On the description and flexibility of state-space assessment model

Shota Nishijima and Momoko Ichinokawa

Fisheries Resources Institute,

Japan Fisheries Research and Education Agency (FRA)

(Corresponding author: Shota Nishijima, nishijima_shota02@fra.go.jp)

Introduction

Through a long way of model selection, it has been concluded that SAM showed the best model performance from the summary metrics of selected performance measures (Rice 2023). Not all members are familiar with SAM, and details of description and usage of SAM are not fully shared in the TWG CMSA except the previous document (Nishijima et al 2022) that only briefly introduce SAM. For transparency and facilitation of collaborative work, the details of SAM as the stock assessment model for chub mackerel should be revisited and shared with the TWG CMSA members.

This document describes model structures of SAM in detail and how to use an R package of SAM ("frasam") developed for the stock assessment of chub mackerel. We then demonstrate that SAM has flexible features and can mimic other candidate models (ASAP, KAFKA, and VPA) in terms of fishery selectivity and the measurement errors in catch at age by posing some constraints. We also show how to treat within-model and among-model uncertainties in SAM. Since SAM can introduce variety types of random components that can be developed by us, 'frasam' can be flexibly adjusted and improved for the chub mackerel stock assessment in a collaborative manner in the TWG CMSA.

Basic model structure

We first introduce the original structure of SAM (Nielsen and Berg 2014) and then describe our adjustments to chub mackerel stock assessment in the next section. The population dynamics in SAM basically follows age-structured models:

2nd Floor Hakuyo Hall,
Tokyo University of Marine Science and Technology,
4-5-7 Konan, Minato-ku, Tokyo
108-8477, JAPAN

TEL +81-3-5479-8717
FAX +81-3-5479-8718
Email secretariat@npfc.int
Web www.npfc.int

$$\log(N_{1,y}) = \log[f(SSB_{y-1})] + \eta_{0,y}, \tag{1}$$

$$\log(N_{a,y}) = \log(N_{a-1,y-1}) - F_{a-1,y-1} - M_{a-1,y-1} + \eta_{a,y}, \qquad 2 \le a \le A\text{-}1 \tag{2}$$

$$\log(N_{A+,y}) = \log(N_{A-1,y-1}e^{-F_{a,y-1}-M_{a,y-1}} + N_{A+,y-1}e^{-F_{A+,y-1}-M_{A+,y-1}}) + \eta_{A+,y}, \tag{3}$$

where $\eta_{a,y}$ is the process error at age a in year y following $\eta_{a,y} \sim N(0, \omega_a^2)$. It was assumed that the recruitment occurs at age 1 and the maximum age class is plus group ($A+$). Although the original paper (Nielsen and Berg 2014) used a stock-recruitment relationship ($f(SSB_{y-1})$), the uploaded code includes another option of random-walk recruitment (https://kaskr.github.io/adcomp/sam_8cpp-example.html):

$$\log(N_{1,y}) = \log(N_{1?,y-1}) + \eta_{0,y}. \tag{4}$$

While other stock assessment models like ASAP usually estimate process errors only for recruitment, SAM has the advantage that process errors for older ages can be estimated, which reflects random variations such as varying natural mortality.

In SAM, the fishing mortality coefficient is assumed to follow a multivariate random walk:

Fy,f = log F_(y-1, f) + …

$$\log(\mathbf{F_y}) = \log(\mathbf{F_{y-1}}) + \boldsymbol{\xi}_y, \tag{5}$$

where $\mathbf{F_y} = (F_{1,y}, \dots, F_{A+,y})^T$, $\boldsymbol{\xi}_y \sim \text{MVN}(0, \boldsymbol{\Sigma})$, and $\boldsymbol{\Sigma}$ is the variance-covariance matrix of multivariate normal distribution (MVN). The diagonal elements of matrix $\boldsymbol{\Sigma}$ were σ_a^2, while off-diagonal elements represent covariance of F process errors between age classes. The original paper tested four covariance structures and found that the assumption that the correlation depends on age differences had the lowest AIC: $\rho^{|a-a'|}\sigma_a\sigma_{a'}$ ($a \ne a'$) with 49 years of North Sea cod data, where $\rho^{|a-a'|}$ corresponded to the correlation coefficient of F between ages a and a' (see details in Nielsen and Berg 2014). In addition, the case study shown by the original paper assumed $F_{A+,y} = F_{A-1,y}$ to stabilize parameter estimation.

