

Exploring a wider approach to OM conditioning in IOTC MSE work

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Contents

1 Background 1

2 Methods 1

3 Results 2

4 Discussion 4

5 Acknowledgements 5

1 Background

For the current suite of IOTC MSE work, the general approach to conditioning the required set of Operating Models (OMs) has been to use the species-specific stock assessment model structure as the basis for the OMs. In [1] an alternate, complementary approach was outlined where instead of the assessment being the basis for conditioning, a suite of possible prior states of historical dynamics and current status are defined. The available, but mostly more contemporary, data are included within an estimation scheme built on emerging Approximate Bayesian Computation (ABC) and Synthetic Likelihood (SL) concepts [2, 3]. The aim is to generate a distribution of current abundance, mortality and status that is consistent with the available data and the suite of possible prior states of nature defined beforehand. This can then be used to initialise the OMs used to project the stock into the future and test the candidate MPs.

A stock assessment, in this context, can be viewed as our attempt to do both of these things at once. Ideally, this is arguably the most sensible option; however, it is not always successful. The ongoing struggles with the Yellowfin tuna stock assessment, and the conditioning of OMs based upon it, outline this problem: what if you cannot adequately reconcile the data, assessment model structures, and the resultant estimates of current status and future projected dynamics? In [1] we proposed an alternate approach arguing that using a stable, agreed and robust stock assessment was the preferable first option, but that the ABC approach was a potentially viable - and scientifically pragmatic - alternative approach if the assessment route was unsuccessful.

In this paper we expand on the ideas outlined in [1] using a relatively simple simulated example of how the approach can work in the tuna MSE context. The mathematical and statistical tools required are mostly in the Appendix, but some general principles are outlined. We explore a flexible approach to fitting to the available data from both parametric and nonparametric viewpoints, depending on the context. We also clarify what key status variables can be assigned priors, and how that feeds into the estimation scheme with the observed data and catch to help produce the abundance, biomass and mortality estimates required to initialise the OMs.

2 Methods

ABC [2] and SL [3] methods can be used to define an *approximate* distribution for the parameters θ we are interested in; subsequently, we obtain an approximate distribution for all the variables that depend on those parameters. Where they differ from more classical frequentist or Bayesian methods is how the data, D , are included. Classical methods posit a likelihood for the data, given the parameters: $\ell(D | \theta)$; for Bayesians we then define a prior distribution, $\pi(\theta)$ to then define the posterior distribution of the parameters given the data:

$$\pi(\theta | D) = \frac{\ell(D | \theta) \pi(\theta)}{\pi(D)}$$

The ABC approach relaxes this requirement for a specific likelihood (i.e. data generating probability model) to the idea of a *discrepancy* statistic that measures the difference between the observed data, and the model-derived process variables, X , that relate to the data. The simplest example would be some distance metric $\rho(D, X)$ whereby we require that this distance between the observed data and our prediction is less than some value $\delta > 0$ (i.e. assumes uniform error on a ball of radius δ). Values whereby $\rho(D, X) \geq \delta$ receive zero probability mass

and, in a sampling scheme, would never be accepted. This simple approach will not necessarily work for certain types of data, especially the types we often have in fisheries contexts, but there are natural generalisations of this simple discrepancy idea.

The other very useful thing we can easily embed within a sampling scheme is informative priors on various elements of the process variables, X , which effectively imply a prior on the key parameters, $\pi(\theta)$. This means we can also define informative priors for the various stock status variables (MSY ratios, SSB depletion *etc.*) and include the most relevant recent data, without having to fully model the historical dynamics and data and define appropriate likelihoods for these data. If we are departing from the stock assessment approach, this implies that we have not really succeeded in being able to robustly estimate the distribution of these key status variables. This approach takes a step back and instead tries to define scenarios (specifically distributional scenarios) for these variables at particular periods in time that are consistent with previous assessment experiences and the data. In terms of likely data sources the two most obvious examples are: CPUE indices of abundance, and catch length composition. For some examples we may also have mark-recapture data (e.g. tropical tuna). As a relatively simple example we will explore an Albacore-like scenario with no spatial structure, catch biomass, a long-line CPUE index and catch composition from a single long-line fishery.

The population models and associated biological relationships will be very similar to the stock assessment, given they have to have the same structure as the existing OMs (which we don't propose need changing at this stage). The main technical challenge is constructing the discrepancy statistics for the data, and the sampling scheme to generate samples from our approximate distribution of the parameter and population dynamic variables. We move the technical details of how these are done to the Appendix to avoid an unnecessary amount of technical exposition in the main body of the paper: what we are trying to demonstrate is that we can get the variables we need for OM conditioning, using plausible status scenarios, key data sets and emerging powerful statistical sampling techniques.

