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Recent developments in the MULTIFAN-CL stock assessment software

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Introduction

MULTIFAN-CL (MFCL) is a statistical, age-structured, length-based model routinely used for stock assessments of tuna and other pelagic species. The model was originally developed by Dave Fournier of Otter Research Ltd for application to south Pacific albacore tuna (Fournier *et al.* 1998).

MFCL is typically fitted to total catch, catch rate, size-frequency and tagging data stratified by fishery, region and time period. Recent tropical tuna assessments (e.g. Davies *et al.* 2011; Hoyle *et al.* 2011, and Langley *et al.* 2011) encompass a time period of 1952 or 1972 to 2011 in quarterly time steps, and model multiple separate fisheries occurring in 3 to 6 spatial regions. The main parameters estimated by the model include initial numbers-at-age in each region (usually constrained by an equilibrium age-structure assumption), the number in age class 1 for each quarter in each region (the recruitment), growth parameters, natural mortality-at-age (if estimated), selectivity-at-age by fishery (constrained by smoothing penalties or splines), catch (unless using the catch-conditioned catch equation), effort deviations (random variations in the effort-fishing mortality relationship) for each fishery, initial catchability and catchability deviations (cumulative changes in catchability with time) for each fishery (if estimated). Parameters are estimated by fitting to a composite likelihood comprised of the fits to the data and penalized likelihood distributions for various parameters.

Each year the MFCL development team works to improve the model to accommodate changes in understanding of the fishery, to fix software errors, and to improve model features and usability. This document records changes made since August 2011 to the model and other components of the MFCL project both for the current release version (1.1.4.2), and the current unreleased development version, and updates the report for the previous period, 2010-11, (Davies *et al.* 2011).

Development overview

Team

The senior developer of MFCL is Dave Fournier, of Otter Software in Canada. Assisting with programming is Nick Davies, with occasional programming carried out by John Hampton (SPC, New Caledonia), and Pierre Kleiber (NMFS Hawaii). Other tasks include testing and debugging (ND, SDH, PK, JH, and Fabrice Bouye (SPC)); documentation (PK, ND); and planning and coordination (DF, ND, JH, SDH, and Shelton J Harley). Related project software are developed or managed by FB (MFCL Viewer, Condor, Gforge), PK (R scripts), and SDH (R4MFCL, Condor).

Calendar

September – December: Planning and ongoing code development

October – January: MFCL development meeting, 1-2 weeks

February – March: Testing and finalizing production version

April-July: Stock assessments

MFCL collaboration and versioning

The project management website based on the open source GForge software was established in 2008-09 has been maintained and provides the nucleus for source code management and versioning. The repository for MFCL source code development is held on the website and uses the open source software SVN (<http://tortoisesvn.net/>). Code developments are consecutively committed to the repository while tracing the different versions chronologically. The repository and overall development are coordinated via the GForge website <http://gforge2.spc.int/>, which is administered by Fabrice Bouye fabriceb@spc.int.

Problems with MFCL operation or compilation have been reported to the project management website so as to maintain a list of desired enhancements, and to allocate tasks among the project team. Some of the tasks identified during the previous reporting period (2010-11) have been addressed in the current period in the way of model developments. A main trunk exists for the MFCL source code, and a development branch has been created to hold these recent developments to the source currently being tested. A formal testing procedure has been designed before source code is committed from the development branch to the trunk, and a manual has been drafted for testing new compilations, standardizing the source code compilation procedure, and posting of executables.

A version of the source code for ADMB (<http://admb-project.org/>) has been added to the project management website in a separate repository. Minor modifications were required to the ADMB source (currently held in a development branch) to facilitate the recent MFCL developments.

Postings to website

There have been two postings of MFCL updates to the website since August 2011.

Version 1.1.3.1 - 25 October 2011

In response to requests for increased speed when running deterministic projections changes were made to minimize file output:

- New input .ini file format entailing a version number that ensures backward compatibility
- Output file controls have been defined for particular report files. Three output options exist: Full; Streamlined; and Silent. Streamlined and silent options achieve faster performance for single model evaluations.

Version 1.1.4.2 - 2 February 2012

A list of the subsequent changes made to version 1.1.4.2 and that are reported here includes:

- New input .ini file format now includes the value of the steepness parameter for the Beverton-Holt stock recruitment relationship where it is initialised or fixed when commencing a model fit.
- The maximum fishing mortality value has been raised to facilitate very high potential "observed" catches being achieved in model projections.

- A new simulation output file containing age-specific fishing mortalities for each time period is produced.
- Simulations can now be operated for projections under zero fishing mortality. This is sometimes required for risk analysis in respect of biological limit reference points in respect of unfished biomass.
- An option has been added for applying a bias correction to the recruitment predictions from the Beverton-Holt stock-recruitment relationship (BH-SRR) so as to approximate the mean of the estimated recruitments. These corrected predictions may then be used for equilibrium yield calculations and deterministic projections.

Tool development

R4MFCL

The R scripts for working with MFCL, developed and released on the internet (<http://code.google.com/p/r4mfcl/>) have been updated to adapt to the recent MFCL file formats. These scripts are used to manipulate the input files, so that runs can be automated. Other scripts can be used to read in the output files, analyze the results, and generate plots and tables. See Hoyle *et al.* (2009) for a list of these R scripts. Further refinements of these tools were undertaken as part of the 2012 stock assessments that consolidated new features to the utilities package. A repository was established in 2012 so as to coordinate current and development versions of the package.

Testing framework

A testing framework for MFCL compilations was developed in 2011-12 that ensures the repeatability and traceability of testing by streamlining the process for new source code developments through a system of model testing procedures and folder locations. The testing criterion is based upon pair-wise comparisons of model run results obtained using an existing MFCL compilation (usually the current release version) versus those from a development compilation. The R scripts for this framework facilitates testing over multiple processor platforms and architectures, with application to multiple input testing data sets, and with various options for the MFCL operation, viz. single or multiple model evaluations, or full do it all model fits to convergence. The tests are submitted to the Condor network that enables the multiple tests to be completed in parallel. Upon completion, the test results are collated and pair-wise comparisons of the screen-output, *.par*, and *plot.rep* output files are made using automated scripts that use functions from the R4MFCL package. Differences in the results may then be evaluated in summary form in relation to the code changes made to the development version to ensure these have integrity.

The streamlined and rapid processing of new MFCL compilations using this framework has eased the workload associated with new releases and ensures a thorough integrity-check of model quantities and components of the objective function prior to the distribution of new versions.

MULTIFAN-CL Viewer

The MFCL viewer was updated with a new diagnostic plot incorporating the new feature for tag release group-specific recapture reporting rates (Davies et al. 2011). A revised, but not yet released, version has been developed to accommodate output files from multi-species

applications of MFCL. Development of this version is ongoing since the multi-species application is not yet complete.

Condor parallel processing facility

The Condor (www.condor.wisc.edu) facility has been used routinely for managing multiple MFCL model runs on a grid currently numbering over 100 processors; being windows or linux platforms, and either 32- or 64-bit architecture. This grid enables intensive model runs for stock assessments, structural sensitivity analyses, and management strategy evaluation. The Condor version was recently updated.

MFCL user's guide

A revision has been completed that documents the developments in version 1.1.4.2 and this has been posted on the website.

New MFCL features

Stochastic population projections

A significant development to MFCL in version 1.1.4.2 and the unreleased development version has been the facility to undertake model simulation runs that include projections into the future with stochastic recruitments, with new features added in 2012 for:

- a) model evaluations under no-fishing in each simulation;
- b) the output of projected fishing mortalities;
- c) generating stochastic recruitments from a defined period of the estimated recruitments; and,
- d) generating stochastic recruitments as deviates from predictions of the SRR in projection years.

These new features entailed changes to the existing operations using the Hessian matrix for generating the inputs to the stochastic simulations, and also for no-fishing projection evaluations, and to the outputs.

Rationale

The concept of the risk associated with a biological reference point, e.g. B_{MSY} , is increasingly being recognised by fisheries managers as having utility since it takes account of model uncertainty and natural variability when interpreting population model estimates. A risk-based limit reference point may therefore be defined, for example, as: a 10% probability of the stock size being less than that which supports B_{MSY} . Risk analysis may be used to evaluate the performance on alternative management strategies against, for example, a threshold 10% probability level. Typically, this analysis would incorporate the main sources of uncertainty, such as statistical uncertainty, model structural assumptions, and natural variability, such as recruitment variation. Incorporating this stochasticity in model projections creates variability in future population states from which estimates of risk relative to a particular reference point can be calculated.

