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1	Accounting for variable recruitment and fishing mortality in length-based stock
2	assessments for data-limited fisheries
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17 Abstract

In fisheries with limited capacity for monitoring, it is often easier to collect length 18 19 measurements from fishery catch than quantify total catch. Conventional stock assessment tools 20 that rely on length measurements without total catch do not directly account for variable fishing mortality and recruitment over time. However, this equilibrium assumption is likely violated in 21 almost every fishery, degrading estimation performance. We developed an extension of length-22 23 only approaches to account for time-varying recruitment and fishing mortality. This Length-24 based Integrated Mixed Effects (LIME) method at a minimum requires a single year of length data and basic biological information, but can fit to multiple years of length data, catch, and an 25 26 abundance index if available. We use simulation testing to demonstrate that LIME can estimate how much fishing has reduced spawning output in the most recent year across a variety of 27 28 scenarios for recruitment and fishing mortality. LIME improves data-limited fisheries stock 29 assessments by its flexibility to incorporate additional years or types of data if available, and 30 obviates the need for equilibrium assumptions.

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32 Introduction

33 Many fisheries worldwide lack the quality and quantity of data used in classical stock 34 assessments, but must deal with limited information to make management decisions (Quinn et al. 35 2016). Stock assessments can provide a quantitative starting point for developing management 36 strategies and monitoring the impacts of management. For example, the Magnuson-Stevens 37 Fisheries Conservation and Management Act mandates fisheries managers in the United States to 38 set catch limits based on the 'best available science', involving advice from stock assessment to inform those limits (Darcy and Matlock 1999; Methot et al. 2014). The Marine Stewardship 39 40 Council (MSC) similarly requires fisheries seeking certification to go through a stock assessment 41 process to determine their sustainability (Gulbrandsen 2009). In the case of small-scale fisheries 42 in developing nations, it is possible to manage a fishery using only harvest control rules to meet 43 management objectives, without formal stock assessment estimating status relative to reference points (Mahon 1997). However, beyond their use to evaluate management strategies for fishery 44 45 resources (Carruthers et al. 2014), modeling tools can help with community engagement in the 46 scientific process, such as conflict resolution (Butler et al. 2006) and integration of local 47 knowledge to support cooperation between fishermen and scientists (Neis 1992; Azzurro et al. 48 2011).

Many stocks worldwide remain unassessed, e.g., the U.N. Food and Agriculture
Organization global fishery statistics database includes 19,624 unique combinations of country
and taxa (FAO 2016), while the RAM Legacy stock assessment database only includes 1,268
stock assessments (Ricard et al. 2012). The regions of the world with the fewest stock
assessments relative to the number of stocks perform worse across fishery management attributes
(Melnychuk et al. 2017), indicating the presence of fishery monitoring and assessment may have

some relation with successful management. In the following, we define "data-limited" as any stock with uninformative data (no contrast to provide information on rates of change) or lacking data types typically used in statistical estimates of stock status (e.g. fishery-independent surveys, proportion-at-ages) (Costello et al. 2012; Dowling et al. 2016). Data-limited stock assessment methods are in great demand in both developed and developing nations due to the ubiquity of data-limited fisheries, and the need for science-based management decisions (Wetzel and Punt 2011; Chrysafi and Kuparinen 2016; Dowling et al. 2015).

Length-based assessment methods are a vital component of the data-limited stock 62 63 assessment toolbox because it is much easier to obtain reliable length measurements of a portion 64 of the fishery catch than to measure total catch or record effort data for many small-scale or nontarget species (Harley et al. 2001; Nadon et al. 2015; Prince et al. 2015b; Kokkalis et al. 2015). 65 66 Similarly, age information and a fishery-independent survey that are representative of total abundance are prohibitively expensive or impossible to collect for most fisheries in the world. 67 68 Prominent length-based methods for estimating reference points in data-limited fisheries include 69 length-based spawning potential ratio (LB-SPR; Hordyk et al. 2015) and mean-length mortality 70 estimation methods (Nadon et al. 2015). LB-SPR uses length-composition data and assumptions 71 about biological parameters to make a rapid assessment of stock status relative to unfished levels 72 assuming equilibrium conditions (Hordyk et al. 2015; Prince et al. 2015b). While LB-SPR can 73 use multiple years of length data, status determination is based on one year of data at a time (i.e. 74 estimates of status over multiple years are based on that year's length composition alone). Mean-75 length mortality estimators (e.g., Gedamke and Hoenig 2006), first developed by Beverton and 76 Holt (1957), assume fishing mortality directly influences mean length of the catch, and have 77 been used for assessments in the U.S. South Atlantic, Pacific islands, and Caribbean (Ehrhardt

and Ault 1992; Ault et al. 2005, 2008; Gedamke and Hoenig 2006; Nadon et al. 2015). As
measures of stock status, these length-based methods derive the spawning potential ratio (SPR)
reference point, defined as the proportion of unfished reproductive potential at a given level of
fishing pressure (Goodyear 1993).

82 Length-based assessment methods estimating stock status assume that recruitment and 83 fishing mortality arise from deterministic relationships or have not changed over a period 84 significant for management and the life history of the species (termed "equilibrium 85 assumptions"). Equilibrium assumptions are often violated (Gedamke and Hoenig 2006), as 86 recruitment is quite variable for most species and fishing mortality changes with markets and 87 other socioeconomic factors in the fishing community (Thorson et al. 2013, 2014a). Stochastic 88 ocean conditions and productivity regime shifts may cause recruitment to vary erratically, 89 gradually, or periodically at any given time (Vert-pre et al. 2013; Thorson et al. 2014b; 90 Szuwalski et al. 2015). However, the violation of the equilibrium assumption may be difficult to 91 detect. For example, the equilibrium assumption may appear valid when the mean length is 92 constant over time (Gedamke and Hoenig 2006; Nadon et al. 2015). If recruitment is then 93 constant over time, increasing fishing mortality will lead to decreasing mean length as the larger 94 individuals are harvested and only smaller individuals remain in the population. However, 95 constant fishing mortality and a recruitment pulse would also lead to a decrease in mean length, with more young individuals entering the population. Given both variable fishing mortality and 96 97 recruitment processes occurring on the same population as well as errors when measuring mean 98 length, a mean-length time series may appear constant when time-varying population processes 99 are instead cancelling each other out.

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100 As an alternative to the equilibrium assumptions, a mixed-effects model can be used to 101 deal with important demographic changes by estimating random variation in recruitment, fishing 102 mortality, or other biological processes, as well as the magnitude (variance) of random variation 103 in each process (de Valpine and Hastings 2002; Buckland et al. 2004; Schnute and Haigh 2007; 104 Thorson and Minto 2015). Mixed-effects models can directly account for variation arising from 105 natural processes or measurement processes separately, and therefore improve performance in 106 nonlinear fisheries models (de Valpine and Hastings 2002; Ono et al. 2012; Thorson et al. 2015b). A main criticism of length-based methods with equilibrium assumptions is that with a 107 single year of length-composition data and general understanding of biological parameters, it is 108 109 impossible to determine whether a larger proportion of small fish in the catch is caused by strong 110 cohort in recent years, or by the removal of larger fish from the system. Accounting for random 111 variation in recruitment, fishing mortality and observation error arising from the process of 112 sampling fish lengths from the population, helps to tease apart each of these processes and better 113 identify the true state of the fish population.

114 The aim of this study is to introduce a new length-based, integrated, mixed-effects (LIME) model and demonstrate its statistical performance when estimating reference points 115 116 assuming only length composition and basic biological information are available. This method 117 builds upon the catch-curve stock reduction analysis (CCSRA) model (Thorson and Cope 2014), 118 which includes an estimate of mortality from the age composition and at least one year of total 119 fishery catch to estimate MSY-based reference points without assuming information about final 120 biomass relative to unfished biomass (as generally used in stock reduction analysis). As an 121 extension, LIME uses samples of length in place of the more resource-intensive samples of age, 122 and can estimate the SPR reference point if catch data are unavailable. To demonstrate the LIME model, we used simulation testing to (i) demonstrate that LIME is unbiased across several lifehistory types and patterns of fishing mortality and recruitment variability and able to include more years of length measurements and catch and/or abundance index data, (ii) examine the sensitivity of the model to sample size of length measurements and error in input parameters, and (iii) compare LIME against LB-SPR to assess performance under various violations of model assumptions, including the timing of sampling within the year and modeling monthly time steps.