3 Results

As a simple expository example, we define an Albacore-like fish population, with associated life-history, and a long-line type fishery from which we can obtain catch length composition and a CPUE-based abundance index. Table 3.1 details the relevant life-history parameters.

Parameter	Value
B_0	1e+6
h	0.75
M	0.4
σ_r	0.5
a_{\max}	20
$a_{1,2}$	2, 10
$l_{1,2}$	50, 120
k	0.2
σ_l	0.15
l_{50}	90cm

Table 3.1: *Life-history parameters for Albacore-like example population.*

For the long-line type fishery we define a double-normal selectivity function with maximum selectivity attained at age $s_{\max} = 4$ with a fast increase $s_l = 1.25$ and a slow declining dome shape $s_r = 25$ (see Figure 3.1).

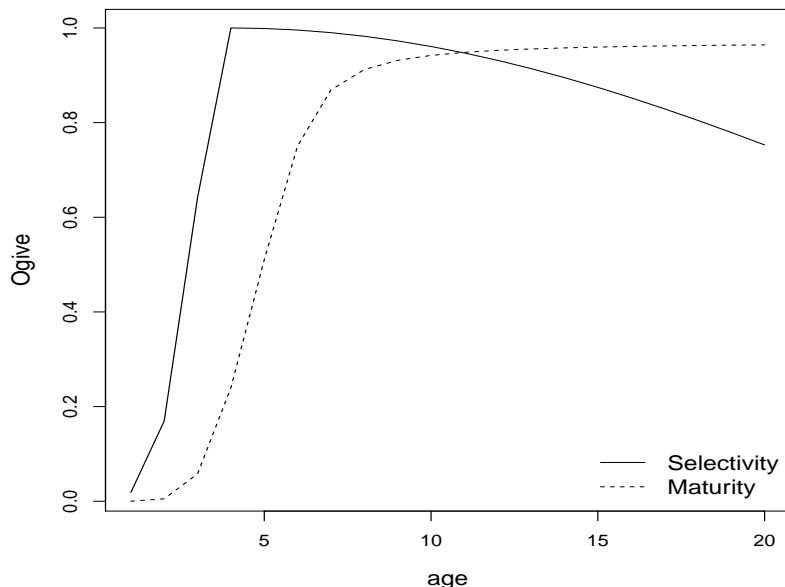


Figure 3.1: *Selectivity (full line) and expected maturity-at-age (dotted line) for simple example.*

In terms of the dynamics simulated over time we explored the following configuration:

1. Start the population from a unfished equilibrium state
2. Simulate forward in time for 50 years
3. Begin with a low harvest rate (0.05) and increase linearly to MSY levels in 50 years
4. Simulate catch length composition from a multinomial distribution with effective sample size of 50
5. Simulated CPUE derived relative abundance index with observation CV 0.15

Figure 3.2 shows the SSB relative depletion and catch summaries for the example simulation. For the example application of ABC/SL estimation techniques we only use the data from the last 20 years and only estimate the population abundance, biomass and mortality over the same time-frame. We do not need to fully reconstruct the dynamics for the construction of a usable OM; we only need to cover enough time so as to capture the recent dynamics and likely current suite of status dynamics.

The purpose of this example is not to explore a full analysis of the estimation accuracy and bias properties of this particular suite of models and scenarios, so we randomly sampled a single iteration from the 1,000 we simulated and fitted the population model to the 20 years of data, using the ABC approximate MCMC algorithm outlined in the Appendix. For the non-recruitment estimated parameters - B_0 , initial equilibrium harvest rate h_{init} , and the three selectivity parameters - vague uninformative priors are assumed; for the recruitment deviations σ_r defines the prior. The key additional priors are what we can call status priors: for a given time range priors on the

MSY ratios and SSB depletion. We use the final three years of the model time period to define this priors - see Table 3.2 for a summary of the true values, the priors, and the approximate posteriors.