Stochasticity in future recruitments is a dominant source of natural variability in fish populations and the functionality for this feature were included in an earlier version 1.1.1.0.

In 2011, requests were received for the generation of outputs from stochastic simulations for reference points entailing the calculation of future population states in the absence of fishing mortality, e.g. $20\%SB_{CurrentF=0}$, and in respect of future fishing mortalities, e.g. F_{future}/F_{MSY} . Accordingly in 2012, new algorithms were added to undertake these calculations and to generate the outputs.

It may be preferable to assume that future recruitments are correlated to the associated adult population state via a spawning stock recruitment relationship. This entails generating stochastic recruitment distributions for projections from the product of a recruitment predictor in each projection year and a set of deviates. Good progress was made towards developing this feature during 2012.

Methods and Testing

MFCL currently incorporates uncertainty in the initial population state, future recruitment and other model parameters into the projection by sampling the parameters from a multivariate probability distribution (i.e. the variance-covariance matrix from the likelihood-based analysis). In MFCL statistical uncertainty for model parameters is calculated by employing the usual second order approximation to the mode of the posterior distribution (Fournier *et al.* 1998), and confidence intervals for derived variables are calculated by the inverse Hessian – Delta method. In this way, the distribution of estimated historical recruitments, numbers-at-age in the final year of the model + 1, and the fishery effort deviates is estimated. During the January 2011 MFCL workshop, it was confirmed the stochastic projection functionality operates according to the formulations, and includes the three sources of stochasticity.

The methods for developing new features a) to d) were as follows.

- a) – c). The operations using the Hessian activated by `parest_flags[145] = 7` and `8`, were extended to include:
 - derivatives calculation of dependent variables for projections with no fishing;
 - output of the no fishing derivatives files (`deplabel_noeff.tmp`, `proparams_noeff.val`)
 - calculate the stochastic no-effort numbers-at-age in the final period of the estimation model
 - output to a file called "simulated_numbers_at_age_noeff"

The implicit model numbers-at-age calculations were then made conditional upon the `parest_flags` values which identify whether the projections are stochastic simulations and have no-effort. An additional report from each simulation was generated for the fishing mortalities-at-age.

These features were fully tested using pair-wise comparisons with deterministic projections using the same set of inputs and by comparing the mean of 200 stochastic projections with the deterministic projection values.

A minor coding change was made to enable a single stochastic simulation to be run. This facilitates repeating a single stochastic simulation but with modified fisheries data in each repetition so as to evaluate future population states under the stochastic recruitments unique to that simulation.

- d) An algorithm was designed for applying the estimated recruitment deviates to generate projection recruitment distributions conditional upon the mean recruitment predicted by the stock-recruitment relationship (BH-SRR) in respect of the spawning stock size in each projection year. A set of comparisons was used to demonstrate the

effect of the assumptions for log-normality and model formulation constraints for recruitment deviates upon the use of these deviates for generating a recruitment distribution from BH-SRR predictions. Initially, to provide background to an application, the method of additive and subtractive correction for log-normal bias was described and demonstrated using a theoretical example. Then, two examples were used to illustrate by comparison the recruitment distributions generated from a BH-SRR predictor using alternative sets of deviates. This comparison illustrated the effect of the model estimation constraints for regional recruitment deviates. Conclusions were drawn on how recruitment deviates should be estimated if they are to be used in generating distributions around a predictor, such as BH-SRR. This has important implications for using these deviates to make unbiased predictions for input to stochastic model projections. Key conclusions were:

- Subtractive log-normal bias correction is an essential adjustment for satisfying the assumption for the mean of a distribution generated from a set of log-normal deviates to be equivalent to the mean of the predictor.
- In the case of the example and given the variance of the recruitment deviates, the effect of the subtractive log-normal bias correction was a 13% reduction in the mean of the recruitment distribution generated.
- If the estimated recruitment deviates are to be applied in a predictive context, (such as for stochastic projections), with the assumption that the mean of the distribution generated from a recruitment predictor, (e.g. BH-SRR), is to be equivalent to the predictor, it is essential for the model estimation constraint in Eq.3 (Kleiber et al. 2012, Appendix A) to be satisfied.

Further work on this new feature is proposed for 2012-13.

Functionality for multiple species/stocks/sexes

This development has been in progress since July 2010 and is to increase the dimensionality of MFCL to accommodate multiple species, stocks and sexes. This development entails a fundamental and large scale modification to MFCL and is the core task in the current project which is still in progress.

Rationale

This is a substantial development to the model since it changes the fundamental structure of the model by expanding the dimensions at the regional level and among all parameters. It has important benefits for modeling Pacific tuna and billfish populations which often have sex-specific growth rates, or regional differences in growth (Nicol et al. 2011). Parameters specific to sex, species, or stocks may be accommodated and, if required, shared among selected dimensions. This may reduce the number of parameters required in fitting models for species that share fisheries having the same characteristics.

Methods

For the development, in 2011 test data sets were created for bigeye and yellowfin for either 5 or 6 regions, using a reduced model time period (1990-2009) so as to facilitate rapid computation while yet retaining the full extent of parameters required for the large tuna assessment models. The input “frq” file format was changed to integrate multiple

sex/spp/stock catch, effort and size composition data within one file. Source code has been adapted for the increased dimensions and model fits to multi-species data have been completed.

A large part of the December 2011 workshop was dedicated to this development, with the aim of achieving convergence of the multi-species model (MSM) fit to multi-species input data with the corresponding single-species model (SSM) fits to the equivalent single-species data. The main development areas of this workshop included:

- A new matrix structure was applied to all multi-species class members to ease their access within various routines, entailing substantial changes for the model variable *nat_mort_coff*;
- Applied the new matrix structure to length-weight parameters *sv*(27, 28) and coded their access throughout;
- Developed new member routines in the class *dvar_fish_stock_history* for returning the appropriate parameters specific to each species via an easy call within any routine;
- Applied the new multi-species structure to *wmid*;
- *age_flags* were extended to the multi-species dimension in order for parameterisations to be specific among species; and a routine was added that returns the *age_flag* value for a given species or region;
- The routine *get_initial_equilibrium_survival_ms()* was made from a copy of the original to deal with the multi-species context;
- Penalty calculations were identified for those to be calculated over all regions and to extend these to the multi-species context using the *region_bounds* object to denote the extent of the regions for each species;
- The new multi-species *age_pars*, *pmsd->age_pars(3)*, were added to the X-vector of estimated parameters in **newmaux.cpp** which required a call to **set_value_partial()**;
- A new member was added to the *multi_species_data* class: *pmsd->region_rec_diff_coeffs(2,num_species, 1, nyears)*; with the constructor allocation made in **rnau2.cpp** These parameters were added to the X-vector of estimated parameters in **newmaux.cpp**. The parameterisation was extended for the initial equilibrium calculations in **getinp2.cpp** to accommodate multi-species and for calculating equilibrium yields for each species.

In summary, substantial progress was made during the workshop with modifications made to 50 source code files. Multi-species *age_flags* were created to make parameterisations and model structural assumptions specific to each species. A number of new routines were added that return parameters, *age_flags*, and species or region identifiers to model routines entailing calculations using length-weight, natural mortality, or growth parameters for multi-species. Test runs using the revised code indicated improved convergence towards the equivalent model fits obtained using the single-species model code, however, differences persisted, indicating certain parameters or functions required extension to the multi-species context.

