



# Evaluation of virgin recruitment profiling as a diagnostic for selectivity curve structure in integrated stock assessment models

Sheng-Ping Wang<sup>a,e,f,\*</sup>, Mark N. Maunder<sup>b,e</sup>, Kevin R. Piner<sup>c</sup>,  
Alexandre Aires-da-Silva<sup>b</sup>, Hui-Hua Lee<sup>d</sup>

<sup>a</sup> Department of Environmental Biology and Fisheries Science, National Taiwan Ocean University, Keelung 202, Taiwan

<sup>b</sup> Inter-American Tropical Tuna Commission, La Jolla, CA 92037, United States

<sup>c</sup> National Oceanic and Atmospheric Administration-Fisheries, Southwest Fisheries Science Center, La Jolla, CA 92037, United States

<sup>d</sup> Joint Institute for Marine and Atmospheric Research, University of Hawaii, Honolulu, HI 96822, United States

<sup>e</sup> Center for the Advancement of Population Assessment Methodology, Scripps Institution of Oceanography, La Jolla, CA 92093, United States

<sup>f</sup> Center of Excellence for the Oceans, National Taiwan Ocean University, Keelung 202, Taiwan

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## ABSTRACT

Virgin recruitment ( $R_0$ ), the equilibrium recruitment in the absence of fishing, is an often used parameter in fisheries stock assessment for scaling population size. We describe and evaluate the use of the  $R_0$  likelihood component profile to diagnose selectivity misspecification, using simulation analysis for bigeye tuna in the eastern Pacific Ocean. The profile is evaluated under two types of selectivity misspecification: (1) misspecified shape and (2) misspecified temporal variation. The results indicate that length-composition data can provide substantial information on  $R_0$  estimation when the model is correctly specified, but can substantially bias estimates of absolute abundance when selectivity is misspecified. Although contradictory profiles for length-composition and abundance index data result from selectivity misspecification, they may not be useful in determining which survey or fishery selectivity is misspecified. The  $R_0$  profile selectivity diagnostic is based on the influence of composition data on absolute abundance. However, perhaps a more problematic and difficult to detect issue is the impact of length-composition data on biomass trends. The age-structured production model diagnostic could be applied to identify bias in both absolute biomass and biomass trend caused by age- or length-composition data in the presence of model misspecification.

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## 1. Introduction

Contemporary stock assessment methods integrate multiple data types in a single analysis (Fournier and Archibald, 1982; Maunder and Punt, 2013; Punt et al., 2013). There are several general computer programs (e.g. Methot and Wetzel, 2013) that implement these methods. In addition to catch data, the two main types of data used in these models are indices of relative abundance and catch age/size composition. These have historically been used in independent analyses. For example, indices of relative abundance have been used to fit surplus production models (Schaefer, 1954; Pella and Tomlinson, 1969), and catch-at-age data have been used in Virtual Population Analysis (VPA) (Fry, 1949) or cohort analysis (Pope, 1972). Catch-at-age data have also been used in catch-curve analyses (i.e. linear regression of log abundance on age)

to estimate total mortality rates and thus fishing mortality if good estimates of natural mortality are available. Relative abundance and composition data provide information on absolute abundance. The decrease in an index of relative abundance caused by a known level of catch provides information on absolute abundance. The decline in the logarithm of the proportion of catch-at-age with age (the catch curve) provides information on fishing mortality (natural mortality assumed known), and when combined with catch data provides information on abundance.

However, both data types require information or assumptions (either explicit or implicit) about population (e.g. growth, natural mortality, and the stock-recruitment relationship) and fisheries (e.g. selectivity) processes. Surplus production models simplify the population dynamics into a single production function that aggregates fishery and biological processes and relies on strong modeling assumptions. Catch curve analysis used to estimate mortality rates generally assumes that recruitment and fishing mortality are in equilibrium, and that selectivity is constant for the ages used in the analysis. There may be information about these processes in data external to the stock assessment model (e.g. growth estimates from age-length data obtained from hard parts or from tag-recapture

\* Corresponding author at: Department of Environmental Biology and Fisheries Science, National Taiwan Ocean University, Keelung 202, Taiwan.  
Tel.: +886 2 24636834; fax: +886 2 24636834.

E-mail address: [wsp@mail.ntou.edu.tw](mailto:wsp@mail.ntou.edu.tw) (S.-P. Wang).

studies) or information used in the model (e.g. information on natural mortality from catch-at-age data; see Lee et al., 2011). Integrated analyses allow simultaneous extraction of information from both indices of abundance and catch-at-age data, with the advantage that assumptions are relaxed through the estimation of parameters based on information from ancillary data external to the assessment or explicitly stated (Maunder and Punt, 2013). Integrated analysis relaxes these assumptions by estimating recruitment, fishing mortality, and selectivity when fitting to the catch-at-age data.