SAM uses the Baranov equation for estimates in catch-at-age:

$C_{a,y,f} = F_{a,y,f}/(F_{a,y}+M_a)(1-\exp(-F_{a,y}-M_a))N_{a,y}$

  if $F_{a,y,f}$ is estimated as random effect, the model is fleet structured (future study)

  if not, we can calculate $F_{a,y,f}$ without errors of $C_{a,y,f}$

$TC_{a,y,f} = \Sigma\, C_{a,y,f} * W_{a,y,f}$ (total catch by fleet)

Selectivity of fleet
$S_{a,y,f} = F_{a,y,f}/\max(F_{a,y,f})$

$$\hat{C}_{a,y} = \frac{F_{a,y}}{F_{a,y}+M_{a,y}}\left(1-\exp(-F_{a,y}-M_{a,y})\right)N_{a,y}. \tag{5}$$

SAM then fit to observed catch-at-age in a lognormal assumption:

$$\log(C_{a,y}) = \log(\hat{C}_{a,y}) + \varepsilon_{a,y}, \tag{6}$$

where $\varepsilon_{a,y} \sim N(0, \tau_a^2)$. SAM was originally fitted to age-specific abundance index in a lognormal assumption (Nielsen and Berg 2014):

$\log(I\_(f,y)) = \log(\Sigma\_a\, q\, S_{a,y,f}\, N_{a,y})$

$$\log(I_{a,y}) = \log(q_a N_{a,y}) + \eta_{a,y}, \tag{7}$$

where $\eta_{a,y}$ is the measurement error of index for age a in year y: $\eta_{k,y} \sim N(0, v_k^2)$.

SAM estimates $\widehat{N}_{a,y}$ and $\widehat{F}_{a,y}$ as random effects using the marginal likelihood with fixed-effect parameters of ω_a, σ_a, ρ, τ_a, q_a, and v_a. The joint likelihood has therefore the components of observation and random effects. Since the integral for the marginal likelihood is difficult to calculate directly, SAM uses the Laplace approximation, which enables fast and accurate computation via TMB (Kristensen et al. 2016). Moreover, SAMs with different settings are quantitatively comparable using criteria such as AIC in terms of whether some parameters are estimated or fixed and how parameter constraints are imposed.

SAM has been developed from the original study by researchers around the world. For example, a recent study extended SAM into multiple fleets (Nielsen et al. 2021), which may be useful for considering chub mackerel fisheries by different members. While it is recommended to estimate natural mortality (M) within a stock assessment model rather than assume M (Punt et al. 2021; Maunder et al. 2023), M may be estimable in SAM. Moreover, we have an experience of extending SAM to Japanese flying squid with longevity of one year so that SAM is applicable to stocks having no age-structure (Nishijima et al. 2021). This extensibility helps us to improve chub mackerel stock assessment by incorporating biological characteristics and fisheries of chub mackerel. We have already revised and extended SAM's configurations for the chub mackerel stock assessment as shown in the next section.

Adjustments to chub mackerel stock assessment

To apply SAM to chub mackerel, we have made several adjustments from the original model configurations as follows:

1. Recruiting age has changed from one to zero.
2. The magnitude of process errors in numbers for ages older than 0 can be fixed at a given value,
3. Random walk of F in a year can be removed from the joint likelihood,
4. Nonlinear relationships can be estimated in fitting abundance indices,
5. Age-aggregate abundance indices can be used.

Revision 1 is required because chub mackerel recruits at age 0. Revision 2 was made because estimating the process errors other than recruitment destabilized parameter estimation and did not match with the assumption of PopSim. We fixed the variance for the ages older than 0 at a small value ($\omega_{S,a}^2 = 0.0001$). We implemented the option of Revision 3 because the fishing effort on chub mackerel possibly greatly decreased in 2011 from the previous year owing to the Great East Japan Earthquake and tsunami in March 2011. Revision 4 was implemented so that the goodness of fit would be improved. Revision 5 was made because we needed to use age-aggregate abundance indices for spawning stock biomass and vulnerable biomass. As a result, the function of fitting abundance indices can be expressed as

$$\log(I_{k,y}) = \log(q_r X_y^{b_k}) + \eta_{k,y} \,, \tag{8}$$

where b_k is the nonlinear coefficient and X_y is the corresponding abundance such as the number of recruits, spawning stock biomass, and vulnerable stock biomass.

the measurement error of index k in year y: $\eta_{k,y} \sim N(0, \, v_k^2)$.

SAM requires estimation of many parameters. We then imposed the following constraints to stabilize estimation and avoid overfitting:

$$\omega_{S,a} = \omega_S \ \left(\forall a \, (a > 0) \right), \tag{15}$$

$$\sigma_0 = \sigma_1, \ \sigma_2 = \sigma_3 = \cdots = \sigma_A \,, \tag{16}$$

$$\tau_2 = \tau_3, \ \tau_5 = \tau_{6+}. \tag{17}$$

These constraints were determined based on the Akaike information criteria (AIC). The other details are shown in the previous working document (Nishijima et al. 2022).