Following the workshop further developments were made including:

- Extending the annual recruitment deviations for multi-species;
- Reporting of multi-species parameters and model estimates into a new file format that could be viewed in a revised version of MFCL-viewer;
- Improving the penalty calculations for estimated recruitments to be robust to the multi-species context;
- Adding the estimation of the multi-species growth parameters *pmsd->vb_coff*;

- Separating the BH-SRR parameters for each species with the equilibrium yield calculated for each. This entailed a large new section for *nwt* calculation and fishery-specific F multipliers for the yield analysis of each species;
- Adding a new object *get_fishing_mortality_by_age_by_year()* and *mean_length_calc()* was adjusted according to the *region_bounds* for each species with a new function call *get_var_coff_species()*;
- Changing to the region loops in **mlcalc.cpp** with fixes to the calculation of multi-species *mean_length_yr* via calls to *get_age_pars_species(isp,3)* for the *mean_length_yr()* calculation, and for the region-specific *lwc* adding a call to *get_len_wt_coff_region(ir)*;
- Assigning *vb_coff* and *var_coff* for each species for the calculations of *sigma* and *obstacatch* in the routines *observed_tags_by_age_from_length()* and *observed_tags_by_age_from_length_pooled()*.

These further developments entailed calculating equilibrium yields and the dynamic annual size compositions for multi-species, and are currently being tested to ensure the integrity of model calculations for each species using the framework described in the following section. Currently, the multi-species calculations for a single model evaluation produce identical results (to at least 6 decimal places) to that of the obtained using the MFCL release version (1.1.4.2) using the equivalent single-species inputs. Differences that persist between a fit to multi-species data to that obtained using single species data are currently being investigated.

Testing

Testing of the components is an ongoing and essential part of the development, with a comprehensive examination of all model quantities occurring upon completion to ensure the model calculations maintain integrity. A comprehensive testing framework was developed based upon that described in the section – Testing framework (above), to undertake pair-wise comparisons of model results obtained using the current release version of MFCL (1.1.4.2) having single-species dimensionality (SSM), versus those obtained using the multi-species development code (MSM). The framework entails two levels of tests, firstly using single-species input data, and secondly using multi-species input data (Table 1). In each level, two types of tests were undertaken, (a) being a single model evaluation using a predefined input parameter file (*.par*), and (b) being a full *doitall* model fit entailing a large number of evaluations in the final phase. The single model evaluation indicates the model functionality to be identical for both the SSM and MSM, and therefore whether the MSM development version maintains the integrity of model calculations of population state and statistical likelihood terms given a deterministic model run using a specific set of input parameters. The full *doitall* model fit indicates whether the MSM maintains the integrity for converging to the original solution over a large number of evaluations as was obtained from the SSM.

The first level of tests using single-species data was to validate that the MSM maintains integrity for its application in a single-species context, and entailed comparing the results of SSM versus MSM for both test types (a) and (b). The second level of tests using multi-species data validated that the MSM maintains integrity for its application in a multi-species context, and entailed comparing the results for each species versus the respective results obtained by the SSM for test type (a), and a comparison of the results for each species versus the MSM fits obtained using the single-species data in test type (b). It was necessary to increase the precision to 8 decimal places for model quantities and objective function components places to ensure the comparisons were comprehensive.

The current results from the testing framework are shown in Table 1. The first level of tests confirm the integrity of the MSM with identical model quantities and almost identical

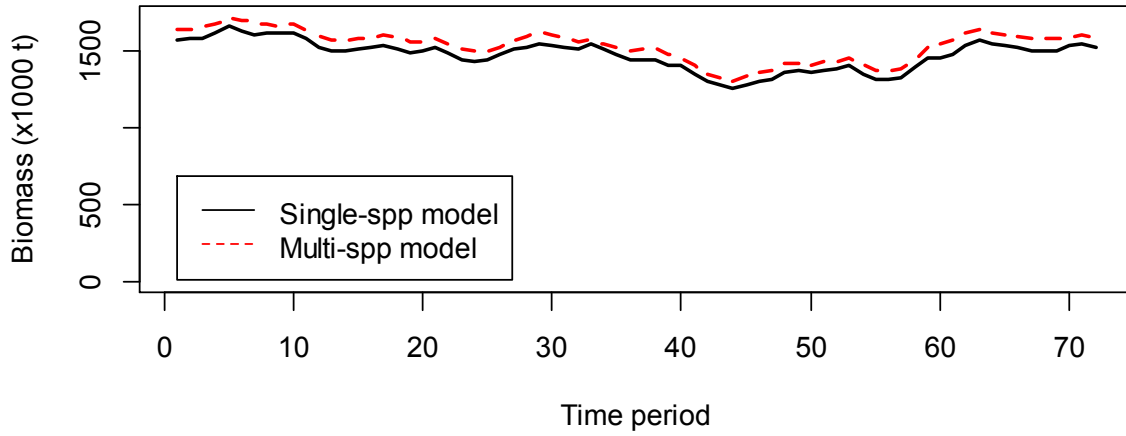
objective function values (to within 8 decimal places) obtained from single evaluations compared to those from the SSM. The MSM converges to an objective function value that is within 0.001% of the solution obtained using the SSM (Table 1), suggesting that the sequences of some calculations are altered in the MSM that slightly affects the likelihood and penalty calculations. However, the model quantities of this solution were essentially identical to that of the SSM solutions. These results satisfactorily attest to the integrity of the MSM in undertaking single-species calculations.

The second level of tests are not yet completed, with current results indicating the MSM is close to achieving integrity when applied to multi-species data. Single evaluations using input parameters in multi-species format (but generated from the SSM fits to single-species data) generate identical model quantities to the SSM, but the objective function value and number of parameters remains different (Table 1). This difference is then reflected in the test results from the doital fit to multi-species data with very similar model quantities but a different objective function value and one less parameter. The close similarity in the model quantities is illustrated in a comparison of the model biomass estimated for each species using the MSM and SSM models (Figure 1). The outstanding differences in the MSM results are currently being investigated and are most likely attributable to the estimation of *age_pars()* associated with the growth function for species 2 which are noticeably different (Figure 2).

Table 1. Testing framework using release version of MULTIFAN-CL (single-species code, SSM) to validate multi-species development version (MSM) using data in either single-species or multi-species formats.

Model operation tested	Input data	Comparison	Result	Objective function	npar
1. Single-species data tests					
a. Single model evaluation using input .par from SSM fitted solution	Single species data for YFT and BET	SSM vs MSM	Identical model quantities. Almost identical objective function (to within 8 decimal places)	Spp1 = 492295.814 Spp2 = 464139.655 Sum = 956435.469	Spp1 = 2553 Spp2 = 2495 Sum = 5048
b. Doitall fit solution (8000 evals in phase 12)	Single species data for YFT and BET	SSM vs MSM	Almost identical objective function (to within 6th sign.digit, 0.001%)	Spp1 = 492351.509 Spp2 = 464344.602 Sum = 956696.111	Spp1 = 2553 Spp2 = 2495 Sum = 5048
2. Multi-species data tests					
a. Single model evaluation using multi-species input both_ssm.par (combined SSM fitted solution .par both spp)	Multi-species data	SSM vs MSM	Identical model quantities; Different objective function value and one less parameter.	953431.227	5047
b. Doitall fit solution (8000 evals in phase 12)	Multi-species data	MSM vs MSM fits to single-species data	Similar model quantities Different objective function value and one less parameter.	955458.190	5047

Single species vs Multi-species Total Biomass: species 1



Single species vs Multi-species Total Biomass: species 2

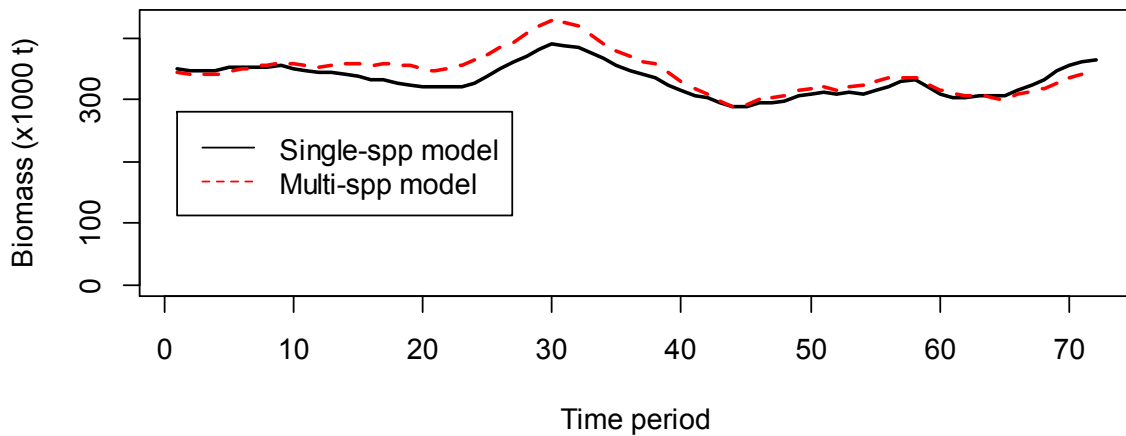


Figure 1. Comparison of the total biomass for species 1 and 2 estimated separately using a single-species model (SSM, black lines) and estimated combined within a multi-species model (MSM, red dashed lines).