130 Methods

129

LIME is an age-structured population dynamics model with the ability to (1) account for 131 variable fishing mortality and recruitment when only length data are available, and (2) to treat 132 133 multiple years and types of data in an integrated manner to improve estimates of fishing 134 mortality changes over time. The minimum inputs for the LIME assessment method are data on 135 the length composition of the catch from a single year as well as assumed life history information, including the length-at-age relationship, an assumed natural mortality rate, and 136 137 length at 50% maturity. LIME estimates annual fishing mortality rates, lengths at 50% and 95% 138 selectivity to the fishing gear, and the Dirichlet-multinomial parameter θ as fixed effects. The effective sample size of length data is linearly related to the input sample size with intercept 139 $(1+\theta)^{-1}$ and slope $\theta(1+\theta)^{-1}$ (Thorson et al. 2017). LIME can be differentiated from other age-140 141 structured models (e.g. Stock Synthesis) in that annual recruitments are treated as random 142 effects, where mean and standard deviation of a distribution for recruitment are additionally 143 estimated as fixed effects. Another key difference is that LIME does not require catch data: if no 144 information on the scale of population size is available, recruitment will be estimated relative to 145 average levels for an unfished population. As measures of stock status, we derived the SPR

reference point to compare results with LB-SPR. We also derived the $F_{30\%}$ and $F_{40\%}$ reference points (the fishing mortality rates that would result in SPR of 30% and 40%, respectively; Clark 2002). We derived MSY by finding the fishing mortality rate that results in the highest yield per recruit. When total catch data were available (thereby providing information on scale of the population size), LIME would estimate equilibrium recruitment, which would scale the MSY based on a per-recruit equation to a scale appropriate for the population size.

152 We developed an operating model to simulate true populations and generate data under a 153 variety of fishing, recruitment, and life history scenarios. We then used this operating model to explore the estimation performance of LIME for different scenarios regarding recruitment, 154 155 fishing mortality, data-availability, and life history (Figure 1). We conducted all simulation 156 modeling using the open-source statistical software R (R Core Team 2016), and all estimation in 157 the R package *Template Model Builder* (TMB; Kristensen et al. 2015) as implemented in our R 158 package LIME (https://github.com/merrillrudd/LIME, doi: 10.5281/zenodo.834404, version 159 1.0.0).

160

161 Operating model

We tested LIME for three different life-history types chosen to reflect the types of taxa for which length-based assessments are commonly demanded (Figure 2). These life-history types were: (a) a short-lived fish, mimicking rabbitfish (*Siganus sutor*, L_{∞} =36.2 cm, k=0.87, M=1.49, L_m^{50} =20.2 cm, maximum age =4, Hicks and McClanahan 2012), (b) a medium-lived fish, mimicking spotted rose snapper (*Lutjanus guttatus*, L_{∞} =64.6 cm, k=0.21, M=0.43, L_m^{50} =34.0 cm, maximum age=15, Bystrom 2015), and (c) a longer-lived fish, mimicking red grouper (*Epinephelus morio*, L_{∞} =90.0 cm, k=0.13, M=0.18, L_m^{50} =50.0 cm, maximum age=26, Heemstra Page 9 of 56

and Randall 1993) (Table 1). Each simulated population began with biomass at a fraction of
unfished biomass, drawn from a uniform distribution between 0.05 and 0.95.

171 For each life history scenario, we tested LIME performance under three scenarios of 172 fishing mortality and recruitment variability (Figure 3). The first is the "equilibrium scenario", 173 which matches the non-variable fishing mortality and recruitment assumptions of LB-SPR. The 174 equilibrium scenario involved fishing mortality and recruitment constant over a 20-year period, 175 with a standard deviation for fishing mortality and recruitment set to a negligible 0.01. The 176 second scenario, the "two-way base scenario", involved a linear change from the fishing 177 mortality that would result in the randomly chosen initial depletion to the rate associated with 20% SPR ($F_{20\%}$) over the first seven years of the 20-year time series. This change could be 178 179 positive or negative depending on the F associated with randomly selected value for initial depletion and $F_{20\%}$. Over the next seven years of the time series, F was constant at $F_{20\%}$, then the 180 181 fishing rate decreased linearly down to half of $F_{20\%}$ for the last six years of the time series. $F_{20\%}$ 182 was calculated deterministically based on the biological information and selectivity associated 183 with each life-history type. Thus, this value would not vary between different scenarios of 184 variability within a life-history type. The fishing mortality time series in the "two-way base 185 scenario" varied between simulation iterations in a) the randomly chosen initial depletion and b) 186 lognormally distributed deviations around this two-way trip (following the same equation for 187 lognormal recruitment deviates in Table 3, eq. 1 except using the standard deviation for fishing 188 mortality, σ_F , equal to 0.2). While we calculated $F_{20\%}$ for the medium-lived and longer-lived life-189 history types, we fixed $F_{20\%}$ to 3.0 for the short-lived life-history type. Based on the assumption 190 of instantaneous annual fishing mortality, $F_{20\%}$ for the short-lived fish was calculated to be much 191 greater than could be supported even by very high fishing capacity. Recruitment was variable

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192 and autocorrelated over a 20-year period (Table 3, eq. 2). This scenario included a standard 193 deviation of recruitment residuals σ_R equal to 0.737 and a first-order autoregressive coefficient 194 equal to 0.426, the mean of the predictive distribution from a meta-analysis of recruitment 195 variability in global fish orders (Thorson et al. 2014b). A third scenario, the "one-way base 196 scenario", involved the same recruitment variability and autocorrelation as the "two-way" 197 scenario, but with fishing mortality changing linearly from the rate that would result in the 198 randomly chosen initial depletion to $F_{20\%}$ over the 20-year period. Thus, this change could be 199 positive or negative depending on the F associated with the randomly chosen initial depletion 200 relative to $F_{20\%}$ for the life-history type. This combination of scenarios tests the ability to track 201 how the population processes are changing over time with variability in the system.

202 In the operating model, we assumed the natural mortality rate was constant, known, and 203 independent of size or age. We modeled individual growth using a von Bertalanffy growth 204 function (Table 2, eq. 1; Figure 2). We assumed maturity at length m_i was based on a one-205 parameter logistic function (Table 2, eq. 2; Figure 2). We converted maturity at length to 206 maturity at age using a normal distribution with standard deviation a function of the coefficient 207 of variation of the age-length curve (Table 2, eq. 3). Selectivity-at-length follows a two-208 parameter logistic model (Table 2, eq. 4; Figure 2), with estimated parameter length at 50% 209 selectivity and a second parameter δ representing the difference between length at 95% and 50% 210 selectivity. We modeled weight at age as an allometric function of individual length at age 211 (Table 2, eq. 5). We calculated annual total biomass as a function of the abundance and weight-212 at-age (Table 2, eq. 6). Spawning biomass was a function of the total annual biomass and the 213 proportion mature at age (Table 2, eq. 7). These processes contributed to an underlying age-214 structured model (Table 2, eq. 8). Parameter definitions and input values are listed in Table 1.

215 216 Data generation 217 We generated length data by simulating underlying age-structured dynamics and then 218 sampling length composition from the vulnerable population instantaneously at the beginning of 219 each year. First we calculated the probability of being in a length bin for individuals of each age 220 (Table 3, eq. 3). We then calculated the probability of harvest in each length bin each year as the 221 proportion of the abundance-at-age vulnerable to the fishing gear each year multiplied by the 222 probability of being in a length bin given age (Table 3, eq. 4). We used a multinomial probability 223 distribution to generate the length frequency of samples of the catch in each length bin over time 224 (Table 3, eq. 5). 225 We assumed a sample size *n* of 200 individuals were measured annually, and that this 226 was the "true" sample size of the length data. We compared the base case of 200 length 227 measurements annually to model performance under sample sizes of 1,000, 500, 100, 50, and 20.

We used the large sample size of 1,000 to confirm the model is unbiased and precise across data availability scenarios under ideal circumstances, and then tested the alternate, lower sample sizes to assess performance under more realistic sample sizes.

We tested seven different scenarios of data availability. Two scenarios included only length data, assuming one or ten years of length data were available (the "one length composition", "ten length compositions" scenarios). Data from these two scenarios were used to demonstrate the value of additional years of length data for each life-history type. We also explored five scenarios of additional data availability to demonstrate the integrated nature of LIME. The data availability scenarios included (i) a "data-rich" scenario with 20 years of total catch, 20 years of an abundance index, and 20 years of length data, used as proof-of-concept that Can. J. Fish. Aguat. Sci. Downloaded from www.nrcresearchpress.com by University of Washington on 09/05/17 For personal use only. This Just-IN manuscript is the accepted manuscript prior to copy editing and page composition. It may differ from the final official version of record.

LIME works when a high amount of informative data exists; (ii) "index plus 10" with 20 years of 238 239 an abundance index and 10 years of length data; (iii) "index plus 1" with 20 years of an 240 abundance index and 1 year of length data; (iv) "catch plus 10" with 20 years of total catch data 241 and 10 years of length data; and (v) "catch plus 1" with 20 years of total catch data and 1 year of 242 length data. We assume that catch and abundance indices are lognormally distributed with a logstandard deviation of 0.2 (Table 1). The "catch plus 1" scenario is essentially a stock-reduction 243 244 analysis while replacing the assumed information regarding final biomass (as used in stockreduction analysis) with a length-based catch-curve to estimate fishing mortality in the final year, 245 which is analogous to Thorson and Cope (2014), except using length-composition samples. We 246 247 calculated the expected catch-at-age, using the Baranov catch equation (Table 3, eq. 6), summing 248 to obtain total annual catch (Table 3, eq. 7), based on the true fishing mortality time series and 249 selectivity specified in the operating model. The generated standardized abundance index I_t was 250 proportional to spawning biomass (Table 3, eq. 8).