A major issue in the application of contemporary integrated analyses is the influence of different types of data (i.e. catch composition, survey, etc.) on estimates of absolute abundance and population trends (Francis, 2011). Based on the logic of catch curve-analysis, catch composition data should provide information on abundance. However, the information provided by the data is highly sensitive to selectivity curves, particularly when these are assumed to be asymptotic. For example, fishing mortality must be very high if fewer old fish than expected are caught given natural mortality. The issue is even more complicated when using length-composition data, since the estimates will be sensitive to the assumed or estimated length of old individuals. Therefore, misspecification of selectivity can bias stock assessment results. The influence of age- or size-composition data on abundance estimates has led to recommendations to de-emphasize age- or size-composition data in stock assessments and, instead, emphasize indices of abundance (Francis, 2011).

Theoretically, it is possible to use statistical approaches to determine the weight assigned to each data set (McAllister and Ianelli, 1997; Maunder and Starr, 2003; Deriso et al., 2007; Maunder, 2011), but these are based on the model being correctly specified. Unfortunately, this is rarely the case and the misspecification can lead to bias, particularly for composition data. Therefore, alternative methods should be used to weight the different data sets and determine model misspecification.

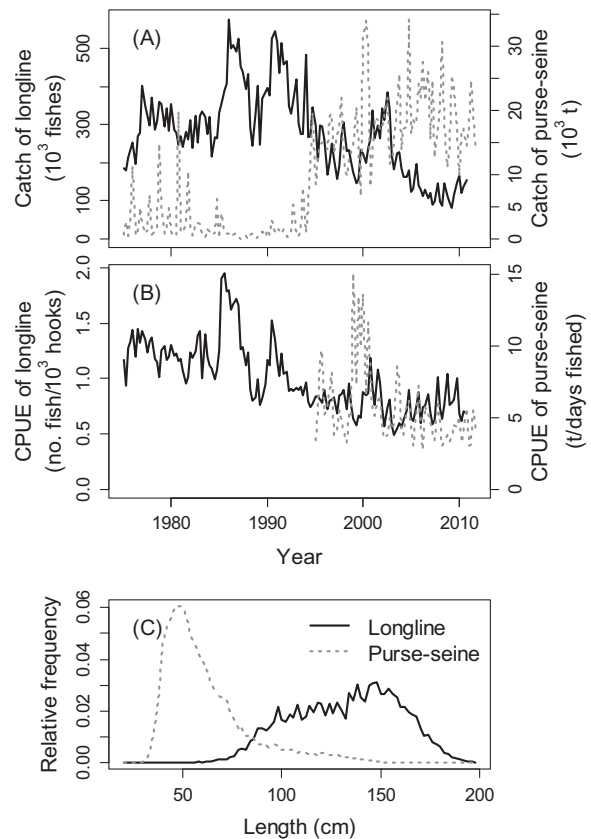
Lee et al. (2014) proposed profiling across a set of levels of a scaling parameter to evaluate the relative contribution of data components and model structure to the estimation of population scale (also see Francis, 2011). Virgin recruitment ( $R_0$ ) or biomass ( $B_0$ ) is the scaling parameter in most contemporary stock assessments. In Lee et al. (2014) approach, profiles of negative log-likelihood of each data component are created and the model is restructured or data down weighted until the change in negative log-likelihood across a reasonable range of virgin recruitment for composition data is low compared to a reliable index of relative abundance. They suggested adding model processes or re-evaluating data weighting to emphasize the data considered most appropriate to provide information on population scale.

This study extends Lee et al. (2014) to include the diagnosis of selectivity pattern misspecification. The  $R_0$  profile is used to explore the contribution of data components for a population exploited under known selectivity patterns when selectivity is either correctly or incorrectly specified in the assessment model. The simulation analysis is based roughly on bigeye tuna (*Thunnus obesus*) in the eastern Pacific Ocean (EPO) and is used to evaluate the  $R_0$  profile diagnostic under two types of selectivity misspecification: (a) asymptotic selectivity when selectivity is dome-shaped and (b) time-invariant selectivity when this is not the case.

## 2. Materials and methods

The most recent assessment of bigeye tuna was carried out using Stock Synthesis (SS) (Methot and Wetzel, 2013; details of the application can be found in Aires-da-Silva and Maunder, 2012).