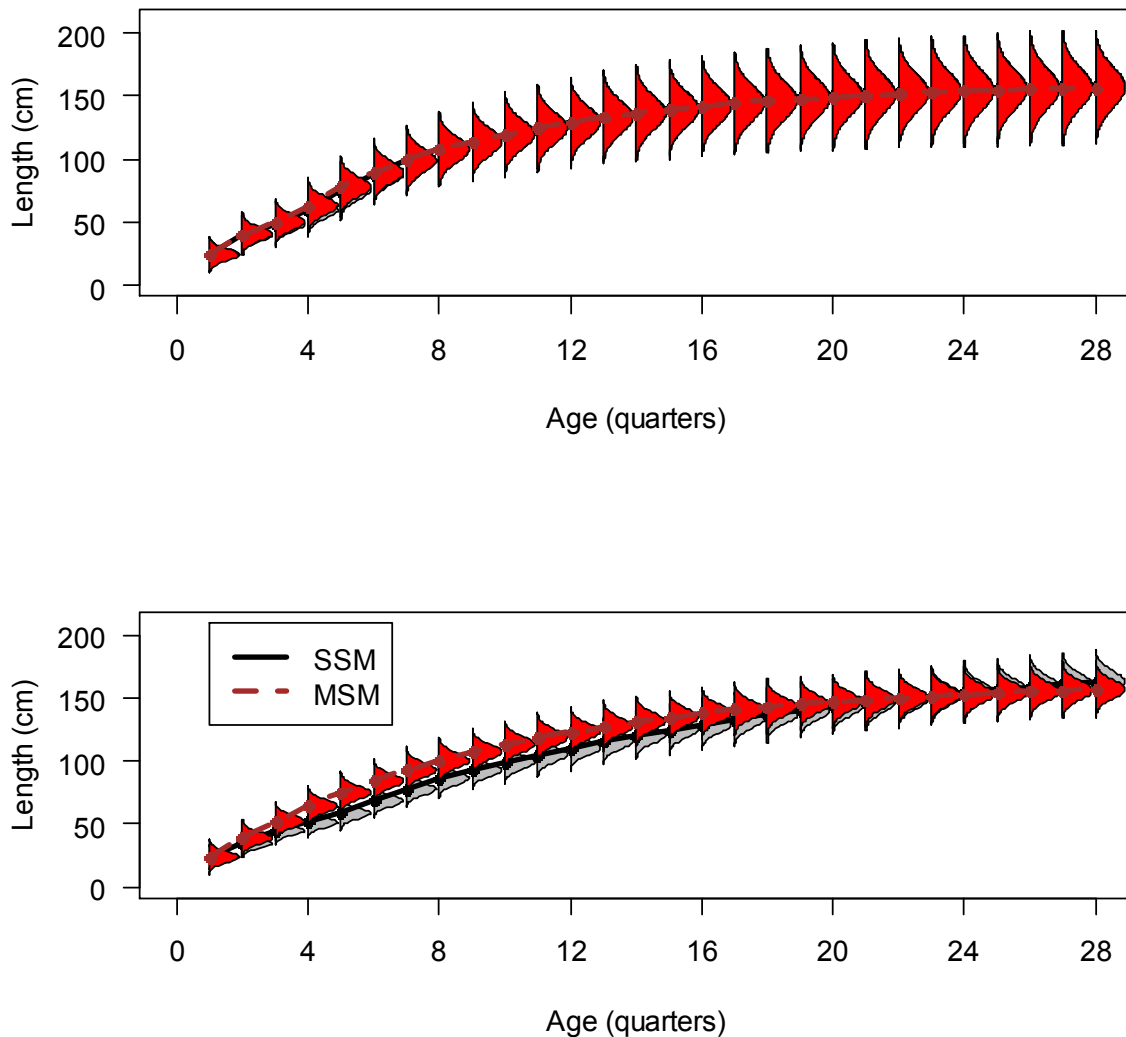


Figure 2. Mean length-at-age for species 1 and 2 (top and bottom, respectively) estimated separately using a single-species model (SSM, black lines) and estimated combined within a multi-species model (MSM, brown/red dashed lines).

Log-normal bias correction of Beverton-Holt stock-recruitment relationship predictions

Comparisons of the biomass trajectories of stochastic projections using random absolute recruitments with those of deterministic projections using recruitments predicted from the Beverton-Holt spawning stock recruitment relationship (BH-SRR) have highlighted differences attributable to model assumptions made for the recruitments. These differences are described briefly to explain the model assumptions and summarise the issues addressed in reviewing these model assumptions by means of applying a correction to predicted recruitments. This has important implications for equilibrium yield calculations and deterministic projections under mean recruitment based upon either the estimated absolute

recruitments or predictions from the BH-SRR. An example is used (BET 2011 assessment model) to illustrate the effects of applying the correction on deterministic projection and equilibrium yield estimates.

Rationale

Estimated annual recruitment (deviates) are highly variable and differ considerably from the SRR predictions in each year (Figure 3). These absolute recruitments appear to be log-normally distributed (in normal space) but are approximately normally distributed when log-transformed. In the example model the differences between the mean of the recruitments estimated and those predicted by the BH-SRR are substantial in normal space, around 14%, and the difference becomes larger for the projection period, around 19% (Table 2). However, the differences in the means are negligible when log-transformed. This difference of 14% is close to that between the median and mean of the estimated recruitments in normal space (15.4%), which indicates that the $\exp(\text{mean of the BH-SRR predictions})$ is equivalent to the median of the estimated recruitments. The BH-SRR therefore appears to be derived from a fit to the estimated recruitments in log-space where the errors are normally distributed. For the BH-SRR predictions to approximate the mean of the estimated recruitments, rather than the median, a correction for log-normal bias may be applied. On this basis, such a feature was added as an option to MFCL.



Figure 3. Recruitments as predicted from the BH-SRR (line) and the estimated recruitments (circles) as deviates from the relationship for each time period, with the SRR predictions for the projection period shown. Example is the BET 2011 assessment model.

Table 2. Summary of mean recruitments as predicted from BH-SRR and as estimated for the model estimation and projection periods. (%differences are with respect to means of SRR predictions).

Notation:

\hat{Y} : the BH-SRR mean predicted recruitment over the estimation period (in log-space)

\hat{Y}_p : the BH-SRR mean predicted recruitment over the projection period (in log-space)

\bar{R} : the mean of the absolute estimated recruitments

md(R): the median of the absolute estimated recruitments

	log-space			normal space				
Estimation period	\hat{Y}	log(\bar{R})	%dif	exp(\hat{Y})	\bar{R}	%dif	md(R)	%dif md(R) vs \bar{R}
	15.708	15.713	0.03	6642591	7564098	13.87	6556500	15.37
Projection period	\hat{Y}_p	log(\bar{R})	%dif	exp(\hat{Y}_p)	\bar{R}	%dif		
	15.731	15.713	0.29	6370243	7564098	18.74		

Methods and Testing

The development was added as part of the December 2011 workshop with the assignment of *age_flag*(161) for adding the option to include a log-normal bias correction to average recruitment predicted from the Beverton-Holt stock-recruitment relationship.

A bias correction may be applied to the recruitment predictions from the BH-SRR. Using the estimated error distribution of the BH-SRR, corrected predicted recruitments (\hat{Z}) may be calculated:

$$\hat{Z} = \exp \left[(\hat{Y}) + \frac{s_{\log(R)}^2}{2} \right]$$

Where $s_{\log(R)}^2$ is the variance of the BH-SRR predicted recruitments (in log-space), and in the example used is equal to 0.277. The effect of the correction is shown in a comparison among the mean recruitments as predicted from the BH-SRR uncorrected and corrected for bias, (Table 3). The percentage difference was of a similar order to that between the mean of the estimated absolute recruitments and the BH-SRR uncorrected predictions, indicating that the bias corrected predictions were consistent with the absolute estimated recruitments.