251 When not otherwise stated, we generated data on an annual time step, which assumes 252 length-composition data are collected instantaneously at the beginning of the year. In fisheries 253 where only length data and biological information are available (i.e. no catch or abundance 254 index) it is possible length data would be available on less than an annual time step. We tested 255 scenarios where length data were collected on a monthly time step, then either pooled into an 256 annual time step or kept on a monthly time step. The monthly data collection scenario is more 257 representative of fisheries occurring year-round, with no specific season. Furthermore, length 258 data on a monthly time step would be more representative of short-lived fish growth, to account 259 for fish observed between the midpoints of each age class.

261 Estimation model

262 The structure of LIME follows the structure of the operating model using equations 1-8 in 263 Table 2 and equations 3-4, and 6-8 in Table 3 to derive the predicted catch, index, and length 264 composition. LIME requires at least one year of length data, but is flexible to include annual 265 fishery catch and/or an abundance index. During our simulation testing, we assumed that LIME 266 had the correct values for the von Bertalanffy length-at-age relationship, including asymptotic 267 length (L_{∞}) , growth coefficient (k), and age at length=0 (t₀), length-weight parameters, natural 268 mortality (M), and the one-parameter logistic maturity-at-length schedule. Future studies can 269 obtain these values from local studies, FishBase (Froese 1990), or global meta-analyses of fish 270 life-history parameters (Thorson et al. In press). We tested LIME performance under violations 271 of these assumptions in sensitivity analyses. We also fixed the values for catch and abundance 272 index observation error and coefficient of variation in the process error for the age-length curve. 273 For all data availability scenarios, the model estimates as fixed effects the annual fishing 274 mortality, lengths at 50% and 95% selectivity, the recruitment standard deviation, and the 275 Dirichlet-multinomial parameter θ related to the effective sample size of length measurements in 276 each year. In scenarios when catch data are unavailable, there is no information on the scale of 277 the population. In these scenarios, we fixed mean recruitment to a relative value of 1.0 so that the 278 model does not estimate the scale of the population but only the annual deviations in recruitment. 279 and estimates of relative reference points (e.g. SPR) can be derived but reference points based on 280 the scale of the population (e.g. MSY) are not meaningful. By contrast, when total catch data are 281 available for at least one year, we can estimate mean recruitment and derive spawning biomass. 282 When an index of abundance was available, we estimated the catchability coefficient for that

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14

index as an additional parameter *q*. A list of parameters estimated and fixed for each scenario is
presented in Table 1.

285 We treated annual recruitment as a random effect in LIME, where recruitment each year 286 is a function of an expected recruitment based on a Beverton-Holt stock recruitment relationship 287 (Table 4, eq. 1), and the estimated recruitment standard deviation (Table 4, eq. 2). For the simulation experiments in this paper, we fixed the steepness parameter h of the Beverton-Holt 288 289 stock-recruitment function at 1.0, meaning that expected recruitment is constant among years and 290 independent of the spawning stock biomass the previous year. It is possible to fix the steepness 291 parameter at a value less than 1.0, where the mean of the lognormal distribution is the predicted 292 number of recruits from the Beverton-Holt stock-recruitment relationship, as opposed to 1.0 or 293 the equilibrium unfished recruitment. We chose to test LIME with 1.0 for the mean of the 294 lognormal distribution to determine how well the model can estimate annual recruitment with all 295 variation from recruitment deviates. Unfished spawning biomass is calculated using the same 296 equation as fished spawning biomass (Table 2, eq. 7) but without the fishing mortality and 297 selectivity terms (Table 2, eq. 9). Unlike the operating model, we did not account for 298 autocorrelation in recruitment in the LIME estimation model.

We applied a random-walk penalty on annual estimates of fishing mortality, which shrinks the estimate of fishing mortality in year t + 1 towards its estimate in year t (Table 4, eq. 3). Drastic changes in fishing mortality between years are unlikely in the real world given costs of entering or leaving a fishery, but the random-walk process accommodates gradual changes in fishing mortality (Nielsen and Berg 2014). However, a fixed value of 0.2 for the standard deviation of the fishing mortality penalty does allow the model to estimate variability in fishing mortality if supported by the data (e.g. exit and entry from the fishery). We also placed a lognormal penalty on the standard deviation of recruitment deviations, σ_R . Based on the meta-analysis conducted by Thorson et al. (2014), the log of the mean was set to the log of 0.737, with a log standard deviation of 0.353 (Table 4, eq. 4). The prior aids in the convergence of the σ_R parameter estimation, preventing the estimate from going to an unlikely value. There is also an upper bound on σ_R at 2.0.

311 The joint log-likelihood of the observed data is the sum of the log-likelihoods of the 312 observed length data, log-probability of fishing mortality and recruitment variation, and the log-313 likelihood of the catch and abundance index, if available. We include bias-correction for recruitment deviations using the TMB bias-correction feature (Thorson and Kristensen 2016). 314 315 For scenarios that include abundance index and catch data, a lognormal probability distribution 316 was assumed to describe error in both data types (Table 4, eq. 7, eq. 8). The respective observation errors σ_l and σ_c are fixed *a priori* (not estimated as parameters). We assumed the 317 318 length data arose from a Dirichlet-multinomial probability distribution with estimated parameters 319 θ_c related to the effective sample size of length measurements each year. Many stock assessment 320 methods use a multinomial distribution to fit age or length data, but the effective sample size 321 must be calculated externally (Francis 2014). By contrast, the Dirichlet distribution can represent 322 variability in the proportions in each length bin, but the parameters do not correspond to the 323 easily interpretable effective sample size of length data for which model results are highly 324 sensitive. The Dirichlet-multinomial is an alternative to these two distributions, estimating an 325 additional parameter θ within the integrated model (Thorson et al. 2016). The effective sample 326 size is a nonlinear function of input sample size (Table 4, eq. 6; Thorson et al. 2016). As θ 327 approaches infinity, the effective sample size is equal to the observed sample size, and the 328 multinomial distribution is a special case of the Dirichlet-multinomial distribution.

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In model runs, we assessed that the model had converged if the final gradient for all parameters was less than 0.001. If the initial model run did not converge (resulting in NAs or a high final gradient), the model would be run up to ten additional times with starting values equal to the estimates from the non-converged model plus a random number drawn from a normal distribution with mean zero and standard deviation 0.2. For each combination of life-history type, data availability scenario, fishing mortality pattern, and recruitment dynamics, we obtained 100 iterations of generated data and ran the estimation model for each set.

336

337 Comparison to LB-SPR

338 We ran LB-SPR from the R package LBSPR (Hordyk et al. 2015) with one year (LBSPR 339 1) and ten years (LBSPR 10) of length data using the operating model described above. LB-SPR 340 requires as input the length data in each year and the ratio of natural mortality to the von 341 Bertalanffy growth coefficient (M/k), as well as inputs similar to those required for LIME: the von Bertalanffy asymptotic length parameter, coefficient of variation of the asymptotic length, 342 343 length at 50% and 95% maturity, length-weight parameters, and starting values for the length at 344 50% and 95% selectivity (Table 1). We assumed the coefficient of variation of the asymptotic 345 length was equivalent to the coefficient of variation of the entire age-length curve. For the base 346 runs, we used the true value for the length at 95% maturity and selectivity from the two-347 parameter logistic curves used in the operating model. LB-SPR uses these inputs to calculate the 348 abundance at relative age at equilibrium. LB-SPR estimates the ratio of fishing mortality to 349 natural mortality and the lengths at 50% and 95% selectivity to best fit the predicted and 350 observed length composition proportions, and derives SPR, outputting estimates for these four 351 values for each year with length data (Hordyk et al. 2015).

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We note that this simulation experiment is comparing performance of LIME and LB-SPR using an operating model that is more similar to LIME. To further compare the strengths and limitations of each method, we used the *LBSPR* package to simulate length data under the LB-SPR equilibrium, length-based structure, so that we could also test LIME and LB-SPR using an operating model that is more similar to LB-SPR.

A major issue in the comparison of models was the time step used. To test model 357 358 performance, we tested both the LIME and LB-SPR methods using the monthly data generation 359 feature in the operating model, where sampling is spread out over all twelve months instead of 360 collected instantaneously at one point. We then compared LIME and LB-SPR performance 361 pooling the monthly length data into an annual distribution and then running each model on an 362 annual time step. These additional simulation tests were designed to compare these two methods 363 under different data-generating models, with the goal of providing guidance for which methods 364 may be appropriate under a variety of real-world conditions.