The definitions of the fisheries in the assessment are based on data collection areas and similarities in catch and length



**Fig. 1.** The data series of catch, CPUE, and length-frequency of bigeye tuna caught by longline (solid line) and purse-seine (dashed line) fisheries in the eastern Pacific Ocean. Length-frequency data are aggregated across years in lower panel to present overall patterns for different fisheries.

frequency of catch. Fishery definitions take into account several factors, including gear type (purse-seine, pole-and-line, and longline), purse-seine set type (fish associated with floating objects, fish in unassociated schools, and fish associated with dolphins), time period, the IATTC length-frequency sampling area or latitude, and whether the catch is reported as numbers or weight (Aires-da-Silva and Maunder, 2012). However, the fisheries definition is simplified here into two categories: longline and purse-seine fisheries to reduce the computational demands of the simulation analysis.

### 2.1. Model structure

A simplified version of the stock assessment model of Aires-da-Silva and Maunder (2012) was used in the simulation analysis as both the simulator and estimator. The model is implemented in SS (version 3.24f) and the parametric bootstrap feature of SS was used to generate the simulated data. The application included two fisheries from 1975 to 2011, and used a quarterly time step. Selectivity for the longline fishery was assumed to be logistic and length-based, while that for the purse-seine fishery was assumed to be a dome-shaped (double normal) and length-based. The data used included catch, catch per unit of effort (CPUE) and length-composition (Fig. 1). The CPUE of the longline fishery has a declining trend before early 2000s, but is relatively flat thereafter. The model is fit to an index of abundance based on longline CPUE and to length-composition data for both fisheries.

Growth, variation in length-at-age, natural mortality, and the steepness of the Beverton–Holt stock-recruitment relationship

were all assumed to be known exactly.  $R_0$ , quarterly recruitment deviates, initial fishing mortality, initial age-structure deviates, and the parameters of the selectivity curves were estimated. The SS option that uses fishing mortality by fishery and year (quarter is treated as a year in this SS application) as parameters was used because a pre-specified catch series could cause the population to crash.

The  $R_0$  likelihood profile was developed by first fitting the model to obtain the maximum likelihood estimate (MLE) of all parameters, including  $R_0$  and then fitting the model with  $R_0$  fixed at a range of values based on  $-10\%$  to  $10\%$  of the MLE of  $R_0$ . The likelihood profiles across  $R_0$  can be obtained for each data component (catch data (“Catch”), indices of abundance (“Survey”) and length-frequency data for each of the two fisheries (“Lfreq.PS” for purse seine and “Lfreq.LL” for longline)) and the recruitment residual penalty (“R\_pen”). The lowest negative log-likelihood for each data component (component MLE) is then subtracted from each negative log-likelihood profile value for the data component so that the gradients are comparable. The lowest value of the negative log-likelihood for each component is referred to as the MLE for that component, but this is not technically correct, as the MLE is technically based on the total likelihood.

## 2.2. Simulation models

Two cases are used to explore the influence of selectivity on  $R_0$  estimation. For examining the misspecification of the selectivity curve for a specific fishery (Case A), the “true” model was based on the assumption that selectivity is logistic and double normal for the longline and purse-seine fisheries, respectively, while the “misspecified” model was based on the assumption that selectivity is logistic for both fisheries. For examining the misspecification of time-varied selectivity for a specific fishery (Case B), the “true” model was the same as for Case A except two time blocks are used for the selectivity of the longline fishery (1970–1992 and 1993–2011), while the “misspecified” model was the same as the “true” model except there are no selectivity time blocks.

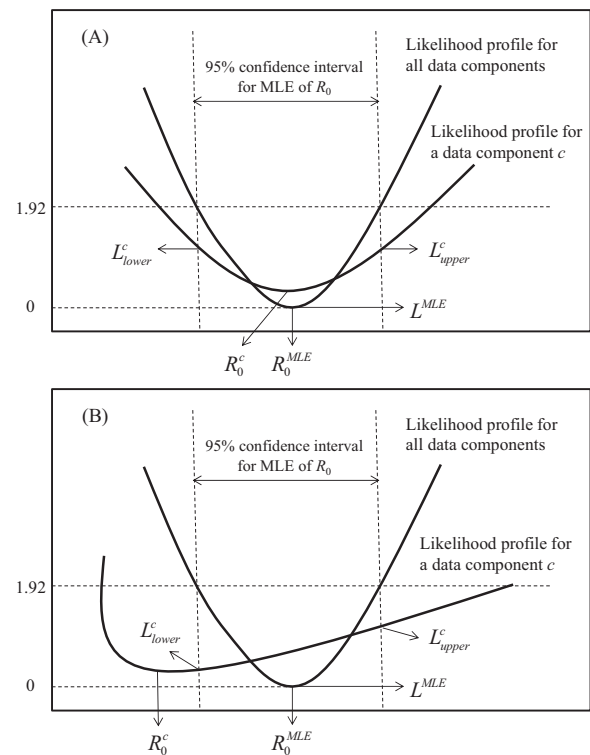
Due to time constraints, the results of only 10 simulation runs were evaluated in this study.