Table 3. Summary of mean recruitments (in normal space) as predicted from BH-SRR, with and without a log-normal bias correction. (%differences are with respect to the mean of SRR predictions uncorrected for log-normal bias).

Estimation period	exp(\hat{Y})	\hat{Z}	%dif
	6642591	7627908	14.83
Projection period	exp(\hat{Y}_p)	\hat{Z}_p	%dif
	6370243	7437127	16.75

When deterministic projections were undertaken assuming constant future recruitment at a level of the average of estimated recruitments, the mean projection biomass corresponded closely to that of the mean of the stochastic recruitments (Figure 4). This simply confirmed the simulation algorithm in which future recruitments are bootstrapped from the estimates. However, in contrast the biomass trajectory of the deterministic projection that assumes recruitments predicted from the BH-SRR uncorrected for log-normal bias was 20% lower by the end of the projection period. Correction for log-normal bias in BH-SRR predictions reduced this difference to only 2% lower than that of projections assuming the average of the estimated recruitments.

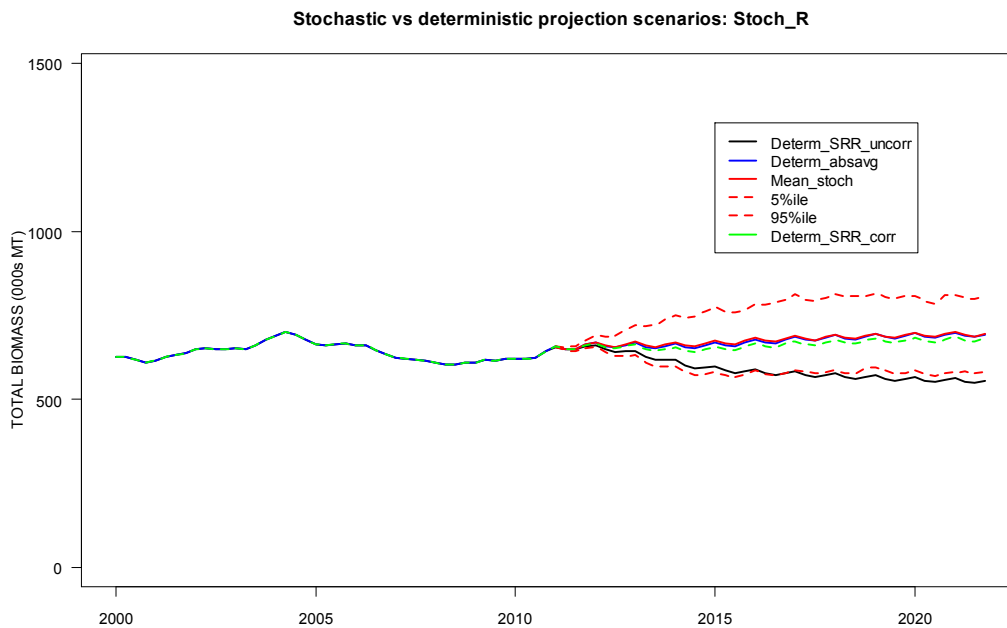


Figure 4. Total biomass over the estimation and projection periods, with deterministic projections assuming three recruitment options: predicted from the BH-SRR uncorrected or corrected for log-normal bias (Determ_SRR_uncorr or Determ_SRR_corr), and the average of the absolute recruitments over the estimation period (Determ_absavg). Mean total biomass is shown from 200 stochastic projections with recruitments sampled from the absolute recruitments over the estimation period (Mean_stoch, and 90 percentiles).

Implications for MULTIFAN-CL yield estimates

Correction for log-normal bias can also be applied to the BH-SRR predictions used for calculating yields, fishing mortalities and population biomass at equilibrium. The percentage difference in the uncorrected and corrected BH-SRR average predictions over the range of the spawning stock biomass corresponding to the estimated recruitments was an increase of 14.83% for the corrected predictions (Figure 5). Consequently, this increased surplus production at levels of spawning biomass (Figure 6) with a higher maximum sustainable yield (MSY) and associated biomass, (SB_{MSY}).

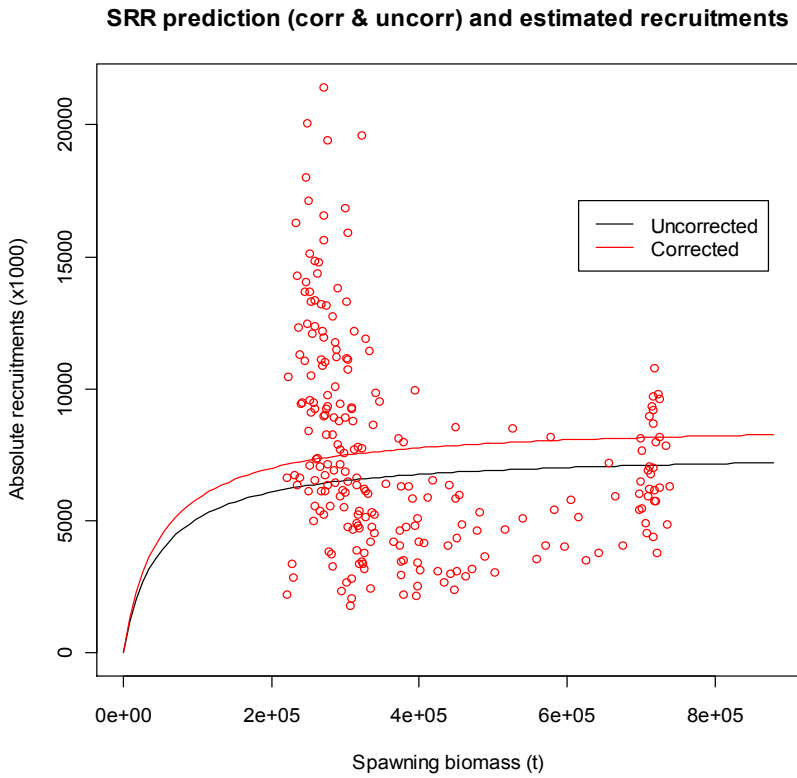


Figure 5. Estimated absolute recruitments (red circles) and the uncorrected (black line) and corrected (red line) predictions of the BH-SRR.

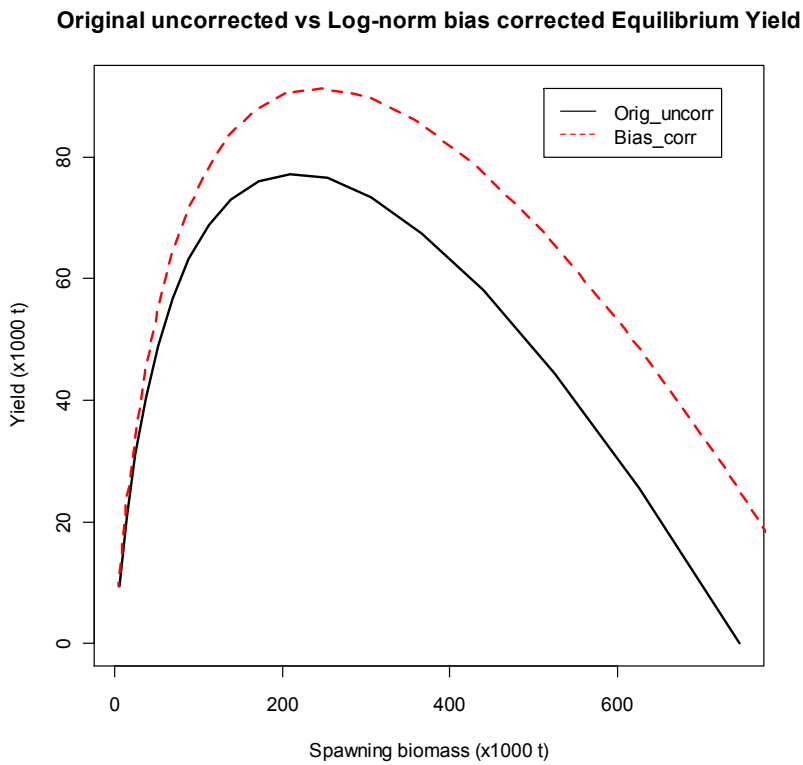


Figure 6. Equilibrium yield at spawning biomass levels derived from BH-SRR predictions uncorrected (Orig_uncorr) and corrected (Bias_corr) for log-normal bias.