Description of R package 'frasam'
We have been developing SAM available for the stock assessment of chub mackerel as a

R package "frasam". The code of "frasam" was evolved from the original C++ code on the website of TMB documentation (https://kaskr.github.io/adcomp/sam_8cpp-example.html) through some revisions including the above points.

The source codes we used are available as R package 'frasam' through GitHub (https://github.com/ShotaNishijima/frasam/tree/dev). One can install as follows:

```
install.packages("devtools") # if not installed
devtools::install_github("ShotaNishijima/frasam", ref="dev")
library(frasam)
```

We here show an example code when we analyzed Scenario A with real data. We firstly formatted data for the input of SAM like this:

```
library(tidyverse)
merged_dat = read.csv("MergedData(chub_mackerel)200928.csv",header=T)
merged_dat = merged_dat %>% mutate(year_label = str_c("X",as.character(year)))
caa0 = merged_dat %>% dplyr::filter(label == "catch-at-age") %>%
   pivot_wider(id_cols=age,names_from=year_label,values_from=value) %>%
   column_to_rownames(var = "age")
maa0 = merged_dat %>% dplyr::filter(label == "maturity-at-age") %>%
   pivot_wider(id_cols=age,names_from=year_label,values_from=value) %>%
   column_to_rownames(var = "age")
waa0 = merged_dat %>% dplyr::filter(label == "weight-at-age") %>%
   pivot_wider(id_cols=age,names_from=year_label,values_from=value) %>%
   column_to_rownames(var = "age")
index0 = merged_dat %>%
pivot_wider(id_cols=c(label,fleet,age),names_from=year_label,values_from=value) %>%
   dplyr::filter(label == "abundance_index") %>%
   select(-label,-age,-fleet) %>%
   mutate(rowname=1:n()) %>%
   column_to_rownames(var = "rowname")
dat1 <- data.handler(caa0, waa0, maa0, index0, M=0.41)
```

We made matrix-style data with columns of years and rows of ages for catch-at-age, weight-at-age, and so on. "data.handler" is a function for data formatting for SAM and VPA in our another package "frasyr" (https://github.com/ichimomo/frasyr). We need to compile and activate the C++ file for SAM ("sam.cpp") before analyzing:

```
use_sam_tmb(overwrite=TRUE)
```

We then analyze SAM as follows:

```
sam_base1 <- sam(
    dat1,
    abund = c("N","N","SSB","SSB","Bs","Bs"),
    min.age=c(0,0,0,0,0,0),
    max.age = c(0,0,6,6,6,6),
    SR = "RW",
    index.key=c(0,0,1,1,2,2),
    b.est=TRUE,
    index.b.key = c(0,1,2,3,4,4),
    b.fix=c(NA,NA,1,1,NA),
    varC = c(0,1,2,2,3,4,4),
    varF = c(0,0,1,1,1,1),
    varN = c(0,1,1,1,1,1,1),
    varN.fix=c(NA,1e-4),
    rho.mode=3,
    bias.correct = TRUE,
    p0.list = NULL,
    map.add = NULL
)
```

Descriptions of above arguments are shown in Table 1. The settings are almost identical to those used for the analyses of real data and pseudo data, but we here did not remove the random walk of F from 2010 to 2011 so that AIC of different settings would be comparable (see below).

This package is still under development, and we will improve its availability by enhancing manuals, functions' helps, test codes and model diagnostic tools so that one can easily understand and analyze SAM via frasam. We can collaboratively work the development and improvement of SAM with TWG members via GitHub. We have uploaded R codes that we used in fitting real and pseudo data in the analyses of SAM and VPA on the Collaboration website (https://collaboration.npfc.int/node/126) for reproducibility and transparency.

SAM as a flexible and intermediate model

One of most important features of SAM is its flexibility including a variety of random components so that SAM naturally has intermediate features between other candidates of

the stock assessment models discussed in the TWG CMSA. A remarkable difference in the model assumption of the other three models (ASAP, KAFKA and VPA) relates to selectivity and measurement errors in catch-at-age. ASAP assumes constant selectivity over time while it estimates measurement errors in catch-at-age. On the other hand, KAFKA and VPA assume no measurement errors in catch at age while they are not subject to selectivity constraints, which means time-varying selectivity. However, SAM can simultaneously estimate both time-varying selectivity and measurement errors in catch at age under the random-walk assumption in fishing mortality at age. This intermediate feature of SAM indicates that it does not require the extreme assumptions made by other candidate models and would represent realistic situations of fisheries with selectivity smoothly and temporally varied (Nielsen and Berg 2014). Because the smoothness of time-varying selectivity can be controlled by imposing some constraints on the parameters of selectivity and measurement errors in catch-at-age in SAM, it can mimic the other models.