## 2.3. $R_0$ component likelihood profile statistic

The negative log-likelihood profile of a data component should decline to an obvious minimum value from at least one side if that component makes a substantial contribution to the estimation of scale (given the structural assumption of the model). A statistic ( $\varphi$ ) was developed based on the MLE of  $R_0$  ( $R_0^{MLE}$ ) and the estimate of  $R_0$  corresponding to the minimum value of a negative log-likelihood for data component  $c$  ( $R_0^c$ ) to explore the impact of each data set and the recruitment penalty on the estimation of  $R_0$ :

$$\varphi = \begin{cases} \max[(L_{lower}^c - L^{MLE}), (L_{upper}^c - L^{MLE})], & \text{if } R_0^c \text{ is located within the 95\% confidence interval for } R_0^{MLE} \\ |L_{lower}^c - L_{upper}^c|, & \text{otherwise} \end{cases}$$

where  $L_{lower}^c$  and  $L_{upper}^c$  are respectively the negative logarithms of the likelihood for data component  $c$  corresponding to the lower and upper boundaries of the 95% confidence interval of the MLE for  $R_0$  based on all the data (total likelihood), and  $L^{MLE}$  is the negative logarithm of the likelihood for data component corresponding to  $R_0^{MLE}$ . A low value for  $\varphi$  for a data or penalty component indicates that it has a relatively small contribution to the estimation of  $R_0$  (Fig. 2).



**Fig. 2.** Calculation of the  $R_0$  component likelihood profile statistic when the minimum component negative log-likelihood for  $R_0$  is obtained within (A) and outside of (B) the 95% confidence interval of the MLE.