Variable	True	Prior CI	Posterior CI
B/B_{msy}	0.97	0.82–1.22	0.87–1.19
B/B_{msy}	0.98	0.82–1.22	0.88–1.19
SSB/B_0	0.26	0.11–0.79	0.24–0.32

Table 3.2: *True values, status priors, and approximate posterior credible intervals for ABC algorithm fitted to example data set.*

Figure 3.3 shows a comparison of the true population dynamic and fishery variables (for the example iteration) compared to their approximate posterior summaries (95% credible intervals). Figure 3.4 shows the approximate posterior summary of the fits to the particular length frequency data and CPUE index for the chosen historical simulation.

4 Discussion

This paper outlines both the theoretical and practical ideas behind the suggestions originally raised in [1], with respect to methods for conditioning OMs that are not built upon the stock assessment model structures and output. The approach uses much if not all the same demographic and life-history parameters the assessment does, and often key subsets of the same data if they are required to be simulated in the OMs. It also includes key prior information on current/recent/historical status variables (MSY ratios, depletion *etc.*) to help estimate the key abundance, biomass and mortality variables required in the OMs. There is a precedent for these types of approach - the original skipjack tuna OM was conditioned in a similar fashion [6] using an approach outlined in [7]. The approach in this paper is built on a more formally probabilistic suite of methods called Approximate Bayesian Computation (ABC) [2]. Using this approach, and the emerging suite of statistical sampling techniques [2], we can obtain samples from an approximating posterior distribution of all the key variables required to condition our OMs.

Using an albacore-like example of a single stock/sex/region population and a single longline fishery we simulated population trajectories and fishery data for 50 years of a familiar “fish down to MSY” one-way trip stock trajectory. Only the last 20 years was used in the estimation phase - emphasising we are not trying to replicate a stock assessment and a full reconstruction of the historical stock dynamics. We are trying to get reliable and robust estimates of current dynamics, given what we think about current status, to initialise the OMs. We include catch composition and a longline CPUE index of abundance using the discrepancy functions detailed in the Appendix. The aim was not to do an exhaustive simulation-estimation analysis of the example model and ABC algorithm; merely to outline how these approaches can work. To this end, we simply selected a single representative iteration of the simulations and summarised how the model fitted to the data and replicated the true key population dynamic trends. We have fitted the model to other iterations and obtained similar quality of fits and replication of dynamics in those cases. Broadly speaking, the models do a good job of fitting to the data and replicating the key features of the stock status information we are interested in for this simple example.

There is some updating of the status priors, but not very strongly if we are being sufficiently

informative with respect to the MSY ratios in particular. If we did have say very informative abundance information and mis-specified status priors any obvious conflict would be clear and simple to identify - this will always be case dependent though. An obvious criticism of these models is that we are supplying strong prior information on status which, when combined with the model structures and the catches and observed data, has a strong impact on the estimated model status. The obvious response is that, if we thought the stock assessment was actually able to robustly estimate stock status and fit to the data given the model structures and biology, we would be using the assessment. The stock status scenarios we define are clearly likely to have a strong impact on the resultant estimates we obtain, and subsequently on the OMs we condition using these estimates. As long as we are both logically clear and consistent about the scenarios we define, and that the suite of possible scenarios covers the range of plausible true status levels, this should avoid any obvious issues.

When we proceed with constructing the actual suite of models when exploring these techniques for application to yellowfin and possibly albacore, they will be more complex than the relative simple example outlined herein. For yellowfin we will have spatial structure and movement, and we will look to try and aggregate similar enough fisheries together and model collective selectivity in a time-varying context to balance reduced fishery complexity with actually fitting to the data (also a problem in the most recent stock assessment). The computational techniques are not limited to just the kind of simple example outlined; we just need to use the computational resources at our disposal when it comes to running the larger more realistic models. The approach outlined in this paper demonstrates the potential for conditioning our suite of OMs without having to rely exclusively on the stock assessment, and will be explored further for the relevant species.

5 Acknowledgements

This work was funded by the Department of Foreign Affairs and Trade of the Government of Australia.