365

366 Reference points

We calculated SPR (Table 2, eq. 10-12) as a biological reference point, used as a proxy for MSY when information on the scale of population size is not available, and for comparison with LB-SPR. A harvest strategy that targets a fishing mortality rate that is expected to result in 40% of unfished spawning output (termed "40% SPR"), is considered risk averse for many species (Clark 2002). Therefore, we calculated these values as examples of possible fishing mortality reference points that could be used to compare to other length-based assessment methods.

375 Sensitivity tests

Preliminary exploration suggested that LIME performed poorly for short-lived species when using an annual time step, therefore we explored LIME performance on a monthly time step. We generated monthly length data for the short-lived life-history type and ran LIME on a monthly time step by specifying the number of years as number of months, ages as fractions of a year, and dividing the input natural mortality rate *M* by twelve so that mortality and growth occurs in each month (Figure A1).

We also included sensitivity tests to LIME base models to understand biases associated with imperfect knowledge about species biology, fishery characteristics, and low sample sizes. We assessed the performance of LIME with (a) parameter misspecification of +/- 25% for each of the life history inputs (M, CV_L , L_{∞} , k, and L_m^{50}) and (b) sample sizes of length data of 20, 50, 100, 500, and 1,000 independent samples annually.

387

388 Model performance

389 To assess the ability of the model to accurately and precisely estimate quantities of management interest, we consider bias and precision (Table 4, eq. 9-10) between estimated and 390 391 true SPR in the last year of data across the 100 iterations of simulated data. We used median 392 relative error (MRE; Table 4, eq. 9) to quantify bias, and median absolute relative error (MARE; 393 Table 4, eq. 10) to quantify precision. To understand the ability of the model to accurately 394 capture uncertainty, we computed the "interval coverage", the proportion of iterations out of 100 395 where the true value of a population parameter in the terminal year is within the 50% confidence 396 intervals. A well-performing model would have close to nominal coverage (i.e., a 50% coverage

interval will contain the true value in 50% of simulation replicates). Coverage is presented toillustrate whether confidence intervals accurately capture model uncertainty.

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400 Results

LIME performance across life history, variability, and data scenarios

Based on the Monte Carlo simulations, LIME can estimate unbiased SPR when length 402 403 data are available and biological characteristics are correctly specified across various scenarios 404 of fishing mortality and recruitment patterns (Figure 4). When tested using the same model structure and assumptions in the operating model, LIME performed best for short-lived fish, with 405 406 increasing bias and decreasing precision for medium-lived fish, and a further deterioration for 407 longer-lived fish (Table 5). The bias in SPR in the terminal year was 0.002 for short-lived, -0.003 408 for medium-lived, and 0.016 for longer-lived fish across all data availability and population 409 variability scenarios with 200 length measurements annually. Additional scenarios illustrate 410 further LIME strengths and weaknesses (Table 5). With only one year of length data, LIME 411 estimated SPR with bias of -0.038 for the short-lived life history, -0.186 for medium-lived, and -412 0.152 for longer-lived across variability scenarios. Integrating ten years of length data improved 413 accuracy in the estimation of SPR in the terminal year on average for each life history type 414 (short-lived from -0.038 to -0.016; medium-lived from -0.186 to -0.048; longer-lived from -415 0.152 to 0.102). The only exception within variability scenarios was decreased accuracy with ten 416 years of length data for the longer-lived life-history type under the one-way variability scenario 417 (from -0.181 to 0.200). While ten years of length data increased precision of SPR estimates for 418 the short-lived life-history type over one year of length data (from 0.072 to 0.041), the additional

length data decreased precision on average for the medium- and longer-lived life-history types
(medium-lived from 0.334 to 0.391; longer-lived from 0.529 to 0.626; Table 5).

421 LIME provides the added advantage over other length-based assessment methods of 422 including a catch time series and abundance index, if available, which further increases accuracy 423 and precision under most cases. Across all scenarios, including an abundance index decreased 424 bias (from -0.047 to 0.020) compared to when only length data were available. An abundance 425 index particularly improved LIME performance for the short- and medium-lived life-history 426 types. Breaking down by life-history types, bias decreases with an abundance index included for 427 the short-lived life-history type (from -0.026 to 0.005) and medium-lived life-history type (from 428 -0.126 to 0.025), but increases for the longer-lived life-history type (from -0.049 to 0.072) on 429 average. Across all life-history types, including an abundance index increases precision (short-430 lived from 0.054 to 0.052; medium-lived from 0.346 to 0.190; longer-lived from 0.594 to 0.257).

431 Adding a catch time series to length data decreased bias minimally on average across all 432 scenarios (from -0.047 to 0.031). The improvement in accuracy is strongest under equilibrium 433 conditions (from -0.036 to -0.007). Given variable fishing mortality and recruitment, including 434 catch data with length composition increased bias (from -0.055 to 0.118). This was mainly due to 435 high bias in the "catch plus one" scenario for short-lived fish (Table 5, Figure 4). Excluding this 436 anomalous scenario, including a catch time series decreased bias for a population with variability 437 (from -0.055 to 0.047). The "catch plus ten" scenario removed the bias from the "catch plus one" 438 scenario for the short-lived life-history type under variability scenarios. However, the "catch plus 439 ten" scenario did not necessarily improve bias nor precision over the "catch plus one" scenario 440 for the medium- and longer-lived life-history types under variability scenarios (Table 5). This 441 indicates that it may be advisable to include a catch time series only when more than one year of

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length data are available for a short-lived life-history type, and consider the possibility of overestimating SPR when fishing mortality is changing over time for medium- and longer-lived lifehistory types when catch data are included.

LIME converged for 95% of iterations of generated data across life-history types, variability scenarios, data availability scenarios, and sample sizes of length data. LIME converged for 100% of iterations of generated data for the data-rich scenario (Figure 5). With only length data, LIME converged for 95% of iterations across scenarios. The LIME convergence rate was 92% including catch data and 94% including an abundance index. Nonconvergence was always due to a high final gradient in parameter estimation, as opposed to any parameter being estimated at the upper or lower bound.

452 The interval coverage for a 50% confidence interval of LIME was 61% across all 453 scenarios of life history, variability scenarios, data availability, and sample sizes of length data. 454 This indicates confidence interval estimates from LIME are generally informative about model 455 uncertainty, but may be wider (more conservative) on average. LIME estimated confidence 456 intervals that were too narrow or wide for individual life history, variation, and data availability 457 scenarios (Figure 5). The "catch plus one" scenario had the lowest coverage across life-history 458 and variability scenarios (42%), likely because this data availability scenario had the most bias, 459 and thus the true SPR would likely not fall within the confidence intervals at the expected rate. 460 For the short-lived life-history type, LIME interval coverage was only 43%. While the method is expected to be unbiased for this life-history type on average, the confidence intervals are often 461 462 too tight to include the true SPR within the 50% intervals at a rate of 50%. LIME estimated 463 wider confidence intervals for the medium-lived life-history type, with interval coverage 72%, and longer-lived life-history types, with an interval coverage of 67%. 464

466 LIME sensitivity to sample size, input parameters, and selectivity estimation

467 With one year of length data, LIME estimated SPR with greater precision with more 468 length measurements, but not necessarily with greater accuracy (Table 6). Across all life history 469 types, accuracy and precision improved greatly in the equilibrium scenario between 20 and 1,000 470 length measurements collected annually. The short-lived life-history type experienced the 471 strongest improvements in accuracy and precision (Table 6). This pattern was strongest with a 472 population in equilibrium, but was generally maintained for scenarios of variability as well. Accuracy generally reached a plateau with greater than 100 samples of length measurements for 473 474 the short-lived life-history type. Alternatively, accuracy and precision improved for the medium-475 and longer-lived life-history types with at least 500 samples of length measurements for a 476 population at equilibrium. With variability, there were no clear patterns in accuracy improvement 477 for the medium- and longer-lived life-history types with increasing sample size of length 478 measurements. This indicates accuracy in SPR estimates is more likely to be improved with 479 more data types than increasing sample size, particularly for medium- and longer-lived life 480 histories (Table 5, Table 6).

481 Like all age or length-based methods, LIME performance is sensitive to the correct 482 specification of life history information (Figure 6). When all biological parameters were 483 correctly specified, LIME estimated unbiased SPR on average with ten years of length data (bias 484 = -0.017). When L_{∞} was misspecified as 25% greater than the truth, bias increased (to -0.554), 485 meaning that on average LIME estimated SPR to be lower than the truth. In this case, we would 486 expect to see larger fish in the observed data. If those fish are not present in the length data, 487 length-based models attribute the difference to a higher fishing mortality, and thus a lower SPR

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488 than the truth. On the other hand, when L_{∞} was misspecified as 25% lower than the truth, LIME 489 estimated SPR higher than the truth on average (bias = 0.761). Assuming k was 25% lower than 490 the truth, LIME estimated SPR higher than the truth on average (bias = 0.478). When k was 491 assumed to be 25% higher than the truth, LIME estimated SPR lower than the truth on average, 492 but to a lower degree than the other biases due to life history misspecification (bias = -0.146). 493 However, this lack of severe bias is simply due some model runs resulting in estimates much 494 greater than or lower than the truth, while none are unbiased. When M was fixed 25% higher 495 than the truth, LIME estimated SPR to be higher than the truth (bias = 0.285). A fish that is faster to die can generally sustain a higher fishing pressure, and the interpretation of the higher SPR is 496 497 that the population has more of its potential spawning biomass than it truly does. When M was 498 assumed to be 25% lower than the truth, LIME estimated SPR lower than the truth (bias = -499 0.352).