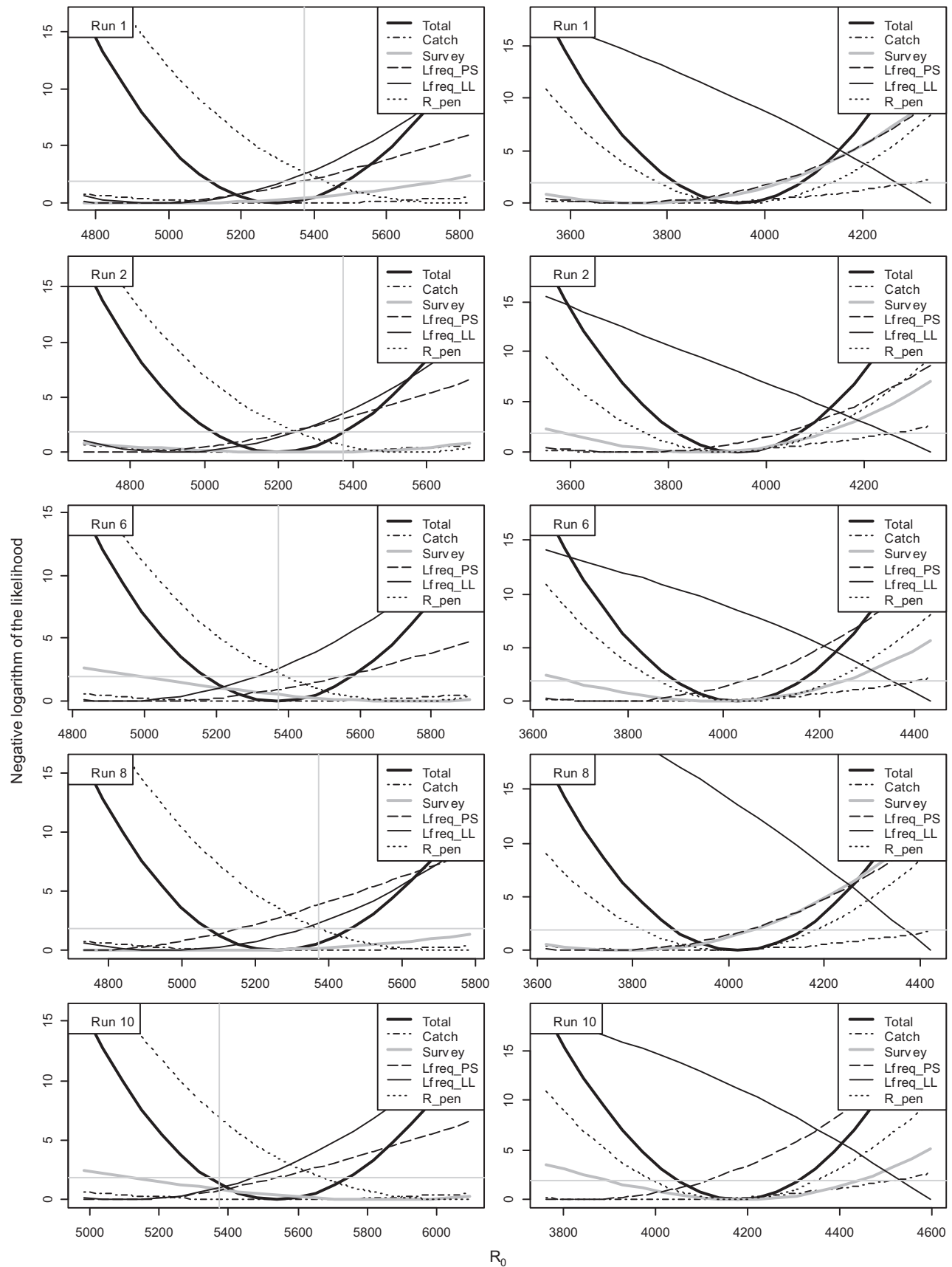
## 3. Results

### 3.1. Misspecified assumption about the shape of selectivity

The profiles of  $R_0$  based on the total likelihood and the component likelihoods for each data set are shown for five representative simulations in Fig. 3. The gradients of the likelihood profiles for the length-frequency data for longline and purse seine and for the penalty on the recruitment deviates are greater than for the likelihood profiles based on other data when the assumptions regarding selectivity are correct (left panels of Fig. 3). Therefore, the length-frequency data are far more informative than the abundance index on the estimation of  $R_0$ . The values of  $R_0$  supported by the length-frequency data are lower than those supported by the total likelihood and the penalty for the recruitment deviates. The estimate of  $R_0$  is determined by the balance between the fits to the length-frequency data and the penalty for the recruitment deviates.

The length-frequency data for the purse-seine fishery and the penalty for the recruitment deviates are still the most informative

components for the estimation of  $R_0$  when the selectivity pattern for the purse-seine fishery is misspecified (right panels of Fig. 3). However, the  $R_0$  values supported by the length-frequency data for the purse-seine fishery are generally lower than those supported by the penalty on the recruitment deviates and the total likelihood. The information on  $R_0$  from all data sources, except the longline length-composition data, supports lower  $R_0$  values than the correctly-specified model. In addition, the MLE of  $R_0$  based on the total likelihood is much lower when selectivity is misspecified.



**Fig. 3.** Likelihood profiles for  $R_0$  based on all data and on various data components for Case A (misspecification of the selectivity curve). Left and right panels respective indicate when selectivity is correctly specified and when it is misspecified. Vertical gray lines indicate the true value of  $R_0$  and horizontal gray lines the 95% confidence interval for  $R_0$ .

**Table 1**

$R_0$  component likelihood profile statistics based on various data components for Case A (misspecification of the selectivity curve).

Simulation	Catch	Survey	Lfreq_PS	Lfreq_LL	R_pen
<i>True</i>					
1	0.11	0.73	2.34	3.75	6.94
2	0.12	0.17	2.56	3.39	6.05
3	0.11	1.09	0.77	4.93	7.20
4	0.09	0.21	1.06	1.56	3.36
5	0.11	0.44	1.28	2.48	4.41
6	0.09	1.06	1.79	4.28	5.20
7	0.11	0.24	2.13	3.08	5.66
8	0.09	0.34	3.30	2.94	6.77
9	0.10	0.95	3.27	3.73	6.23
10	0.08	0.95	2.66	4.51	6.40
Mean	0.10	0.62	2.12	3.46	5.82
<i>Misspecified</i>					
1	0.61	2.82	2.88	5.97	1.38
2	0.76	1.23	2.58	5.20	1.47
3	0.41	4.19	2.99	6.73	1.65
4	0.44	1.79	4.99	10.38	2.66
5	0.70	1.16	5.11	9.99	2.85
6	0.59	0.88	3.86	4.75	1.41
7	0.65	0.62	6.31	7.58	1.43
8	0.35	3.74	3.53	8.45	1.51
9	0.65	0.60	4.99	7.41	2.26
10	0.77	0.63	5.35	6.39	1.51
Mean	0.59	1.77	4.26	7.29	1.81

The  $R_0$  component likelihood profile statistic also shows that the longline and purse-seine length-frequency data and the penalty on the recruitment deviates provide a much greater contribution to the estimation of  $R_0$  than do the catch and abundance-index data (Table 1). The influence of the penalty on the recruitment deviates on the estimation of  $R_0$  decreases when the selectivity pattern for the purse-seine fishery is misspecified, and the catch and abundance-index data components become more influential, while the influence of the length-composition data increases as well. In addition, a greater fraction of the MLEs of  $R_0$  based on the likelihood profile of the abundance index lie within the confidence interval for  $R_0$  based on total likelihood than those based on the likelihood profiles of other data components (Table 3).