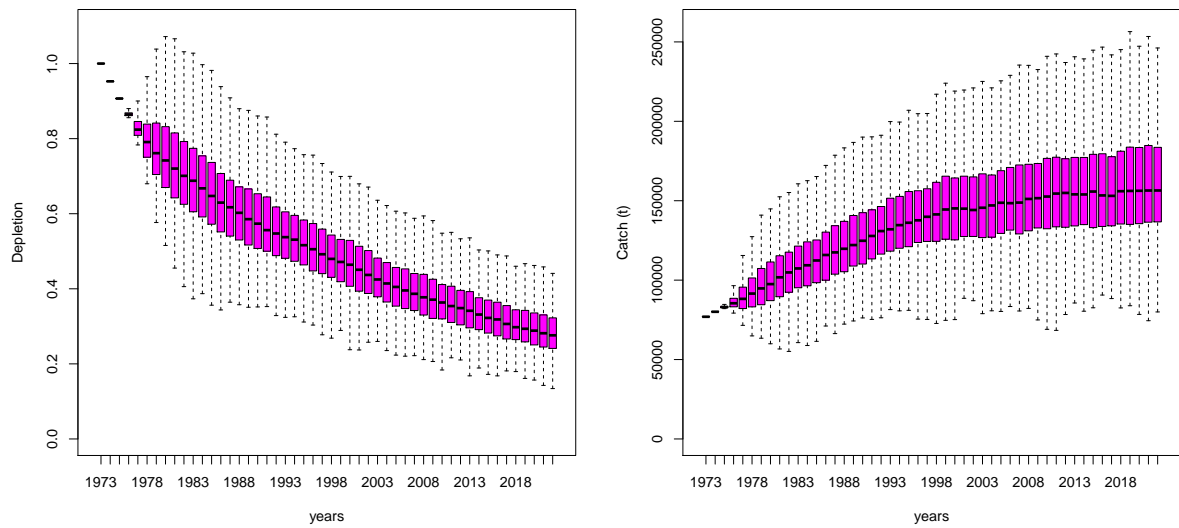


Figure 3.2: *Simulated SSB depletion (left) and catch (right).*

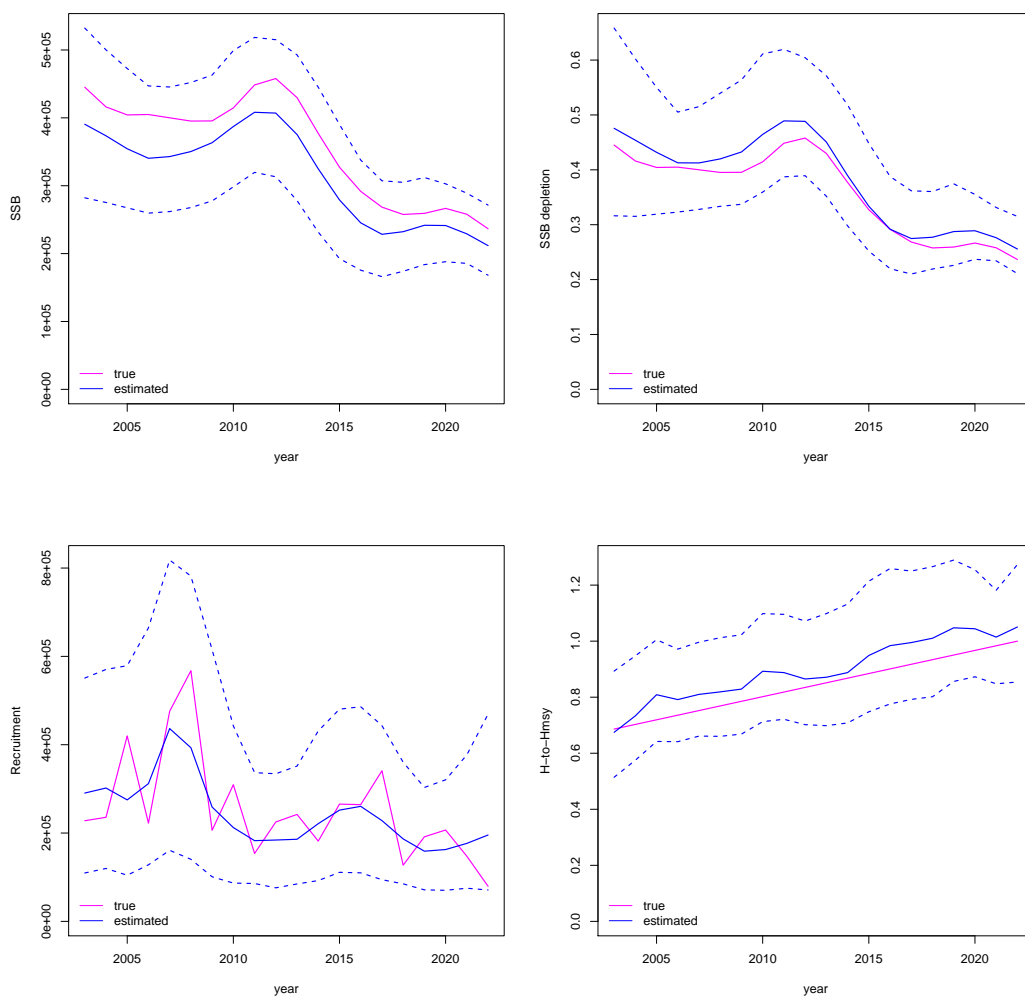


Figure 3.3: Comparison between true (magenta) and approximate posterior summaries (blue; median full and 95% credible interval dotted) for SSB (top left), SSB depletion (top right), recruitment (bottom left), and harvest rate MSY ratio (bottom right).