The constant selectivity assumed by ASAP is achievable if each element in the variance-covariance matrix of F random walk is assumed to have a same value:

$$\boldsymbol{\Sigma} = \begin{pmatrix} \sigma^2 & \cdots & \sigma^2 \\ \vdots & \ddots & \vdots \\ \sigma^2 & \cdots & \sigma^2 \end{pmatrix}, \tag{4}$$

This means that F at each age changes in the same way, causing selectivity constant over time. This is possible if one fixes at $\rho = 1$ and estimates a common value of σ across all age classes. This constraint makes SAM close to the assumption of ASAP (but error structures of catch at age are different because ASAP assumes a lognormal error for total catch and multinomial errors in catch composition). This revision to constant selectivity is easily feasible in frasam:

```
input <- sam_base1$input
input$varF <- rep(0,7)
input$rho.mode <- 1
input$bias.correct <- FALSE
asap_like1 <- do.call("sam",input)
```

The list of arguments is stored as 'input'. We changed the arguments of 'varF' (constraints on the variance in F random walk process) and "rho.mode' (correlation structure of variance-covariance matrix in F random walk process) and removed the option for bias correction (Table 1). The other model configurations were assumed to be identical in SAM. We call here this model 'ASAP-like' model.

No measurement errors of catch-at-age as assumed by VPA and KAFKA are almost achievable if the variance of measurement errors in catch-at age (τ_a^2) is fixed at a very small value. This constraint makes SAM close to the assumption of KAFKA and VPA. In frasam, two steps are needed for posing this constraint:

```
input <- sam_base1$input
input$varC <- rep(0,7)
input$bias.correct <- FALSE
temp <- do.call("sam",input)
```

In this first step above, we assumed and estimated a common value of measurement errors in catches for all age classes. We then fixed at the measurement errors at $\tau_a^2 = 0.0001$ $(\tau_a = 0.01)$ as follows:

```
p0_list = temp$par_list
p0_list$logSdLogObs[1] <- log(0.01) #fixed at SD=0.01
map_add = list("logSdLogObs" = factor(c(NA,0:2)))
input = temp$input
input$map.add <- map_add
input$p0.list <- p0_list
vpa_like1 = do.call("sam",input)
```

The estimated parameters are stored as 'par_list' in a list format, which would be used for initial parameters in the second-step analysis. The initial value for measurement errors in catches was changed to the small value by the second line. The argument of 'map.add' was used to fix the parameter for catch at age. The other model configurations were assumed to be identical in SAM. We call here this model 'VPA-like' model (there is no particular reason why we don't call it 'KAFKA-like' model).

As a result, while SAM shows a gradual change in selectivity at age, the VPA-like model exhibits the highest levels and ASAP-like model has constant selectivity over time (Fig. 1). For the fits to the catch at age, the VPA-like model estimated the almost same values of observed catch-at-age and the ASAP-like model showed the lowest fitting to observation while SAM moderately fitted to observed catch-at-age (Fig. 2). Abundance estimates were similar between SAM and the ASAP-like model, although the ASAP-like model estimated slightly lower abundances than SAM (Fig. 3). The VPA-like model estimated higher abundances than the other two models (Fig. 3).

Importantly, performances of the different settings of SAM are easy to be compared by using AIC and other criteria. In this example data of chub mackerel, it is shown that

SAM has achieved the minimum AIC. This suggests that the intermediate assumptions

```
> c("SAM"=sam_base1$aic,"ASAP-like"=asap_like1$aic,"VPA-like"=vpa_like1$aic)
    SAM    ASAP-like   VPA-like
 1012.649   1035.778   1145.855
```

on time-varying selectivity and the measurement errors in catch at age for SAM are plausible compared with their extreme assumptions in the other three models. We have also uploaded the R code for this demonstration on the Collaboration website (https://collaboration.npfc.int/node/126).

Parameter uncertainties and model averaging
While the TWG CMSA has focused on point estimates from stock assessment models in evaluating model performances, parameter uncertainties in estimation will be a matter of debate for judging latest stock status and considering future projection and management advice. SAM outputs standard deviations of fixed effects, random effects, and derived parameters by the delta method via TMB. On the other hand, SAM can iteratively generate the parameters with random errors from a variance-covariance matrix or joint precision matrix under the assumption of multivariate normal distribution as with other stock assessment models. This feature will be useful for not only quantification of uncertainty in stock status but also future projection with estimation uncertainty because it is ideal for future predictions to incorporate the uncertainties of both estimated parameters and future processes. Sample sets of parameters generated from multivariate normal distributions will be respectively used for future projection with process errors mainly from recruitment variability.

Quantification of estimation uncertainty is also useful to treat multiple models with different settings and assumptions. For example, it is one of the most difficult things in stock assessments to determine natural mortality (M). TWG CMSA currently considers two sets of natural mortality scenarios: age-common M and age-specific M. Here we demonstrate a way of model averaging of different M assumptions using scenarios A and B.