The correction resulted in a proportional increase in B_{msy} , B_0 , and SB_{msy} , SB_0 of 13 to 16% with negligible change in the ratios (Table 4). MSY increased by 18.3%. Since dynamic model absolute biomass estimates were relatively unaffected by the correction, the increase in the equilibrium yield reference point quantities resulted in a 12% decline in stock status; making the assessment more pessimistic. Equilibrium fishing mortalities were less affected by the correction with a 5.3% increase in F_{msy} and a 3% reduction in the overfishing quantity F_{curr}/F_{msy} (Table 4).

Table 4. Stock assessment output quantities affected by the correction for log-normal bias in BH-SRR predictions for the BET 2011 example uncorrected (orig) and corrected (corr) and showing the percentage difference in respect of the uncorrected quantity.

	orig	corr	%dif_to_orig
YF_{curr}	68720	83440	21.42
MSY	77200	91360	18.342
$YF_{curr}.MSY$	0.89	0.913	2.584
$C_{curr}.MSY$	1.829	1.545	-15.528
$C_{latest}.MSY$	1.514	1.279	-15.522
F_{msy}	0.038	0.040	5.263
F_{mult}	0.683	0.706	3.367
$F_{curr}.F_{msy}$	1.464	1.417	-3.21
B_0	1441000	1668000	15.753
B_{msy}	501600	572100	14.055
$B_{msy}.B_0$	0.348	0.343	-1.437
BF_{curr}	290700	352900	21.397
SB_0	744400	862200	15.825
SB_{msy}	216100	244700	13.235
$SB_{msy}.SB_0$	0.29	0.284	-2.069
SBF_{curr}	112200	136200	21.39
$B_{curr}.B_0$	0.432	0.374	-13.426
$B_{latest}.B_0$	0.447	0.386	-13.647
$BF_{curr}.B_0$	0.202	0.212	4.95
$B_{curr}.B_{msy}$	1.242	1.089	-12.319
$B_{latest}.B_{msy}$	1.284	1.126	-12.305
$BF_{curr}.B_{msy}$	0.58	0.617	6.379
$SB_{curr}.SB_0$	0.343	0.296	-13.703
$SB_{latest}.SB_0$	0.314	0.271	-13.694
$SBF_{curr}.SB_0$	0.151	0.158	4.636
$SB_{curr}.SB_{msy}$	1.181	1.043	-11.685
$SB_{latest}.SB_{msy}$	1.082	0.955	-11.738
$SBF_{curr}.SB_{msy}$	0.519	0.557	7.322

Other enhancements and bug fixes

A listing of the current and proposed tasks in the project is presented in Table 5. The main developments against tasks 40, 25, 4, 41, 42 and 46 completed to date and in progress have been discussed above, and other lesser enhancements and fixes are briefly mentioned below.

New input .ini file format

For MFCL version 1.1.2.0 the *.ini* file format was modified to entail the streamlined input of the parameters associated with estimating recapture rates of tagged fish relative to both release group and fishery group. This required including an *.ini* file version number at the top of the file. For MFCL version 1.1.3.1 the reading of the *.ini* file was modified to ensure backward compatibility for early MFCL versions. In the absence of a file version number, the earlier format is assumed, otherwise the new version number is input from the first line and the format is defined.

Output file control

It may not always be efficient to produce the full output from a MULTIFAN-CL model as this requires more processing time and entails producing what are sometimes large files. For example when multiple model projections are undertaken, it is efficient to reduce the output from a single model evaluation. This output can be controlled using *parest_flags*(186 to 190) and is as follows.

parest_flag (190) = 0 : generates par file, turns off output of *plot.rep*, *plotq0.rep*, *ests.rep*, *temp_tag_report*, *fishmort* files and other report files.

parest_flag (190) = 1 : turns on output of report files subject to options specified by *parest_flag*(186 to 189) as follows:

- *parest_flag* (188) = 0 : turns off *ests.rep*, *tag.rep*, *.fit*
 - *parest_flag*(189) = 0 : turns off output of the *.fit* files
- *parest_flag* (187) = 0 : turns off *temporary_tag_rep*
- *parest_flag* (186) = 0 : turns off *fishmort* and *plotq0.rep*

This facilitates output according to three options:

- Full output: 1 189 1 1 190 1 1 188 1 1 187 1 1 186 1
- Streamlined option: 1 189 0 1 190 1 1 188 0 1 187 0 1 186 0
- Silent option: 1 189 0 1 190 0 1 188 0 1 187 0 1 186 0

Note that output of the *.fit* files requires *parest_flags*(190, 188, 189) to be set to 1.

Fixes

A single fix was made to the formulations in MFCL in 2012.

Maximum projection fishing mortality

The maximum fishing mortality value has been raised to facilitate very high potential "observed" catches being achieved in model projections. This prevents Newton-Raphson

solutions that result in model catches in projections being lower than the values input in the *.frq* file fisheries data for projection years.

Application of new features

Several of the new features described above have been used as part of the 2012 tuna assessments. The general nature of the application is described and the significance of its utility for the management of tuna outlined.

Log-normal bias correction of the Beverton-Holt stock-recruitment relationship calculation

Equilibrium yield estimates calculated using a SRR derived from the stock-recruitment relationship with the log-normal bias correction were routinely reported for the striped marlin (Davies et al. 2012) and albacore (Hoyle et al. 2012) stock assessments. In both cases it was considered that the mean of the estimated absolute recruitments was the preferred basis for calculating equilibrium yields rather than the median, and therefore the option for log-normal bias correction was applied. This preference is consistent with the advice given by an independent review panel that the bias-correction be applied if estimates from the deterministic yield function are presented (Ianelli et al. 2012).

Stochastic projections

Berger et al. (2012) introduced the concept of harvest control rules (HCRs) for Western-Central Pacific Ocean (WCPO) tuna management and presented specific example HCRs applied to the skipjack (effort-based rules) and South Pacific albacore (catch-based rules) fisheries to demonstrate the process for evaluating alternative HCRs. This study employed the stochastic simulation tools for projections with no fishing and used the output of projected fishing mortalities. Figure 7 shows estimates for the probability of future biomass exceeding a reference point that is a percentage of the unfished future biomass (40% B unfished), and the probability of the ratio of future fishing mortality and F_{MSY} exceeding 0.8, for a range of six alternative HCRs considered for skipjack. A similar application of these features by Harley et al. (2012) enabled the evaluation of stock status of tunas and striped marlin against potential reference points, including those relating to fishing mortality and biomass predicted in the absence of fishing. These studies demonstrate the immediate utility of the newly developed applications and outputs from stochastic simulations for formulating advice to fishery managers on the relative performance of alternative management strategies.

The new MFCL facility that enabled repeating a single stochastic simulation but with modified fisheries data in each repetition was used by Berger et al.(2012). For each projection a HCR might be evaluated several times over the projection period. This entailed re-running the same simulation so as to evaluate future population states under the stochastic recruitments unique to that simulation, and evaluating the HCR, after which the fisheries data for the subsequent period was modified, and then to repeat this process. Customised R script was drafted that modified the input file containing stochastic recruitments and the `age_flags[20]` option was set to 1.