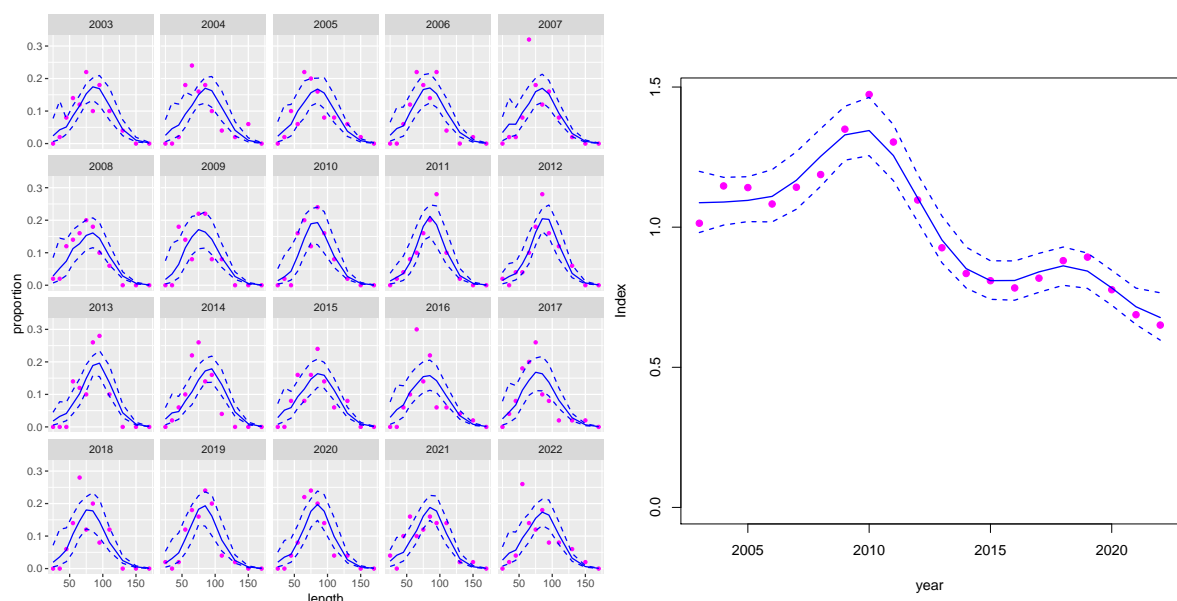


Figure 3.4: Comparison between observed (magenta dots) and approximate posterior predictions (blue; median full and 95% credible interval dotted) for the length frequency (left) and CPUE index (right).

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Appendix

The underlying population model used to simulate the data was a fairly straightforward age structured single sex and area model, that can generate length composition data and abundance indices. It uses a simple harvest rate-based catch equation, not the more complex fishing mortality based Baranov equation, which can be easily extended to account for seasonal distributions of fishing pressure. A Beverton-Holt steepness parameterised stock-recruit stochastic relationship is also used.

Approximate MCMC ABC algorithm

There are a wide variety of possible algorithms that can be used to generate a sample from the approximate posterior distribution [2, 3, 4]. Given the relative complexity of our likely suite of models, we consider that Algorithm D from [4] is the most applicable. It is basically an ABC-configured Metropolis-Hastings accept-reject algorithm used in classic Bayesian MCMC contexts. At time t , we have our joint parameter and process variable state $\Xi_t = \{\theta_t, X_t\}$. We generate a proposal for a new parameter vector θ' (and $X' = f(\theta')$) from the pre-specified transition kernel $q(\theta_t, \theta')$. We define the following acceptance probability for $\Xi' = \{\theta', X'\}$:

$$\alpha(\Xi_t, \Xi') = \min \left(1, \frac{\pi(D, X')q(\theta', \theta_t)\pi(\theta')}{\pi(D, X_t)q(\theta_t, \theta')\pi(\theta_t)} \right)$$