Scenario B can easily be analyzed by replacing data of scenario A in frasam:

```
dat2 = dat1
dat2$M[] <-
matrix(rep(c(0.57,0.47,0.38,0.32,0.28,0.26,0.24),ncol(dat2$M)),ncol=ncol(dat2$M))
input = sam_base1$input
input$dat <- dat2
input$p0.list <- sam_base1$obj$env$parList()
sam_base2 = do.call("sam",input)
```

```
> delta = c(sam_base1$aic,sam_base2$aic)
> (delta = delta - min(delta))
[1] 0.0000000 0.4191264
> (weight = exp(-delta/2)/sum(exp(-delta/2)))
[1] 0.5521999 0.4478001
```

SSB under the age-specific M scenario (B) in the last year (2019) was estimated to be lower than that under the age-common M scenario (A) and their probability distributions generated from their joint precision matrices of fixed-effect and random-effect parameters are shown in Fig. 4. One may consider the need to incorporate the uncertainty from different M assumptions into the chub mackerel stock assessment. AIC of these two scenarios is comparable and showed that the age-common M scenario had slightly better goodness-of-fit (ΔAIC = 0.42). This suggests that putting a heavier weight on the age-common M scenario according to Akaike weights may be plausible.

For model averaging, we therefore took samples from the scenario A with weight of 55.2% and from the scenario B with weight of 44.8%. The probability distribution of SSB in the model averaging was located at an intermediate position, but relatively close to age-common M (Fig. 4). Although this demonstration is a preliminary idea for model averaging, it highlights the ability of SAM to easily deal with among-model uncertainty as well as within-model uncertainty and employ model averaging with appropriate weighting.

Final remarks

Ensemble modeling has increasingly been used in fisheries stock assessments (Jardim et al. 2021; Stewart and Hicks 2018; Stewart and Martell 2015). One of the pros in the ensemble modeling is better consideration of uncertainty (Ducharme-Barch and Vincent 2022), while its cons are costs for time and efforts and potential biases by inclusion of

biased and/or flawed models. Neubauer et al. (2023) illustrated that using a simple simulation, an ensemble of multiple models with wrong assumptions estimated more biased stock status and productivity than a single model (see Fig. 6 in https://meetings.wcpfc.int/file/13043/download).

In the case of chub mackerel stock assessment, there is no evidence that the prediction skill will be improved by the ensemble approach at this moment, while there is a potential risk of estimation bias because some candidate models showed serious biases even in the self-test (Joel 2023). Ensemble modeling in fisheries stock assessments is used to cover structural and parameter uncertainties (Jardim et al. 2021). For structural uncertainty, we demonstrated in this document that SAM can mimic the structures and assumptions of the other models. We also showed that SAM can incorporate the uncertainty of fixed parameters using different scenarios of natural mortality as an example. Accordingly, there seems to be no clear advantages of taking the ensemble modeling in the TWG CMSA from a scientific view.

From an operational view, the ensemble approach requires a lot of things to be considered such as how to ensemble different models (Ducharme-Barch and Vincent 2022; Neubauer et al. 2023), but we don't have sufficient time to the first stock assessment. More importantly, it appears that taking the ensemble modeling will require much human effort and labor cost. Consider situations where each member analyzes different models independently by using their methods of computer languages, codes, and packages. This means that each member must do the best every time of stock assessment and efforts on analyses and review inevitably increase as much as the number of stock assessment models. More invited experts may be needed to review each stock assessment model and approve individual results. We already know from the previous demanding process how difficult it is to align the data to be used, to keep pace among members, and to reach a clear understanding of all models. It will be better to learn from our experience through the simulation works for the model competition.

Another concern is that naive ensemble of candidate models proposed by members is just a collection of 'independent' results, which is far removed from scientific collaborative work in the true sense. To be more productive, we would like to suggest that members collaboratively work on the improvements of SAM rather than ensemble modeling. SAM can flexibly adjust model configurations, suggesting high extensibility to treat structural and parameter uncertainties. While the one of most important pros in ensemble modeling is consideration of wide range of uncertainty, the uncertainty on model structures and assumptions such as selectivity and natural mortality can be represented within the range of model configurations by SAM, as illustrated in this

document. Because of its flexibility, SAM will be improved by adding a new idea that a member thinks of for model improvements. This collaborative work will keep transparency and save our effort and labor cost, because we can use the same format and quantitative measures such as AIC when evaluating and comparing models. Such collaborative development of the single model specific for chub mackerel, rather than simple competition of existing models, would promote further understanding of chub mackerel population dynamics more deeply and thereby help international management of this species in a collaborative manner.