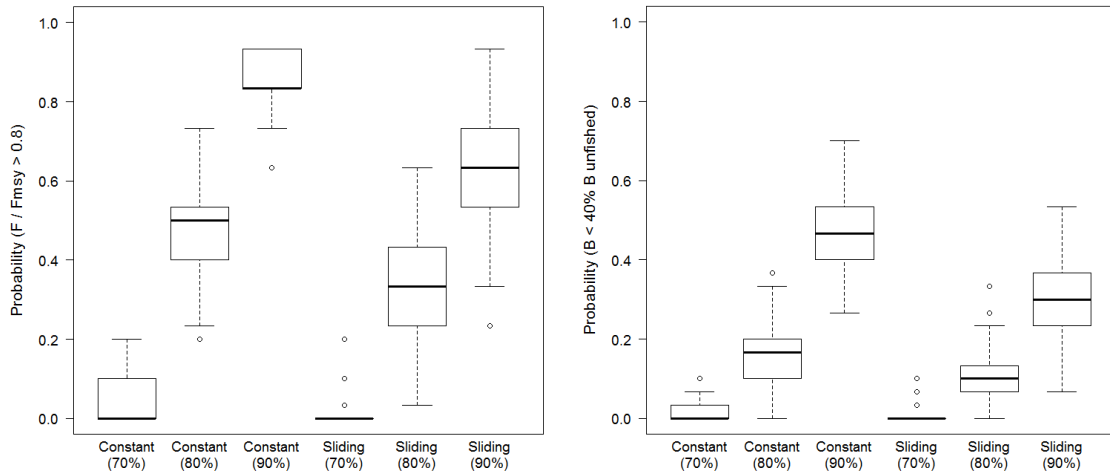


Figure 7. Boxplots showing the distribution across simulations for the probability of exceeding hypothetical skipjack target and limit reference points for each of the example HRCs examined. Median represented by the horizontal line of the box. Boxes represent the 25th, and 75th percentiles, whiskers show 5th and 95th percentiles. (Taken from Berger et al. 2012).

Future work

The current and future work plan for MFCL is outlined in Table 2 with those having high priority being assigned a priority identification of 5. Tasks of immediate priority are discussed in the following section.

Discussion

Substantial changes have been made to MFCL during 2011-2012, with most relating to the multi-species development and stochastic simulation functionality. Although a fix was made to the source code addressed problems with model formulations, this related to model projections and did not change the management implications of model results, such as stock status relative to reference points employed by the Commission, in any significant way.

The most significant development made during 2011 in terms of both developmental effort expended, and importance for tuna stock assessments, has been in modifying the underlying structure of MFCL by expanding the regional dimension to accommodate multiple species, stocks or sexes. This has entailed substantial coding modifications for dealing with additional inputs, expanded parameter structure, and modifying object structures at a basic level. Progress on this development has been good with the comprehensive testing of the multi-species application showing positive results with convergence nearly being achieved against the single-species test case. The significance of this development for tuna stock is increasing, with recent important findings of heterogeneity in growth among regions and sexes (Nicol et al. 2011). This development will continue to attract the highest priority for 2012-13 and is anticipated to be completed in the next year.

Increasingly MFCL is being used to evaluate potential management strategies and so the stochastic projection functionality has a significant role in the advice supplied to the Commission. Good progress was made with adding functionality to the structural projection assumptions (i.e. future recruitments derived from a pre-defined model period), but in particular the capability for stochastic projections under zero-fishing. The work completed in

2012 in this respect has been valuable, enabling evaluations of alternative management strategies (e.g. harvest control rules) and references points to be done over a wide range of species and reported to the Scientific Committee. Given the computationally-intensive nature of these applications for MFCL, the control of output files being written during projection model evaluations has greatly improved efficiency. Further progress is needed to consolidate these developments with testing of the stochastic variables: numbers-at-age in the first projection year, and fishery effort deviates. This has been given priority for 2012-13, but it also identified a need to complement MFCL with the SVD diagnostic tool (Table 5).

As in previous years, considerable further work is required to comprehensively test all changes to the model made in the past and currently, and to update all the changes to the manual. The development of the automated testing framework in 2012 is anticipated to increase the rate at which new compilations and specific new features are tested. This remains a high priority task for 2012-2013, with the new features relating to tagging being top of the list.

A necessary task for 2013 is to update the support utilities for MFCL because increasingly model evaluations are made within the structure of a particular project such as a stock assessment analysis. Examples include, structural uncertainty grid analysis, risk analysis, or evaluation of alternative management options (TUMAS). These tools have been developed somewhat independently of the MFCL project repository. Generalizing these tools for their wider application and including them in the R4MFCL repository would assist in avoiding conflicts among their applications in combination with R4MFCL tools, and would keep track of their developments needed in line with new versions of MFCL.

Table 5: 2012-2013 work plan for MFCL, including work completed and suggested future enhancements. TBA = to be assigned

GF ID	Item	Description / Comment	Priority (high=5)	Who	Comments
PROBLEMS					
TBA	Projection recruitment problem	For the projection recruitment option with full period SRR average recruitments, when run with F _{q0} , projection recruitments are distributed uniformly and not according to the average regional distribution used when F>0.	5	Nick	Pending
TBA	Projection problem	SKJ model crash under FMSY harvest strategy	5	Nick	In progress
Add	Projection problem	Possible problem with effort devs and catchability dev with zero effort devs in the projections. Large change in F. May require change to projection approach. Cause needs more analysis - initially try q devs at shorter time step.	5	Dave	Pending
NEW FEATURES					
40	Multi-species/stock/sex dimensionality	<ul style="list-style-type: none"> - merge Dave's Multi-spp. version of the source with release version (1.1.4.2) and place in the repository development branch - complete testing of development version - extend application to multiple sex and various input formats 	5	Dave/Nick	In progress - inputs and operation complete; development executable being tested.
19	Region-specific environmental recruitment correlates	Allowing for recruitment deviates in each region to be correlated with some environmental variable. See the following file for a discussion of recruitment modelling options: I:\assessments\Pop dy modelling\MFCL\Recruitment.doc	3		Pending
20	Selectivity varying with a covariate	Implement a scheme to allow time-series variation in selectivity, both as a random effect and correlated with an environmental or other index (e.g. mean latitude fished)	2		Pending

21	Individually-specified penalty weights for movement coefficients	Allow individually-specified penalty weights (priors) for movement coefficients to constrain parameters and make them estimable. Probably best done in conjunction with 23 and 24 when the new tagging data is incorporated.	3		Some structure there now but we probably want something more flexible. Pending
22	Seasonally varying selectivity coefficients	Implement a scheme to estimate seasonal variability in selectivity coefficients	4	Dave	Pending
24	Time-series variation in movement coefficients	Implement a scheme to allow time-series variation in movement coefficients correlated with an environmental index. Probably best done in conjunction with 21 and 23 when the new tagging data is incorporated.	3	Dave	Pending
25	Stochastic projections	Generate "simulation_numbers_at_age_F0" directly from the Hessian and integrate Fnorm and F0 deterministic projections; Option for defined period over which stochastic recruitments are bootstrapped Develop an algorithm that accounts for future spawning biomass: random resampling from historical recruitment deviates (as a proportion of SSR predicted recruitment given SB) and apply to f(SSR,SB) in year t_proj.	5	Dave, Nick	Complete - variability in recruitment (resampled). Further testing of effort devs, and numbers-at-age in 1st projection year in progress. Deviates on the BH-SRR still being developed.
26	Estimate biological parameters at length	Maturity, fecundity, spawning fraction are typically length-specific properties (at least the data on them is) and so they are converted to age based on the initial growth curve. As soon as a growth curve is estimated there is an inconsistency.	3		Pending
36	Yield-related analysis capabilities	Estimate indicative yields by fishery for both MSY and Equilibrium yield. Also estimate region-specific scalars. the current MSY calculations estimate a single F-scalar across all fisheries. Anything more than scalars would cause estimation difficulties. Required for management options project	5	Dave	Region-specific yield calculations are already an option in MFCL. (See section in code called "Daves_folly"). Pending