### 3.2. Misspecified assumption about time-varied selectivity

The correctly-specified models for Cases A and B led to similar  $R_0$  profiles for each data component (left panels of Fig. 3 and Fig. 4). However, the true values of  $R_0$  differ between the two cases. The gradient of the  $R_0$  profile based on the abundance index changes from preferring lower values of  $R_0$  compared with the other data components to higher values when selectivity is incorrectly assumed to be time-invariant (right panels of Fig. 4).

The  $R_0$  component likelihood profile statistic also shows that the length-frequency data for the longline and purse-seine fisheries and the penalty for the recruitment deviates provides a much greater contribution to the estimation of  $R_0$  than the catch and abundance index data for the correctly specified model (Table 2). The abundance-index data component becomes more influential when selectivity is incorrectly assumed to be time-invariant, while the influence of the length composition data increases as well. However, all of the MLEs of  $R_0$  based on the likelihood profile of the abundance index lie outside the confidence interval of  $R_0$  based on total likelihood (Table 3).

## 4. Discussion

The  $R_0$  profile diagnostic was not able to correctly identify selectivity pattern misspecification. The index of abundance should provide reasonable information on the estimation of population

**Table 2**

$R_0$  component likelihood profile statistics based on various data components for Case B (misspecification of time-varied selectivity).

Simulation	Catch	Survey	Lfreq_PS	Lfreq_LL	R_pen
<i>True</i>					
1	0.12	0.33	2.42	3.27	6.18
2	0.13	0.30	1.97	3.16	5.47
3	0.10	0.25	1.86	5.38	7.67
4	0.12	0.35	2.47	1.50	4.87
5	0.09	1.27	1.08	4.49	4.44
6	0.14	0.90	2.63	3.25	5.12
7	0.12	0.61	2.98	4.22	7.91
8	0.11	0.17	2.51	3.60	6.18
9	0.11	0.28	2.70	2.58	5.23
10	0.10	0.14	1.80	6.06	8.08
Mean	0.11	0.46	2.24	3.75	6.12
<i>Misspecified</i>					
1	0.20	1.08	3.15	5.04	7.11
2	0.20	1.32	3.22	4.88	6.71
3	0.17	1.32	2.86	6.86	8.43
4	0.18	1.42	3.69	3.73	6.01
5	0.15	2.27	2.34	5.60	5.70
6	0.26	2.84	4.13	5.47	6.70
7	0.20	1.45	4.01	6.06	8.59
8	0.19	2.05	3.78	5.27	7.02
9	0.22	2.05	3.51	4.71	6.17
10	0.18	1.33	2.84	7.44	8.95
Mean	0.19	1.71	3.35	5.51	7.14

scale because there is a long history of using the effects of different catch levels on population abundance for estimating both the productivity and scale of a population (Schaefer, 1954; Pella and Tomlinson, 1969; Lee et al., 2014). In contrast, the index of abundance in our example provided almost no information on population scale. This lack of information was a due to a lack of contrast in the index, and because bigeye tuna are relatively productive, with large variation in recruitment, implying a weak production function or that historical fishing has yet to define the relationship. Therefore, the estimate of population scale was defined almost completely by the length-composition data and model structure in the correctly-specified models. It is unclear whether the profile diagnostic would have performed better had the production relationship been stronger or the index of abundance more informative.

It is a relatively common for indices of abundance to be uninformative, so the diagnostic as proposed by Lee et al. (2014) to reduce profile gradients to composition data and emphasize abundance index information may not be feasible and could potentially result in degrading model performance. Downweighting the composition data could, as in the bigeye tuna example, lead to substantial uncertainty in the estimates of absolute abundance. Naturally, the information from the composition data will also bias estimates of abundance if selectivity is misspecified.