References

Ducharme-Barch ND, Vincent MT (2023) Focusing on the front end: A framework for incorporating uncertainty in biological parameters in model ensembles of integrated stock assessments. Fisheries Research 255: 106452.

Jardim E, Azevedo M, Brodziak J, Brooks EN, Johnson KF, Klibansky N, Millar CP, Minto C, Mosqueira I, Nash RDM, Vasilakopoulos P, Wells BK. (2021) Operationalizing ensemble models for scientific advice to fisheries management. ICES Journal of Marine Science 78: 1209–1216.

Joel R. (2023) Recommendation to TWG CMSA07 on a stock assessment model platform based on work completed as part of the TWG CMSA assessment modeling project. NPFC-2023-TWG CMSA07-WP03.

Kristensen K, Nielsen A, Berg CW, Skaug H, Bell BM (2016) TMB: Automatic differentiation and Laplace approximation. Journal of Statistical Software 70:1–21.

Maunder MN, Hamel OS, Lee HH, Piner KR, Cope JM, Punt AE, Ianelli JN, Castillo-Jordán C, Kapur MS, Methot RD (2023) A review of estimation methods for natural mortality and their performance in the context of fishery stock assessment. Fisheries Research 257: 106489.

Neubauer P, Kim K, A'mar T, Large. K. (2023) Addressing uncertainty in WCPFC stock assessments: Review and recommendations from WCPFC Project 113. WCPFC-SC19-2023/SA-WP-12.

Nielsen A, Berg CW. (2014) Estimation of time-varying selectivity in stock assessments using state-space models. Fisheries Research 158:96–101.

Nielsen A, Hintzen NT, Mosegaard H, Trijoulet V, Berg CW. (2021) Multi-fleet state-space assessment model strengthens confidence in single-fleet SAM and provides fleet-specific forecast options. ICES Journal of Marine Science 78: 2043–2052.

Nishijima S, Kubota H, Kaga T, Okamoto S, Miyahara H, Okamura H. (2021) State-

space modeling clarifies productivity regime shifts of Japanese flying squid. Population Ecology 63: 27–40.

Nishijima S, Oshima K, Ichinokawa M, Shinohara N. (2022) Update of virtual population analysis and state-space assessment model for operating models of chub mackerel stock assessment in NPFC. NPFC-2021-TWG CMSA05-WP06.

Punt AE, Castillo-Jordán C, Hamel OS, Cope JM, Maunder MN, Ianelli JN. (2021) Consequences of error in natural mortality and its estimation in stock assessment models. Fisheries Research 233: 105759.

Stewart IJ, Martell, SJD. (2015) Reconciling stock assessment paradigms to better inform fisheries management. ICES Journal of Marine Science 72: 2187–2196.

Stewart IJ, Hicks AC. (2018) Interannual stability from ensemble modelling. Canadian Journal of Fisheries and Aquatic Sciences 75: 2109–2113.

Table 1: Descriptions of arguments in the 'sam' function.

Argument	Description
abund	Targets of abundance indices. "N": population number, "SSB": spawning stock biomass, "Bs": vulnerable biomass, and "B": biomass (default).
min.age	The minimum age for the abundance indices in the argument 'abund'.
max.age	The maximum age for the abundance indices in the argument 'abund'. The same values of 'min.age' and 'max.age' indicate age-specific abundance index, whereas otherwise indicate age-aggregate indices.
SR	The form of stock-recruitment relationships. "BH": Beverton-Holt (default), "RI": Ricker, "RW": Random walk, and "Const": Constant average recruitment with random errors. The option of hockey-stick ("HS") is under development.
index.key	Constraints on measurement errors for abundance indices. The same value indicates a common value shared among abundance indices (default: NULL).
b.est	Whether nonlinear coefficients for abundance indices are estimated (default: FALSE)
b.fix	Able to fix nonlinear coefficients at a certain value (mostly 1). Its length should be the number of abundance indices (default) or the number of different values of 'index.b.key' (otherwise). The fixed values should be inputted and NA for otherwise.
varC	Constraints on measurement errors in catch at age. Its length should be