500 Fixing length at 50% maturity at a value 25% higher than the truth resulted in negative 501 bias in SPR (bias = -0.383). In this case the LIME model attributes a lower proportion of the 502 population as being mature, leading the estimated SPR to be lower than the truth. The opposite is 503 true when length at maturity was 25% lower than the truth; estimates of SPR were biased higher 504 than the truth (bias = 0.152). LIME was relatively insensitive to misspecification of CV_L for the 505 age-length curve, but a higher CV_L resulted in a relatively lower estimate of SPR on average 506 (bias = -0.044), and a higher CV_L resulted in a relatively higher estimate of SPR on average (bias 507 = 0.047).

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509 *Comparing LIME and LB-SPR*

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510 Simulation testing demonstrated that the LIME and LB-SPR methods perform well under 511 different conditions. LB-SPR is biased when the equilibrium conditions are violated (Table 5). 512 However, testing of LB-SPR against the age-structured LIME operating model with 513 instantaneous sampling at the beginning of each year resulted in poor performance for the short-514 lived life-history type under equilibrium conditions (Table 5, Table 7, Figure 7). We verified that LB-SPR performs well across life-history types when tested using an operating model that 515 516 matches its model assumptions. LIME, on the other hand, over-estimated SPR for the short-lived 517 life history type with one year of length data and, similar to the performance under its own operating model, had low precision for the medium- and longer-lived life history types with ten 518 519 years of length data (Table 7). When length data were collected monthly and pooled into an 520 annual length composition, LB-SPR performance improved over the annual model for the short-521 lived life history type, but LIME over-estimated SPR (Table 7, Figure 7). Running LIME on a 522 monthly time step with monthly length data decreased bias compared to running on an annual 523 time step (from 0.468 to -0.040 with ten years of monthly length data and 0.484 to 0.034 with 524 one year of monthly length data; Table 7).

526 Discussion

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This study demonstrates that the length-based integrated mixed-effects (LIME) method can be a valuable tool for fisheries stock assessment when at least one year of length data and basic biological information are available for the species (Table 8). LIME estimates reference points more accurately than LB-SPR under many common scenarios. The LIME assessment method has several characteristics that make it particularly useful in situations where an abundance index and/or catch data cannot be collected reliably, as data collection programs 533 improve to include more data types, and when recruitment and fishing mortality are believed to 534 be changing more rapidly than would match the equilibrium assumptions required for existing 535 methods with the same data requirements.

536 The *length-based* aspect of the model setup allows the analyst to fit to length, rather than 537 age, composition data from the catch. The current toolbox of data-limited stock assessment 538 methods includes length-only methods with equilibrium assumptions (Hordyk et al. 2015; Nadon 539 et al. 2015; Kokkalis et al. 2015), ad hoc assumptions about changes in mortality (Gedamke and 540 Hoenig 2006), or age-structured models that cannot fit to length-composition data (Martell and Froese 2013; Thorson and Cope 2014). MULTIFAN (Fournier et al. 1990) and Stock Synthesis 541 (Methot and Wetzel 2013) can use length instead of age data to gain information on cohort 542 543 strength and total mortality, but require a catch time series to estimate stock status. The 544 flexibility of LIME to fit to length composition, as opposed to age-composition, is more realistic 545 for capacity-limited fisheries. LIME can be used in conjunction with other length-based methods 546 as a diagnostic tool to see if variations in recruitment or fishing mortality are being predicted by 547 the model based on the length data, and how the results of the multiple assessment types would 548 vary in light of those possibly violated assumptions.

The *integrated* nature of LIME is useful in situations where monitoring programs are continuing to be developed over time, incorporating more years of length data or other data types in the same assessment framework. LB-SPR is a quick way of conducting an assessment with only one year of length data, but as monitoring programs improve, the method must be applied independently over multiple years (Prince et al. 2015a, 2015b). There are also many catch-based methods that assume a catch time series is available, but they are not thoroughly tested in fitting to length, rather than age, composition data (Sabater and Kleiber 2013; Martell and Froese 2013;

Thorson and Cope 2014). LIME allows for these data to be included into the same assessment framework, rather than requiring a switch between assessment models as monitoring programs develop and new data types become available (Maunder and Punt 2013). Also, few existing models can incorporate an abundance index and length data without catch data. LIME can be used in this scenario to estimate a relative SPR reference point with no measure of scale. This scenario is common for small-scale fisheries, bycatch species, or other fisheries where trends in abundance are available but total harvest is not.

563 Finally, the *mixed effects* aspect of LIME extends length-based methods by estimating changes in recruitment and fishing mortality over time. Estimating random effects has been 564 565 integrated into existing stock assessment models, such as Stock Synthesis (Thorson et al. 2015a) 566 and the state-space assessment model (SAM) framework (Nielsen and Berg 2014). Many 567 assessments for European stocks now use SAM to separate process and observation errors as an 568 objective method of weighting data in age-structured models (Berg et al. 2014). Computing the 569 marginal likelihood for mixed-effects models was previously too computationally challenging, 570 hindering wide application of mixed-effects models. Now, programs such as TMB can do these 571 computations much faster than previous options (Nielsen and Berg 2014). To illustrate the 572 benefits of LIME, a vignette is available on the repository site that walks the user through a 573 simple example, with tips for model interpretation and convergence. An app using the R package 574 shiny (Chang et al. 2017) is also available on the repository site 575 (https://github.com/merrillrudd/LIME shiny) that allows analysts to run the model in a graphical 576 user interface.

577 Simulation testing in this study demonstrated the best LIME performance with only 578 length data for the short-lived life-history type, with comparatively lower performance for Page 27 of 56

579 medium- and longer-lived fish. With only length data, LIME performs well for the shorter-lived 580 fish likely because the model is tracking cohorts through the length data to estimate recruitment 581 deviations. This is likely difficult for the longer-lived life histories due to variation in the age-582 length relationship (especially for older fish), and because each individual cohort represents a 583 small proportion of total abundance (hence requiring more samples to track each individual 584 cohort). The increasing uncertainty in a longer-lived fish's age with increasing length blurs the 585 cohorts as they age, making it difficult to track recruitment events without a much longer time 586 series of length data. With ten years of length data, accuracy in estimating SPR increases but 587 precision decreases for the medium- and longer-lived life-history types, providing support for the 588 increased ability to track recruitment events but propagating uncertainty in the age-length curve 589 for older individuals. With short-lived fish that only live to four years old, each length more 590 clearly matches up with an age group. Regardless of fish growth, one year of length data holds 591 information on an entire generation for a short-lived fish. Even if recruitment is occurring 592 monthly or seasonally and not annually, a ten-year time series of length data can inform variation 593 in cohort strength across several generations of the short-lived fish.

594 By testing LIME and LB-SPR using multiple operating models, we identified scenarios 595 in which each method excels. LB-SPR performs better than LIME for estimating SPR if the 596 population is at equilibrium and only length data are available. If the population is not in 597 equilibrium, then LIME performs better. If the data are collected continuously throughout the 598 year (e.g. monthly), LIME is expected to estimate higher SPR than the truth for short-lived fish. 599 In this case, analysts should run LIME using monthly (or shorter) time steps to account for fish 600 growth during the year. This bias does not occur for medium- or longer-lived fish, where the 601 growth during the year is less rapid. On the other hand, LB-SPR likely under-estimates SPR for

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short-lived fish if data are collected instantaneously, but is unbiased if data are collectedcontinuously.

604 An important question for management is often how many years or how much data are 605 enough, particularly for fisheries where funding for monitoring is limited. The simulation testing 606 in this study demonstrated that we can get accurate but highly uncertain estimates of SPR, 607 fishing mortality, and recruitment from only one year of length data on average (Figure 8). As 608 expected, collecting more data (ten years of length data instead of one) resulted in greater 609 accuracy and precision in LIME estimates of SPR (Figure 4, Table 5). When using only length 610 data, LIME performance is best with at least 500 independent length measurements per year for 611 medium- and longer-lived life histories, but is expected to perform well with 100 or more length 612 measurements per year for short-lived life-history types (Table 6). However, including an 613 abundance index or catch time series improves bias and precision to a greater extent than 614 collecting more independent length measurements (Table 5, Table 6). Managers must determine 615 how much uncertainty they are comfortable with to set monitoring goals. Collecting more years 616 of length data, taking more independent length measurements during each year of length data 617 collection, conducting surveys, and monitoring catch data hold varying levels of information 618 used to estimate variable fishing mortality and recruitment. Their costs and benefits should be 619 weighed to help managers prioritize data collection.