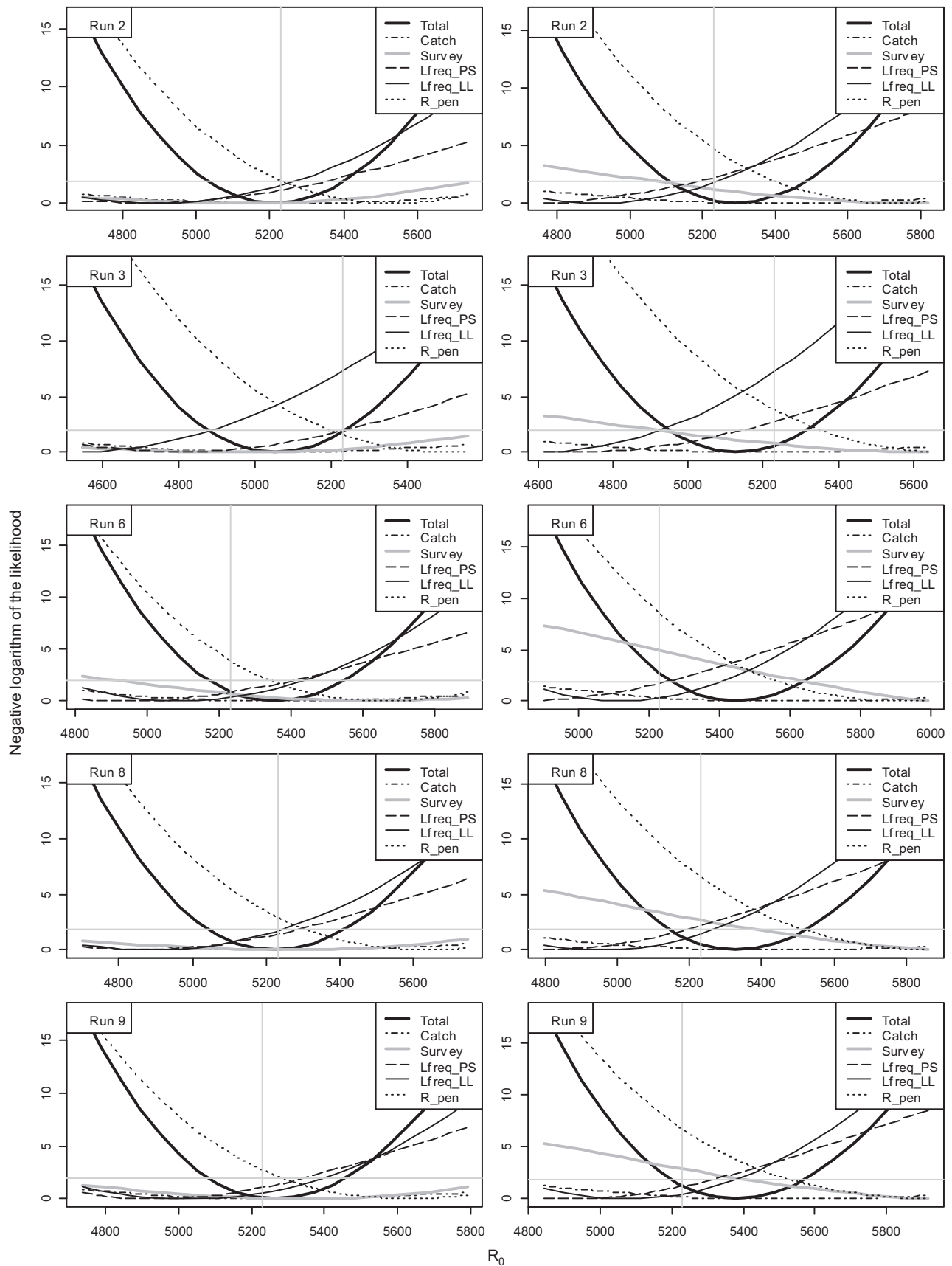
Although the likelihood profile was not able to identify the fishery or survey with misspecified selectivity, there is some indication that it may provide information on the general shape of the

**Table 3**

Number of simulations in which the estimate of  $R_0$  corresponding to the minimum value of the likelihood profiles based on various data components occurs with the 95% confidence interval of the MLE of  $R_0$  for Case A (misspecification of the selectivity curve) and Case B (misspecification of time-varied selectivity).

Source	Case A		Case B	
	True	Misspecified	True	Misspecified
Catch	10	3	10	10
Survey	2	7	7	0
Lfreq_PS	1	0	0	0
Lfreq_LL	1	0	1	0
R_pen	0	10	0	0





**Fig. 4.** Likelihood profiles for  $R_0$  based on all data and on various data components for Case B (misspecification of time-varied selectivity). Left and right panels respective indicate when selectivity is correctly specified and when it time-varying selectivity is ignored. Vertical gray lines indicate the true value of  $R_0$  and horizontal gray lines the 95% confidence interval for  $R_0$ .

selection pattern. When there was contradictory information on population scale, the data component fitting better at smaller population scale was consistent with a dome-shaped selectivity pattern and that fitting better at higher population scale an asymptotic selectivity pattern. This last point is important, because it identifies an action that may be taken to correct a problem identified by the diagnostic.

Prioritization of data sources is intended to insure that population dynamics are influenced by the most reliable data. It can be achieved by increasing the weights assigned to data sources or by reducing the number of parameters used to fit that data component (Lee et al., 2014). The  $R_0$  profile diagnostic was originally proposed as way to evaluate the prioritization of different data. Prioritization of an abundance index (Francis, 2011) using the  $R_0$  profiling method appears to be appropriate for estimating the population scale when a strong production relationship is apparent in the data (Lee et al., 2014). Within SS, a simple means to evaluate the strength of the underlying production relationship is to fit an age-structured production model. This involves first fitting the full integrated model to all data and estimating all model parameters. The model is then fit fixing the selectivity parameters at those estimated in the full integrated model, leaving out the composition data, and setting the recruitment deviates to zero. It can be concluded that the data support a well-defined production function if the removal of catch from approximately the right ages can recreate the trends in the index of abundance. Conversely, a strong production function is not apparent in the data (i.e. there are trends in recruitment or the index of abundance is biased) if removal of catch in the simplified model does not approximate the trends in the index of abundance. In the latter case, diagnostics such as  $R_0$  likelihood profiling should be interpreted with this understanding.