37	Hyperstability	Implement fishery-specific hyperstability, as a relationship between vulnerable biomass and catchability	3		Pending
38	Projections for mgmt options project	<p>1. Modify MULTIFAN-CL to run under the control of the management options application. [Probably no changes needed, but output cleanup might help]</p> <p>2. Automate production of input files for projections under alternative management options. Adding projection period into par file could be done in R.</p> <p>3. Link to an encrypted catch-effort database in order to define effects of time-area closures at one month (or less) and 1 degree square resolution (as in IATTC-77-04). (N.B. the model itself will still run at a regional level). Area boundaries will be selected from a predefined set, in order to help maintain data confidentiality.</p> <p>4. Link to encrypted catch-effort database and estimate indicative yields by location.</p>	5	Fabrice + Dave + Simon + Shelton + Nick	Mostly completed as input to the TUMAS project. Tasks 3 and 4 are still in progress
TBA	Kobe mode	Create a "Kobe" mode of operation that does a single evaluation with no output to .par and output to new kobe.rep containing: year, F/FMSY, SB/SBMSY, B/BMSY	3	Nick	Pending
TBA	Calibrate model over-parameterisation	<p>Design a survey of model runs with alternative penalty weights on catch devs and recruitments to attempt to reduce overparameterisation and reduce variance</p> <p>The survey involves increasing the penalty on total catch errors and evaluate if the minimisation time is reduced and there is convergence to a shared solution.</p> <p>Recruitments could be restricted in some way in the last so many years because these are always highly variable. The amount of restriction could be justified by likelihood ratio tests. Check to see if there is existing code to put specified penalties on the terminal recruitment deviates (something with pf(148)), but if not, draft some.</p> <p>There is also the orthogonal recruitment code (perhaps that applying to seasonal recruitment indices with deviates), which needs to be checked and tested.</p>	3	Nick	Pending
TBA	Dynamic MSY	<p>Develop a dynamic MSY calculation for each year that uses all parameters (incl. annual recruitment) for that year and applies the Fmsy to the population state in that year to generate a predicted ""MSY"" catch. It is likely that this MSY catch will be more comparable to actual catches.</p> <p>Output formats for MFCL_viewer (Fabrice)</p>	2	Nick/Dave	Pending

TBA	Singular value decomposition	Singular Value Decomposition: confirm its utility as a tool for model selection or diagnostic tool. If it is to be included as a standard feature, then get Lapack libraries for windows and develop Windows compilation. Get mini SVD code compiled and evaluate.	2	Dave	Pending
OUTPUT					
13+	Report likelihood components	A new output file should be created that provides all values for penalties and likelihood components. For diagnostic purposes it would be good to have it for each phase. Generate an output table of likelihood components and develop an index of data conflict (likelihood ratios) that is output for each cell of the SUA grid. This may be used to indicate those cells with parameters that reduce the conflict.	5	Nick/Dave	Pending
TBA	Cut down dep vars	Design a new dependent variable report (i.e. *.dep -> *.var) that is relevant for what we now need for our assessments. The existing one, if it works, contains a lot of time consuming stuff that is no used.	4	Pierre	Pending
TBA	Tagging results output	Determine which of the three alternative tag output files is correct. (see notes in Appendix A); Which contains the correct report? Output formats for MFCL_viewer (Fabrice)	5	Nick/Dave	In progress
OTHER					
4	Testing 1	Set up an automated procedure for testing MFCL executables before use. 1. Design a set of doitall files that test the full range of important MFCL options. This would initially be the current doitall's for the YFT SKJ BET and ALB assessments. 2. Store the output files the above runs with a stable version of MFCL in a test directory. 3. Write an R script to produce figures that compare outputs between the 'good' runs and the new runs. 4. Write an R script to automate the whole procedure including (as an option) submitting all the runs to condor.	5		Completed
41	Testing 2	Set up "cut-down" models (say 1987 init-year) for quick runs and testing, one for each species. Follow John's approach for modifying the *.par file according to a specified 00.par file. Enables rapid runs for checking code operation.	5	Nick	cutbet - completed; cutyft - complete
42	Testing 3	1. Release group-specific tag reporting rates; any changes to format may entail new output formats for MFCL_viewer (Fabrice)	5	Nick	1. Is complete 2. to 5. Are in progress

		<ol style="list-style-type: none"> 2. Tag-fishery-specific reporting rates: the short time span obviates the need for time series changes does not necessarily apply to the pooled tags. The effect of this should be tested when the time-period pre-pooling is short and the tagged fish lifetime is long. 3. Fit to tags during the mixing period - test alternative parameterisations (remove observed, estimated + scaled by reporting rates) 4. Catch-conditioned model (see Appendix B) 5. Length-based selectivity 6. Structured recruitment estimates - seasonal recruitments +annual deviates; find out if this is the orthogonal recruitment feature; test to see if this works" 			
43	Compilation 1	Create standard VS2010 platform with SP1 for windows compilations.	4	Nick	Complete
44	Compilation 2	Include Lapack library for single value decomposition in Windows compilation	4	Dave, Nick	Pending
45	Compilation 3	Review outputs and temporary file use (Gforge tasks 47 - 50)	4	Nick	Complete
46	Equilibrium yield calculations	Check whether the equilibrium yield calculations include a log-normal bias correction for the recruitments (if not, this might explain the generally lower eq.yield estimates relative to catch)	5	Nick/Dave	Complete
TBA	Tagging likelihood negative binomial	Clarify and test the current parameterisation of the tagging negative binomial and zero-inflation used in the tagging likelihood term for the options of pf(111) either 3 or 4, and confirm the effects of the mixing terms	5	Nick/Dave	Pending
TBA	Static linking	External dlls currently have to be ported with the Win32-bit executables: msvcP100.dll, msvcr100.dll. For MFCL to be completely portable, on its own or with TUMAS, we need to identify what DLLs are required. Ideally, these should all be statically linked during compilation. A test should be developed on a "naked" windows platform that could identify all the required DLLs. Then revise the build options make them all statically linked.	5	Nick/Fabrice	Pending

Reference List

1. Berger, A., Harley, S., Pilling, G.M., Davies, N. and Hampton, J. 2012. Introduction to harvest control rules for WCPO tuna fisheries. WCPFC-SC8-MI-WP-03
2. Davies, N. and Harley, S. 2010. Stochastic and deterministic projections: a framework to evaluate the potential impacts of limit reference points, including multi-species considerations. Secretariat of the Pacific Community No. WCPFC-SC6-MI -WP-01
3. Davies, N., Hoyle, S., Fournier, D., Kleiber, P., Hampton, J., Bouyé, F., and Harley, S. 2011. Update of recent developments in MULTIFAN-CL an related software for stock assessment. WCPFC-SC7-ME -IP-04
4. Davies, N., Hoyle, S., Harley, S., Langley, A., Kleiber, P., and Hampton, J. 2011. Stock assessment of bigeye tuna in the western and central Pacific Ocean. WCPFC-SC7-2011/SA-WP-02
5. Davies, N., Hoyle, S., and Hampton, J., 2012. Stock Assessment of Striped Marlin in the southwestern Pacific Ocean. WCPFC-SC8-2012/SA-WP-05.
6. Fournier, D.A., Hampton, J., and Sibert, J.R. 1998. MULTIFAN-CL: a length-based, age-structured model for fisheries stock assessment, with application to South Pacific albacore, *Thunnus alalunga*. *Can. J. Fish. Aquat. Sci* 55:2105-2116
7. Harley, S., Hoyle, S., Williams, P., Hampton, J., and Kleiber, P. 2010. Stock assessment of bigeye tuna in the western and central Pacific Ocean. WCPFC-SC6-2010/SA-WP-04
8. Harley, S., and Davies, N. 2011. Application of alternative reference points to WCPO stock assessments. WCPFC-SC7-2011/ME-WP-03
9. Harley, S., Berger, A., Pilling, G., Davies, N., and Hampton, J. 2012. Evaluation of stock status of bigeye, skipjack, and yellowfin tunas and southwest Pacific striped marlin against potential limit reference points. WCPFC-SC8-2012/MI-WP-01
10. Hoyle, S.D., Fournier,D., Kleiber, P., Hampton, J., Bouyé, F., Davies, N., and Harley, S. 2009. Update of recent developments in multifan-cl and related software for stock assessment. Secretariat of the Pacific Community No. WCPFC-SC5-2009/ SA-IP-06.
11. Hoyle, S., Hampton, J., and Davies, N. 2012. Stock assessment of albacore tuna in the south Pacific Ocean. WCPFC-SC8-2012/SA-WP-04
12. Ianelli, J., Maunder, M., and Punt, A. 2012. Independent review of 2011 WCPO bigeye tuna assessment. WCPFC-SC8-SA-WP-01
13. Langley, A., Hoyle, P., and Hampton, J. 2011. Stock assessment of yellowfin tuna in the western and central Pacific Ocean. WCPFC-SC7-2011/ SA-WP-03
14. Nicol, S., Hoyle, S., Farley, J., Muller, B., Retalmai, S., Sisor, K., and Williams, A. 2011. Bigeye tuna age, growthm and reproductive biology (project 35). WCPFC-SC&-2011/SA-WP-01