Including an abundance index or catch time series improves LIME performance in most scenarios. Catch data provides useful information on the scale of the population, which is not possible with length data alone. The abundance index provides useful information to help inform the trajectory of the population from which the length data arose. The abundance index could be more informative on the state of the population than length data alone, as long as the abundance Page 29 of 56

index is proportional to abundance and any significant changes in fishing mortality and
recruitment occurred during the surveyed time series. Our simulation study shows that the biases
associated with including a time series with one year of length data are often overcome with
more years of length data. The exception is for the longer-lived life history type, for which LIME
performs worse when including an abundance index with ten years of length composition data
than if the abundance index was excluded.

631 However, the simulation study also identified some potential issues with data conflict 632 when an abundance index or catch time series are included with length data. Data conflict can be 633 diagnostic of poor data quality, such as catch misreporting, indices from spatial areas with 634 ontogenetic differences, or length data not representative of the fishery. Data quality is an 635 equally important issue as limited data types and should be considered in LIME applications. In 636 the case of this study, however, poor data quality was not the culprit behind any data conflict 637 because we used the true catch data, abundance index from a single area, and representative 638 length data to test LIME. To avoid data conflict, Maunder and Piner (2015) recommend 639 modeling process error explicitly, most commonly via time-varying recruitment, as a better 640 alternative to down-weighting or eliminating data conflicts. LIME takes this approach, but data 641 conflict may still occur, particularly because recruitment deviations are treated as a random 642 effect even if this is not the correct model process for which the data hold conflicting information 643 (Maunder and Piner 2015). Other options to avoid data conflict are to estimate the variance 644 parameter for observed data outside of the stock assessment model (Lee et al. 2014; Maunder 645 and Piner 2015). Alternatively, an analyst could identify whether data conflict is occurring in the 646 LIME model by likelihood profiling individual data components (Ichinokawa et al. 2014) or

retrospective analysis, which quantifies the impact of additional years of data on the stockassessment output (Hurtado-Ferro et al. 2014).

649 Like all length-based assessment methods, fixing the biological parameters at their true 650 values is an important first step for estimating unbiased reference points. LB-SPR circumvents 651 this strong assumption by using Beverton-Holt life history invariants to estimate the expected 652 age or length structure, as opposed to assuming known values of natural mortality and growth 653 (Prince et al. 2015a). Sensitivity tests in this study demonstrating the impact of misspecifying 654 biological parameters provide support for local studies of species growth rates for stocks 655 assessed using LIME. Analysts should be aware of how SPR is expected to be biased given their 656 assumptions on fixed values for input parameters or model structure. A next step for LIME is to 657 use Bayesian priors on biological parameters to more thoroughly represent the uncertainty in 658 population parameter estimates relevant to management (e.g., from FishLife; Thorson et al. In 659 press). Sensitivity tests and likelihood profiles should be conducted on different levels of dome-660 shaped selectivity to understand how SPR is expected to be biased if the model structure is 661 misspecified.

Length-based stock assessments are good starting-points for making management 662 663 decisions with limited data and monitoring capacity. The shrinkage of poorly estimated 664 parameters towards an estimated distribution (as implemented within mixed effects models) has 665 been shown to increase accuracy and precision in stock assessments (Thorson et al. 2013; 666 Nielsen and Berg 2014), but high uncertainty in estimates of stock status will always result if 667 there are only one or two years of length data. Any stock assessment deals with data limitation 668 and uncertainty, and it is vital to appropriately represent and communicate this uncertainty to 669 managers.

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670 Ideally, conclusions on stock status should be drawn using an ensemble of assessment 671 models with varying structure and assumptions (Stewart and Martell 2015; Anderson et al. 672 2017). In the data-limited context, existing models represent a relatively small range of 673 alternative model assumptions. We have shown that LIME presents a way to represent both 674 process and observation uncertainty. LIME can complement other length-based (Hordyk et al. 675 2015; Nadon et al. 2015; Gedamke and Hoenig 2006) and catch-only methods (Rosenberg et al. 676 2014; Carruthers et al. 2014), with the strength of estimating recruitment variability. More 677 accurate and precise estimates of recruitment variability can help decipher whether decreased 678 mean length is due to fishing pressure or recruitment variability, and understanding the range of 679 possible levels of recruitment into the future. We therefore conclude that LIME is a step forward 680 in dealing with uncertainty in decision-making for fisheries where length data are collected.

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Table 1. Parameter definitions, including parameter input values for the base scenario for each of
the three life history types, and whether the parameter is fixed ("Fixed") or estimated ("Est.")
depending on the data availability scenario, or if the parameter is used in data generation only
("Sim."). Values separated by commas indicate alternate values for sensitivity analysis. Note that
scenarios including "LC" are each divided into two scenarios with either one or ten years of
length data. Parameter input values are based on short-lived *Siganus sutor* (Hicks and
McClanahan 2012), medium-lived *Lutjanus guttatus* (Bystrom 2015), and longer-lived

	884	Epinephelus mo	rio (Heemstra	a and Randall	1993).
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	Description	Input value			Data Scenario			
Symbo	1	Life history type			Index	Catch	LC	
Biological			Medium	Longer	Rich	+ LC	+ LC	only
L_{∞}	Asymptotic length	36.2cm	64.6cm	90.0cm	Fixed	Fixed	Fixed	Fixed
k	Brody growth coefficient	0.87	0.21	0.13	Fixed	Fixed	Fixed	Fixed
t_o	Age at length=0	-0.01	-0.01	-0.01	Fixed	Fixed	Fixed	Fixed
L_{m}^{50}	Length at 50% maturity	20.2cm	34.0cm	50.0cm	Fixed	Fixed	Fixed	Fixed
α	Length-weight scalar	0.0597	0.0245	0.0264	Fixed	Fixed	Fixed	Fixed
β	Length-weight allometric	2.75	2.79	2.96	Fixed	Fixed	Fixed	Fixed
A	Maximum age	4	18	26	Fixed	Fixed	Fixed	Fixed
M	Natural mortality	1.49	0.43	0.18	Fixed	Fixed	Fixed	Fixed
h	Steepness parameter	1	1	1	Fixed	Fixed	Fixed	Fixed
CV_L	Coefficient of variation for the length- age curve	0.1	0.1	0.1	Fixed	Fixed	Fixed	Fixed
J	Maximum length bin	54cm	97cm	135cm	Fixed	Fixed	Fixed	Fixed
R_{0}	Equilibrium recruitment	1	1	1	Est.	Fixed	Est.	Fixed
σ_R	Recruitment standard deviation	0.737	0.737	0.737	Est.	Est.	Est.	Est.
ρ	Recruitment autocorrelation	0.426	0.426	0.426	Sim.	Sim.	Sim.	Sim.
Non-bi	ological							
L_{s}^{50}	Length at 50% selectivity	11.3cm	20.0cm	25.0cm	Est.	Est.	Est.	Est.
δ	Difference L_s^{95} - L_s^{50}	1.3	1.3	1.3	Est.	Est.	Est.	Est.
	(expressed here as ratio L_s^{95}/L_s^{50} to compare across life histories)							
q	Catchability coefficient	1e-5	1e-5	1e-5	Est.	Est.	Fixed	Fixed
σ_F	Fishing mortality penalty standard deviation	0.2	0.2	0.2	Fixed	Fixed	Fixed	Fixed
σ_c	Standard deviation for observed catch	0.2	0.2	0.2	Fixed	Fixed	Fixed	Fixed
σ_I	Standard deviation for observed abundance index	0.2	0.2	0.2	Fixed	Fixed	Fixed	Fixed
θ	Dirichlet-multinomial parameter related to effective sample size	10	10	10	Est.	Est.	Est.	Est.
п	Sample size of length measurements	200	200	200	Fixed	Fixed	Fixed	Fixed
ϕ	Cumulative normal probability distribution							