An alternative  $R_0$  likelihood profile could be constructed by simulating data without error and fitting the model when the effective sample sizes and standard deviations are based on those from the actual data, and comparing the  $R_0$  component likelihood profile with that from the original data. This model is correctly specified and there is no sampling error, so the  $R_0$  component likelihood profile shows what information should be in the data, and any difference from the original indicates model misspecification. The annual recruitment deviates penalty needs special treatment (e.g. fixed at zero or generated randomly) in the simulation because the estimator assumes that they are random and any trend in the deviates may misrepresent the profile. However, this diagnostic has not been used extensively or evaluated and more research is needed before it can be recommended.

The use of  $R_0$  profiling undoubtedly is informative about the influence of data and model structure on estimates of population scale. However, the subject of prioritization of different data types remains an unsettled question. For those situations where a trusted survey with good contrast is available, the prioritization of a data source may be justified and the  $R_0$  profile is one potential tool to

evaluate the process of prioritization. Prioritization of a single data source using the  $R_0$  profile may be more questionable when the survey is not informative or where a production relationship is not apparent. Each modeling situation is likely to be different and a range of tools will be needed to construct a reasonable recreation of the population dynamics.

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## References

- Aires-da-Silva, A., Maunder, M.N., 2012. Status of bigeye tuna in the eastern Pacific Ocean in 2011 and outlook for the future. *Inter-Am. Trop. Tuna. Comm. Stock Ass. Rep.* 13, 18–29.
- Deriso, R.B., Maunder, M.N., Skalski, J.R., 2007. Variance estimation in integrated assessment models and its importance for hypothesis testing. *Can. J. Fish. Aquat. Sci.* 64, 187–197.
- Fournier, D., Archibald, C.P., 1982. A general theory for analyzing catch at age data. *Can. J. Fish. Aquat. Sci.* 39, 1195–1207.
- Francis, R.I.C.C., 2011. Data weighting in statistical fisheries stock assessment models. *Can. J. Fish. Aquat. Sci.* 68, 1124–1138.
- Fry, F.E., 1949. Statistics of a lake trout fishery. *Biometrics* 5, 27–67.
- Lee, H.H., Maunder, M.N., Piner, K.R., Methot, R.D., 2011. Estimating natural mortality within a fisheries stock assessment model: an evaluation using simulation analysis based on twelve stock assessments. *Fish. Res.* 109, 89–94.
- Lee, H.H., Piner, K.R., Methot, R.D., Maunder, M.N., 2014. Use of likelihood profiling over a global scaling parameter to structure the population dynamics model: An example using blue marlin in the Pacific Ocean. *Fish. Res.* 158, 138–146.
- Maunder, M.N., 2011. Review and evaluation of likelihood functions for composition data in stock-assessment models: estimating the effective sample size. *Fish. Res.* 109, 311–319.
- Maunder, M.N., Punt, A.E., 2013. A review of integrated analysis in fisheries stock assessment. *Fish. Res.* 142, 61–74.
- Maunder, M.N., Starr, P.J., 2003. Fitting fisheries models to standardised CPUE abundance indices. *Fish. Res.* 63, 43–50.
- McAllister, M.K., Ianelli, J.N., 1997. Bayesian stock assessment using catch-at-age data and the sampling-importance resampling algorithm. *Can. J. Fish. Aquat. Sci.* 54, 284–300.
- Methot, R.D., Wetzal, C.R., 2013. Stock synthesis: a biological and statistical framework for fish stock assessment and fishery management. *Fish. Res.* 142, 86–99.
- Pella, J.J., Tomlinson, P.K., 1969. A generalized stock production model. *Inter-Am. Trop. Tuna. Comm. Bull.* 13, 421–458.
- Pope, J.G., 1972. An investigation of the accuracy of virtual population analysis using cohort analysis. *Res. Bull. ICNAF* 9, 65–74.
- Punt, A.E., Haug, T.C., Maunder, M.N., 2013. Review of integrated size-structured models for stock assessment of hard-to-age crustacean and mollusc species. *ICES J. Mar. Sci.* 70, 16–33.
- Schaefer, M.B., 1954. Some aspects of the dynamics of populations important to the management of commercial marine fisheries. *Inter-Am. Trop. Tuna. Comm. Bull.* 1, 25–56.