upper limit Herring**	**Lower limit Herring**	**ΔAICc**
Final model	0.84[0.61 1.49]	-	0.62[0.39 1.16]	-0.53[-1.75 -0.25]	0.39[0.24 0.79]	-1.65[-6.65 -0.79]	0
Single species model	0.68[0.42 1.25]	-	0.81[0.45 1.61]	-	0.44[0.19 0.90]	-	10.71
Full model	0.98[0.58 2.25]	-2.93[-25.18 -0.35]	0.57[0.33 1.20]	-0.48[-1.76 -0.21]	0.35[0.18 0.78]	-1.31[-7.31 -0.63]	8.89

[§] Final model represents the model found through model selection; Single species model represents a model fitted assuming no interspecific interactions, i.e. assuming a diagonal **B**-matrix; and Full model represents a model fitted assuming that all species interact with each other. Note that limits for ESER are reported as anomalies, i.e. the number of standard deviations above (positive values) or below (negative values) mean historical exploitation rate levels (for 1988-2014). Confidence intervals are based on 500 bootstrapped parameter sets. Some of the data-points represent exploitation anomalies that would infer zero catch or less. Exploitation rate anomalies smaller than: -1.52, for cod; -2.23, for herring; and, -2.38, for sprat represent zero catch and can be referred to as parameter sets with no exploitation rate limits (See Tab. S5).

Table S4. Indirect effects caused by increased exploitation rate in our example of applying ESERs.

	Sensitivity to change in μ_{FCod}	**Sensitivity to change in μ_{FSprat}**	**Sensitivity to change in $\mu_{FHerring}$**
Cod	-0.4[-0.55;-0.26]	0.26[0.01;0.5]	-0.1[-0.26;0]
Sprat	-	-1.04[-1.58;-0.62]	0.39[0.1;0.76]
Herring	-	0.36[0.09;0.72]	-0.53[-0.77;-0.33]

[§] The response (rows) of the stationary mean (eq. 3 in Methods) of the final model to a unitary increase in exploitation rate for each species (columns). The values presented are the partial derivatives of the stationary mean (eq. 3 in Methods) with respect to a change in mean exploitation rate for each species. Values within square brackets are 95% confidence intervals based on 500 bootstrapped data sets.

Table S5. The number of cases where it is impossible to find an ESER limit (No limit), and the number of cases where the lower limit for ESERs would represent an exploitation rate lower than zero on the original untransformed scale (Unfeasible limit), i.e. an exploitation rate inferring no exploitation, in our application example of ESERs.

	Final model			**Single species model**			**Full model**		
	Cod	**Sprat**	**Herring**	**Cod**	**Sprat**	**Herring**	**Cod**	**Sprat**	**Herring**
No limit	0	0	1	0	0	0	76	0	8
Unfeasible limit	0	3	184	0	0	0	242	6	126

§For each species and model, numbers are based on numerical investigations of 500 bootstrapped parameter sets. Note that no limits for ESERs infers that the multispecies objective cannot be attained when a given focal species' mean exploitation rate is changed, and the other two species' mean exploitation rates are kept at mean historical levels.

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