and generate a random variable $u \sim U[0, 1]$. If $\alpha(\Xi_t, \Xi') > u$ we accept the proposal and $\Xi_{t+1} = \Xi'$; if $\alpha(\Xi_t, \Xi') \leq u$ we reject the proposal and set $\Xi_{t+1} = \Xi_t$. By choosing a symmetric normally distributed transition kernel $q(\theta_t, \theta') = q(\theta', \theta_t)$ this term disappears from the acceptance rate calculations. The prior distribution, $\pi(\theta)$, is for the estimated parameters. The $\pi(D, X')$ term is our likelihood analogue or discrepancy function - it includes both the observed data (catch length composition, abundance indices) and our additional information on the key status variables contained in the suite of process variables, X (e.g. MSY and depletion ratios). The Markov chain transition kernels $q()$ are defined to use the random walk approach to sampling the posterior surface. To make the MCMC algorithm more efficient we implement a Metropolis-within-Gibbs sampling approach [5], where parameters are grouped together depending on expected correlation to make the algorithm more efficient. Each block is updated using the Metropolis-Hastings algorithm, conditional on the parameters not included in that block being fixed at their most recent value. After doing this for each block of parameters (the Gibbs sampling part of the algorithm) we have fully updated all the parameters of the model and repeat the same process many times. Random walk variances are adjusted to achieve acceptance rates around 40% - long considered generically optimally efficient [5]. A suitable burn in period is used to get the sampler moving on the surface before we decide to keep the samples and the samples themselves are thinned to remove autocorrelation in the Markov chain. When this is done we have 1,000 samples from the approximate posterior distribution of interest and we use the Geweke statistic [5] to test for non-convergence of the Markov chains.

For the CPUE based abundance index, in the IOTC MSE context CPUE is the key candidate MP data input so we are going to have to simulate the CPUE data in the OMs (which requires catchability and variance parameters). For this reason we actually used a modified log-normal distribution for these data. The data were log transformed and standardised to have mean zero (this removes the need for estimating catchability at estimation run time). The catchability can

be efficiently estimated post-estimation so this treatment doesn't cause issues later on in the OMs. The *overall* variance in the distribution was estimated by fitting a LOESS smoother to the log-transformed index and using the residual SD in the likelihood - in this regard this part of the discrepancy function is closer to SL than ABC.

For the length composition data we took a nonparametric approach using the concept of the Kullback-Leibler divergence (KLD): this is a measure of the divergence between in this case a discrete probability distribution Q_i , relative to a reference distribution P_i . It is defined as follows:

$$D_{KL}(P \parallel Q) = \sum_i P_i \ln \left(\frac{P_i}{Q_i} \right) \geq 0$$

with the convention that

$$\lim_{x \rightarrow 0^+} x \ln(x) = 0.$$

The KLD serves as a potentially very useful option in the ABC sense for the following reasons:

1. It is nonparametric so the underlying generating distribution of the length data does not need to be assumed
2. It reduces to zero when $P_i \equiv Q_i$ and increases the further Q_i diverges from P_i - by defining P_i as our observed data and Q_i our model prediction it makes an obvious candidate as a discrepancy measure of lack of fit
3. The units are interpretable. For natural logarithms the units are called nats - 1 nat is basically a difference in probability of $1/e$. This means we can set tolerance levels for how much divergence we are willing to accept in our predicted data that have a grounding in information theory

In practice we would use the *negative* KLD - it reaches a maximum at perfect prediction of the data and decreases as this gets progressively worse, much like a likelihood does. If we define $p_{y,l}$ as our observed length data and $\hat{p}_{y,l}$ as our predicted length composition this part of the discrepancy function can be defined as

$$\mathcal{D}_{LF} = -\lambda_{LF} \sum_y \sum_l p_{y,l} \ln \left(\frac{p_{y,l}}{\hat{p}_{y,l}} \right)$$

and λ_{LF} is a weighting parameter that we can change depending on how much divergence we are willing to accept between the observed and model-predicted length composition.

For the status variables (MSY and depletion ratios) we simply defined quadratic kernels for the log-transformed variables averaged over the relevant time frame:

$$K(x, y | \epsilon) = \frac{\|x - y\|^2}{\epsilon^2}$$

In this case the tolerance for each kernel ϵ can basically be interpreted as twice the standard deviation of a normal distribution. The summation of the CPUE and length composition discrepancies and the status prior kernels makes up the overall discrepancy function $\pi(D, X)$.

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