|	
	the number of age classes or one (i.e., common for all age classes). The same value indicates a common value shared among age classes (default: 0).
varF	Constraints on process errors in F random walk. Its length should be the number of age classes or one (i.e., common for all age classes). The same value indicates a common value shared among age classes (default: 0).
varN	Constraints on process errors in numbers by age. Its length should be the number of age classes or one (i.e., common for all age classes). The same value indicates a common value shared among age classes (default: 0).
varN.fix	Able to fix the variances of process errors in numbers at a certain value. Its length should be the number of different values of 'varN'. The values of fixed variances should be inputted and NA for otherwise.
rho.mode	Correlation structure of variance-covariance matrix in F random walk. 0: almost no correlation for all combination of age classes (accurately $\rho=0.000001$), 1: almost complete correlation for all combination of age classes (accurately $\rho=0.999999$), 2: same correlation between any two age classes, 3: correlation following the power-law function of age differences $\rho^{|a-a'|}$.
bias.correct	Whether the generic method of bias correction is implemented for random effects (default: TRUE).
p0.list	Initial parameter values as a list format (default: NULL).
map.add	Additional parameter that are fixed at initial values. A list format with parameter names is needed (default: NULL).
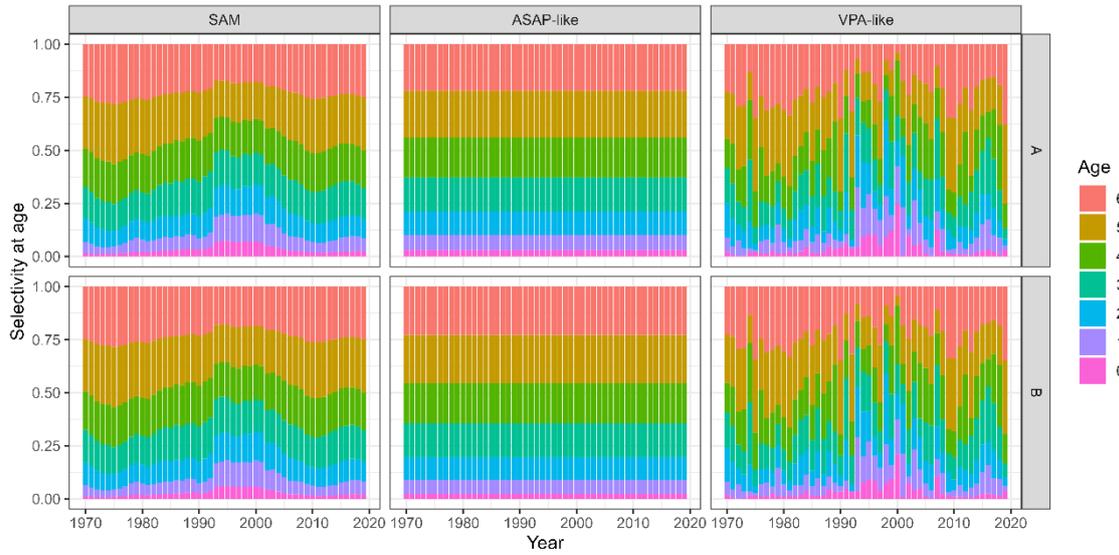
Figure 1: Temporal changes of selectivity at age in different model assumptions. Selectivity at age a in year y was obtained as $s_{a,y} = F_{a,y}/\sum_a F_{a,y}$.
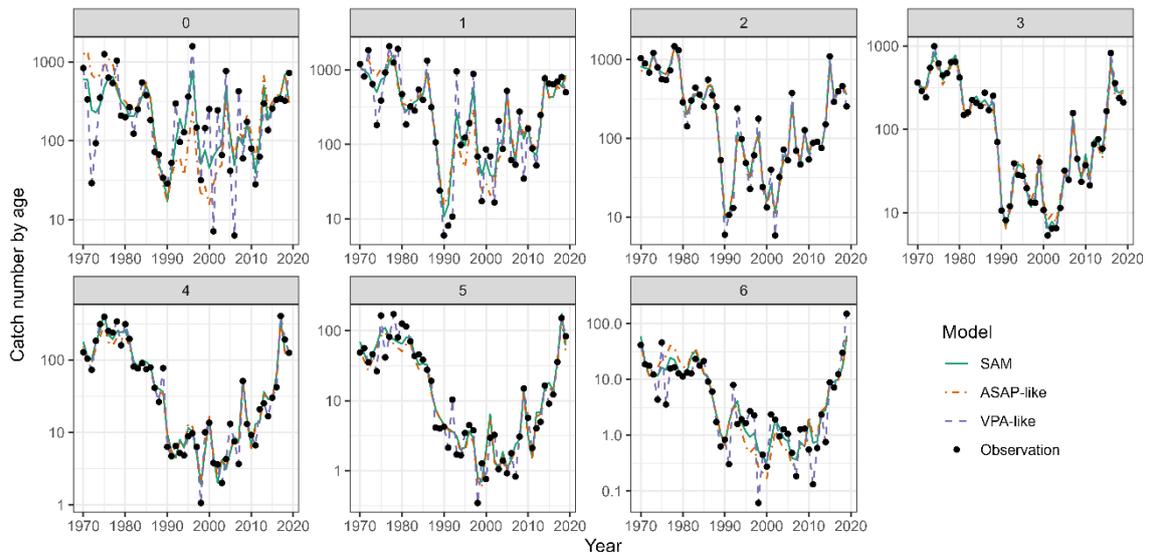