E	Equation	Description
1	$L_a = L_{\infty}(1 - \exp(-k(a - t_0)))$	Von Bertalanffy length-at-age <i>a</i>
2	$m_j = 1/(1 + \exp(L_m^{50} - j))$	Maturity-at-length
3	$m_{a} = \sum_{j=1}^{J} m_{j} \left(\frac{1}{L_{a} C V_{L} \sqrt{2\pi}} \right) \exp(-\frac{(j - L_{a})^{2}}{2 L_{a} C V_{L}^{2}})$	Maturity-at-age
4	$S_j = 1/(1 + \exp\left(-\frac{\ln(19) (j - L_s^{50})}{L_s^{95} - L_s^{50}}\right))$	Logistic selectivit at-length
5	$w_a = \alpha L_a^{\beta}$	Weight-at-age
6	$B_t = \sum_{a=1}^A N_{a,t} w_a$	Annual total population biomas
7	$SB_t = \sum_{a=0}^{A} N_{a,t} w_a m_a$	Annual spawning biomass
8	$N_{a,t} = \begin{cases} R_t, & a = 0\\ N_{a-1,t} \exp(-M - F_t S_{a-1}), & 0 < a < A \text{ and} \\ \frac{N_{a-1,t} \exp(-M - F_t S_{a-1})}{1 - \exp(-M - F_t S_{a-1})}, & a = A \text{ and } t=1\\ N_{a-1,t-1} \exp(-M - F_t S_{a-1}), & 0 < a < A \text{ and} \\ (N_{a-1,t-1} + N_{a,t-1}) \exp(-M - F_{t-1} S_{a-1}), & a = A \text{ and } t > 1 \end{cases}$	Abundance at age d t=1 over time d t > 1 1
9	$SB_0 = \sum_{a=0}^{A} R_0 \exp(-aM) w_a m_a$	Unfished spawnin biomass
10	$E_0 = \sum_{a=0}^{A} \exp(-aM) w_a m_a$	Expected lifetime egg production (unfished)
11	$E_f = \sum_{a=0}^{A} \exp(-a(M + FS_a))w_a m_a$	Expected lifetime egg production (fished)
12	$SPR = \frac{E_f}{E_0}$	Spawning potenti ratio

890	Table 3. Functions for generating data in th	e operating model. All except Equations 2 and 5 are
891	also used in the LIME estimation model to	predict values for the observed data.

Equation	1	Description
1	$\varepsilon_t \sim Lognormal(0, \sigma_R)$	Non-autocorrelated recruitment deviations
2	$\begin{aligned} \tau_t &= \varepsilon_t & t = 1 \\ \tau_t &= \varepsilon_t \tau_{t-1} \rho \sqrt{1 - \rho^2} & t > 1 \end{aligned}$	Autocorrelated recruitment deviations
3		Probability of being in a length bin given age
	$p_{j,a} = \begin{cases} \varphi\left(\frac{J - L_a}{L_a C V_L}\right) - \varphi\left(\frac{J - 1 - L_a}{L_a C V_L}\right), & 1 < j < J \end{cases}$	
	$\left(1 - \phi \left(\frac{J - 1 - L_a}{L_a C V_L} \right), j = J \right)$	
4	$\pi_j = p_{j,a} \frac{\sum_{a=0}^A N_{a,t} S_a}{N_t}$	Predicted probability o harvest by length bin
5	$\tilde{\pi}_j \sim Multinomial(n, \pi_j)$	Generated probability of harvest by length bi
6	$C_{a,t} = \frac{F_t S_a}{M + F_t S_a} N_{a,t} (1 - \exp(-M - F_t S_a))$	Annual catch at age
7	$C_t = \sum_{a=0}^{A} C_{a,t}$	Annual catch
8	$I_t = qB_t$	Abundance index

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odel, as we	ell as performar
1	Description
	Expected annual
1	recruitment based
	on Beverton-Holt
:	stock-recruit
1	relationship
	Annual recruitmen
	R_{t} arising from a
1	lognormal
	distribution
	Danalty on annual

894	Table 4. Components of the joint likelihood function in the LI	ME model, as well as performance
895	metrics across iterations of generated data.	
	Equation	Description

 $\mu_{Rt} = \frac{4hR_0SB_{t-1}}{SB_0(1-h) + SB_{t-1}(5h-h-1)}$

		1
2	$R_t \sim Lognormal(\mu_{Rt}, \sigma_R^2)$	Annual recruitment R_t arising from a lognormal distribution
3	$F_t \sim Normal(F_{t-1}, \sigma_F^2)$	Penalty on annual fishing mortality F_t
4	$\sigma_R \sim Lognormal(0.7, 0.2^2)$	Recruitment standard deviation penalty
5	$logL(\pi_{j},\theta \tilde{\pi}_{j},n) = log\Gamma(n+1) - \sum (log\Gamma(n\tilde{\pi}_{j}+1)) + log\Gamma(\theta n) - log\Gamma(n+\theta n) + \sum (log\Gamma(n\tilde{\pi}_{j}+\theta n\pi_{j}) - log\Gamma(\theta n\pi_{j}))$	Dirichlet- multinomial log- likelihood
6	$n_{eff} = (1 + \theta n) / (1 + \theta)$	Effective sample size
7	$C_t^{obs} \sim Lognormal(\sum_{t}^{A} C_t, \sigma_c^2)$	Lognormal likelihood (catch)
8	$I_t^{obs} \sim Lognormal(qB_t, \sigma_I^2)$	Lognormal likelihood (abundance index)
9	$MRE = median\left(\frac{x_{estimated} - x_{true}}{x_{true}}\right)$	Median relative error to quantify bias
10	$MARE = median\left(\left \frac{x_{estimated} - x_{true}}{x_{true}}\right \right)$	Median absolute relative error to

 x_{true}

relative error to quantify precision

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Table 5. LIME performance in estimation of SPR in the terminal year across life-history types, scenarios of data availability, and patterns in fishing mortality and recruitment variability, compared with LB-SPR. Bias (top) is measured as median relative error and precision (bottom) is measured as median absolute relative error from 100 iterations of generated data using the LIME age-structured operating model assuming instantaneous sampling with 200 length measurements annually. Dark green indicates bias/precision less than 5%, light green indicates bias/precision less than 10%, yellow indicates bias/precision less than 20%, light blue indicates bias/precision greater than 30%.

Data									
availability	Short			Medium			Longer		
scenario									
		Variability,	Variability,		Variability,	Variability,		Variability,	Variability,
Bias (MRE)	Equilibrium	two-way F	one-way F	Equilibrium	two-way F	one-way F	Equilibrium	two-way F	one-way F
Rich	-0.019	-0.017	0.023	-0.004	0.005	0.034	0.001	0.012	0.023
Index+LC10	-0.014	-0.039	0.023	-0.049	-0.001	0.094	0.125	0.173	0.076
Index+LC1	0.012	-0.006	0.033	-0.003	0.060	0.065	0.040	-0.061	0.029
Catch+LC10	-0.018	-0.045	0.018	-0.021	0.150	0.165	-0.002	0.124	0.280
Catch+LC1	0.029	0.796	0.972	-0.056	0.119	0.193	0.010	-0.146	0.236
LC10	-0.022	-0.056	0.016	-0.086	-0.137	0.072	0.104	-0.006	0.200
LC1	-0.045	-0.082	-0.025	-0.140	-0.355	-0.154	0.166	-0.468	-0.181
LBSPR10	-0.570	-0.676	-0.708	0.006	-0.405	0.196	0.062	-0.359	0.452
LBSPR1	-0.603	-0.698	-0.738	-0.030	-0.372	-0.181	0.059	-0.403	0.296
Precision (MAI	RE)								
Rich	0.027	0.069	0.028	0.038	0.044	0.101	0.038	0.042	0.089
Index+LC10	0.039	0.051	0.038	0.185	0.176	0.295	0.244	0.449	0.352
Index+LC1	0.046	0.079	0.062	0.105	0.207	0.235	0.180	0.223	0.223
Catch+LC10	0.025	0.055	0.035	0.080	0.382	0.476	0.077	0.423	0.630
Catch+LC1	0.060	0.796	0.972	0.129	0.429	0.496	0.161	0.313	0.714
LC10	0.028	0.063	0.031	0.246	0.499	0.470	0.498	0.743	0.702
LC1	0.072	0.126	0.039	0.216	0.437	0.362	0.301	0.705	0.549
LBSPR10	0.570	0.676	0.708	0.066	0.412	0.404	0.078	0.367	0.486
LBSPR1	0.603	0.698	0.738	0.113	0.478	0.432	0.120	0.501	0.536

Table 6. LIME bias and precision in estimating SPR in the terminal year for a variety of sample size of independent length measurements. In all cases one year of length data are provided to the model. Bias (top) is measured as median relative error and precision (bottom) is measured as median absolute relative error from 100 iterations of generated data using the LIME age-structured operating model assuming instantaneous sampling. Dark green indicates bias/precision less than 5%, light green indicates bias/precision less than 10%, yellow indicates bias/precision less than 20%, light blue indicates bias/precision less than 30%, and dark blue indicates bias/precision greater than 30%.