Figure 2: Estimates in catch numbers at age 0 to 6+ in different model assumptions. Note that y-axis is a logarithmic scale.
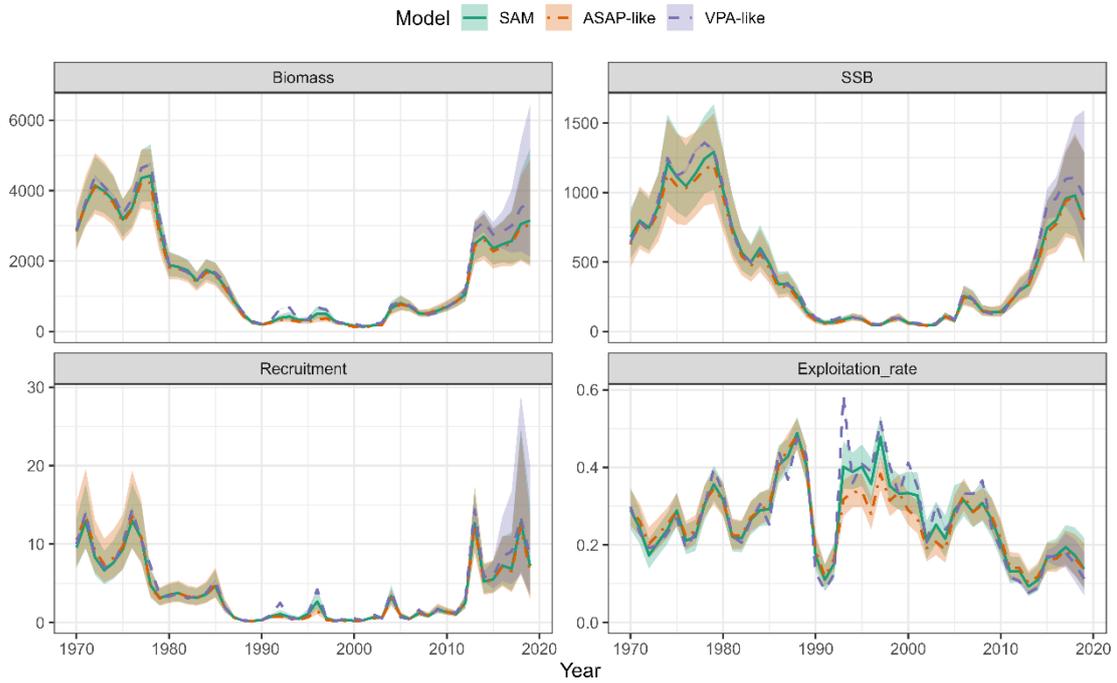
Figure 3: Estimates of biomass, SSB, the number of recruits, and exploitation rate in different model assumptions.
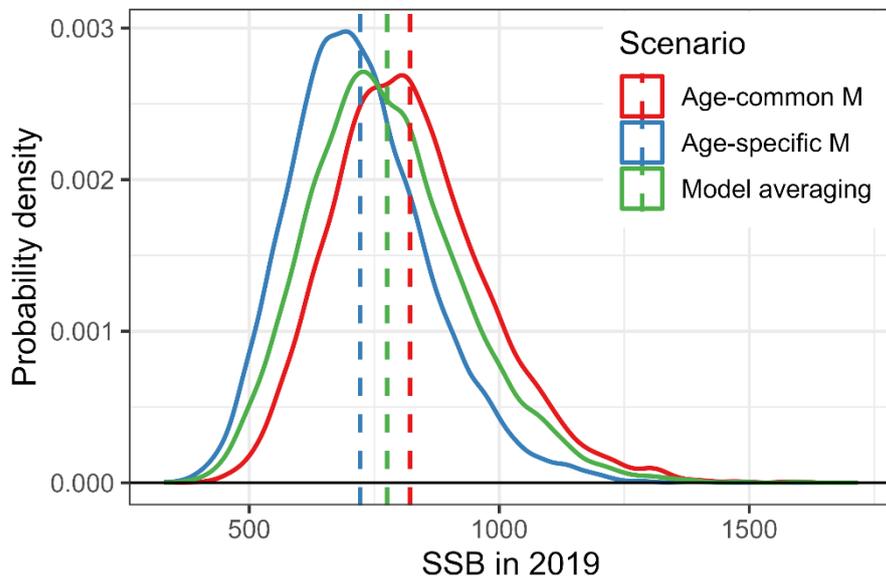

Figure 4: Probability distributions of SSB in the last year (2019) under scenarios of age-common M (A), age-specific M (B) and their weighted average by Akaike weights. The vertical dash lines represent mean values.