Sample size	Short			Medium			Longer		
		Variability,	Variability,		Variability,	Variability,		Variability,	Variability,
Bias (MRE)	Equilibrium	two-way F	one-way F	Equilibrium	two-way F	one-way F	Equilibrium	two-way F	one-way F
1000	-0.033	-0.070	-0.029	0.034	-0.369	-0.201	-0.061	-0.449	-0.201
500	-0.028	-0.117	-0.041	-0.001	-0.505	-0.157	-0.031	-0.621	-0.145
200	-0.045	-0.082	-0.025	-0.140	-0.355	-0.154	0.166	-0.468	-0.181
100	-0.027	-0.070	-0.028	-0.055	-0.370	-0.201	-0.127	-0.480	-0.206
50	-0.082	-0.124	-0.041	-0.182	-0.499	-0.163	-0.141	-0.621	-0.107
20	-0.171	-0.153	-0.043	-0.295	-0.431	-0.214	-0.465	-0.751	-0.451
Precision (MARE)									
1000	0.070	0.148	0.048	0.110	0.443	0.422	0.240	0.648	0.474
500	0.053	0.172	0.047	0.125	0.514	0.423	0.245	0.663	0.519
200	0.072	0.126	0.039	0.216	0.437	0.362	0.301	0.705	0.549
100	0.087	0.147	0.046	0.217	0.453	0.429	0.397	0.665	0.503
50	0.108	0.178	0.046	0.343	0.510	0.455	0.421	0.665	0.506
20	0.228	0.168	0.045	0.374	0.469	0.610	0.547	0.754	0.615

Table 7. Comparison of LIME and LB-SPR performance in estimation of SPR in the terminal year between equilibrium scenarios with length data collected annually and using an annual model, length data collected monthly but pooled annually for an annual model, and using the LB-SPR operating model. We also compared the annual model runs with monthly length data run on a monthly time step for the short-lived life-history type. Bias (top) is measured as median relative error and precision (bottom) is measured as median absolute relative error from 100 iterations of generated data. Dark green indicates bias/precision less than 5%, light green indicates bias/precision less than 10%, yellow indicates bias/precision less than 20%, light blue indicates bias/precision less than 30%.

Data availability scenario	Short		Medium			Longer				
	Annual data	Monthly data,	Monthly data,		Annual data	Monthly data,		Annual data	Monthly data,	
Bias (MRE)	and model	annual model	monthly model	LB-SPR	and model	annual model	LB-SPR	and model	annual model	LB-SPR
LC10	-0.022	0.468	-0.040	0.068	-0.086	0.072	-0.133	0.104	0.184	-0.112
LC1	-0.045	0.484	0.034	0.195	-0.140	-0.104	-0.097	0.166	0.168	-0.113
LBSPR10	-0.570	0.136	NA	-0.005	0.006	0.090	0.002	0.062	0.117	0.010
LBSPR1	-0.603	0.111	NA	0.021	-0.030	0.056	-0.003	0.059	0.114	-0.030
Precision (M	ARE)									
LC10	0.028	0.468	0.102	0.140	0.246	0.272	0.260	0.498	0.442	0.429
LC1	0.072	0.484	0.130	0.233	0.216	0.209	0.133	0.301	0.311	0.167
LBSPR10	0.570	0.138	NA	0.050	0.066	0.094	0.048	0.078	0.117	0.050
LBSPR1	0.603	0.154	NA	0.152	0.113	0.139	0.138	0.120	0.157	0.149

	Objective	Conclusion
1.	Is LIME unbiased:	
a.	Across life-history types?	Yes, if the assumption of instantaneous length sampling is met, and growth parameters are known with no error. Performance is best for life histories with longevity less than 20 years under this assumption.
b.	With population variability?	Yes. It is recommended to use more than one year of length data for short- and medium- lived life-history types, and include catch or an abundance index if longer-lived.
c.	With inclusion of catch and/or an abundance index?	Yes, with more than one year of length data for short-lived species. May over-estimate SPR for medium and longer-lived species if the population is not in equilibrium.
2.	Is LIME sensitive to:	
a.	Sample size of length measurements?	Yes, accuracy and precision generally improve with higher annual sample size. There is a performance plateau for 100 samples for short-lived fish and 500 samples for medium- or longer-lived fish.
b.	Error in input parameters?	Relatively insensitive to error in the CV of the age-length curve. If asymptotic length, von Bertalanffy growth coefficient, or length at 50% maturity are input lower than the truth, or natural mortality input higher than the truth, SPR will be estimated higher than the truth (and vice versa).
3. a.	<i>Comparison of LIME and LB-SPR under</i> Instantaneous annual sampling from age-structured model	<i>equilibrium conditions</i> LIME unbiased across life-history types; LB- SPR estimates lower SPR for short-lived life history.
b.	Continuous sampling (monthly) from age-structured model	LIME should use monthly time steps for short-lived species, but can use annual time steps for medium and longer-lived species.
c.	Length-structured operating model	LIME over-estimates SPR for short-lived and under-estimates SPR for medium- and longer- lived. LB-SPR unbiased across life-history types.



Figure 1. Diagram of the simulation study. "LC" stands for length data, numbers indicate number of years in the 20-year time-period modeled. In the case of the instantaneous, annual length measurement scenario, we compared multiple sample sizes of length measurements annually (1,000, 500, 200, 100, 50, and 20). For the other scenarios, we assumed the base case of 200 length measurements annually.



Figure 2. Selectivity, maturity, and length at age curves for the three life-history types tested in the simulation study, mimicking: (a) rabbitfish (*Siganus sutor*), a short-lived fish (L_{∞} =36.2 cm, k=0.87, M=1.49, a_m^{50} =1 year, maximum age A=4 years, Hicks and McClanahan 2012), (b) spotted rose snapper (*Lutjanus guttatus*), a medium-lived fish (asymptotic length L_{∞} =64.6 cm, von Bertalanffy k=0.21, natural mortality M=0.43, length at 50% maturity a_m^{50} =4 years, maximum age A=15 years; Bystrom 2015), and (c) red grouper (*Epinephelus morio*), a longer-lived fish (L_{∞} =90 cm, k=0.13, M=0.18, a_m^{50} =7 years, maximum age A=26 years; Heemstra and Randall 1993).



Figure 3. Scenarios of fishing mortality and recruitment under equilibrium and variable conditions for the three life-history types, with corresponding trajectories of relative spawning biomass. Shaded regions represent the area between the 5th and 95th percentile of generated data, and the lines show three randomly chosen iterations out of 100, as examples. Scenarios labeled "equilibrium" demonstrate that the initial depletion may start between 0.05 and 0.95, but fishing mortality remains constant to produce that level of depletion, and recruitment is constant at 1.0 over time. Scenarios labeled "two-way" demonstrate fishing mortality that increases to a fishing mortality rate $F_{20\%}$ that results in 20% SPR over the first seven years, stays at $F_{20\%}$ for seven years, and then drops to half of $F_{20\%}$ for the last six years. Scenarios labeled "one-way" demonstrate a change from equilibrium fishing mortality resulting in an initial depletion between 0.05 to 0.95 to the fishing mortality $F_{20\%}$ over the 20-year period.



Figure 4. Distribution of relative error ((estimated-true)/true) for spawning potential ratio (SPR) in the current year for 100 iterations of simulated populations across the LIME and LB-SPR data availability scenarios for the three life-history types and scenarios of equilibrium and variable fishing mortality and recruitment with 200 samples of length measurements annually. The gray bean represents the "data-rich" scenario, which verifies LIME is unbiased and most precise when an unrealistically high amount of data are available. Darker colors represent data availability scenarios with 10 years of length data, and lighter colors represent the scenario with one year of length data available. Each life-history type has a different y-range.



Figure 5. Proportion of iterations out of 100 where the true value of the spawning potential ratio (SPR) lies within the 50% confidence intervals for each life-history type across various patterns of fishing mortality and recruitment (gray circles) compared to the convergence rates for the same scenario (pink triangles).



Figure 6. Comparison of the distribution of estimation error for spawning potential ratio (SPR) in the terminal year with the life history parameters fixed at +/- 25% of their true value from 100 iterations of generated data across the various life history scenarios for the equilibrium (blue) and the two-way fishing mortality scenario with variable and autocorrelated recruitment (red), with other biological parameters fixed at their true values, including 10 years of length data with 200 length measurements annually. Life history parameters include natural mortality, asymptotic length, von Bertalanffy growth coefficient, length at 50% maturity, and the coefficient of variation for the age-length curve.



Figure 7. Comparison of the LIME and LB-SPR methods in the equilibrium state via the distribution of relative error *(estimated-true)/true* for spawning potential ratio (SPR) in the current year for 100 iterations of simulated populations from the LIME age-structured operating model using annual length composition collected instantaneously in the year (a-c), monthly length data collection pooled into annual length compositions (d-f), and the LB-SPR operating model based on relative ages. The methods are compared across life-history types. Darker colors represent data availability scenarios with 10 years of length data, and lighter colors represent the scenario with one year of length data available. Each scenario has a different y-range.



Figure 8. Example of model estimates (color lines) with 95% confidence intervals (shaded areas) and the true simulated population dynamics (black dotted line) for each of the data availability scenarios for one iteration of a simulated population with medium-lived life history, 200 length measurements annually in the length data, for the base variation scenario.



Figure A1. Size at age for the yearly (blue) vs. monthly (white-orange) time steps for the shortlived life-history type. White lines (monthly) overlapping blue lines (yearly) demonstrate that size-at-age is identical at the start to each year, and orange lines increasing in density indicate the size-at-age distributions during the following months within each year.