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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 2012 to the model and other components of the MFCL project both for the current release version (1.1.5.4), and the current unreleased development version, and updates the report for the previous period, 2011-12, (Davies *et al.* 2012).

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 (2011-12) 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 developed and tested. A formal testing procedure has been designed before source code is committed from the development branch to the trunk, and a manual for the testing of new compilations, standardizing the source code compilation procedure, and posting of executables has been drafted.

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.

Developer's Workshop

A developer's workshop was hosted by the primary developer Dr Dave Fournier at North Saanich, British Columbia, Canada, 25 October – 2 November 2012. The participants were Dr Dave Fournier and Mr Nick Davies. The main areas of development were:

- Multi-species/sex model development
- Stochastic projections
- Fixes to projections
- Compilation for Mac OS X

The specific details of these developments and corrections are provided in the relevant sections that follow.

Postings to website

There have been two postings of MFCL updates to the website since August 2012.

15 November 2012 – version 1.1.4.3

- Refinements have been made to the Hessian options 7 and 8, and improvements to the operations for stochastic simulation projections under zero fishing. These allow simulations under no fishing mortality to be run simultaneously with those under specified levels. Input and output filenames have been revised. Should simulations need to be run incrementally, e.g. to undertake Harvest Control Rule evaluations, this is now possible.

- A small fix has been made to the month doubling in respect of tagging data
- An additional output has been added to the report file *plot.rep* to include the `tag_fish_group_flags` so as to facilitate labeling the unique tagging reporting rates in the MULTIFAN-CL viewer.

25 March 2013 – version 1.1.5.4

- New age_flags[178] for applying the constraint on the sum-product of regional recruitment proportions and the regional recruitment deviates to equal 1 in each model time period. Set age_flags[178] = 1 to activate the constraint.
- New parest_flags[239] that activates stochastic recruitments in projections as deviates about the Beverton-Holt stock-recruitment relationship (BH-SRR) predictions where the deviates, including situations where the relationship are taken over a subset of the model time period.
- Revision to the application of age_flags[145] such that negative values will enable low penalty weights upon the fitting of the BH-SRR.
- A small improvement to a routine that returns the BH-SRR parameters.
- Improvements to several routines to maintain stability during the control phases.

Independent Peer Review of 2012 Bigeye stock assessment

An outcome of an independent peer review of the 2011 bigeye tuna stock assessment (Ianelli et al. 2012) was a set of recommendations for improvements and developments to the MFCL software. These aim not only to improve the software's application in the context of the bigeye assessment specifically, but also its stock assessment application more generally.

From this list, a subset of the recommendations were identified for the developments to be undertaken for 2013:

- Posting for release a completed development and implementation of a 'multi-sex' version of MULTIFAN-CL, with application to example multi-sex stock assessments. (recommendation "f")

- Completion of the development and implementation for time-varying selectivities and a scheme to estimate seasonal variability in selectivity coefficients. (recommendation "a")

- Completion of the development and implementation for conditional age-at-length data to be included in the likelihood function. (recommendation "e")

- Completion of the development and implementation of an output table which lists all of the likelihood components by fleet and automates the process of computing effective sample sizes (and other summary statistics related to the model fit). (recommendation "g")

- Completion of the development and implementation for assuming a multinomial likelihood for the compositional data in the first phases and only transition to the robust normal likelihood in the later phases. (recommendation "j")

Of the five listed above, that relating to the multi-sex application has the highest priority and has comprised the majority of work done to date in 2013. Substantial progress has been made on this task and is reported in the next section of this report. Work towards the other recommendations will be done later in 2013 and early 2014.

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 2013 stock assessments that consolidated new features to the utilities package. The repository was updated in 2013 for the current and development versions of the package.

Testing framework

The testing framework for MFCL compilations developed in 2011-12, was improved and extended during 2012-13. This framework 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. Tests are undertaken 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 doitall model fits to convergence. This ensures a thorough integrity-check of model quantities and components of the objective function prior to the distribution of new versions.

During 2012-13 the test data sets were expanded so as to include all the major tuna and billfish stock assessment data used at the Oceanic Fisheries Programme (bigeye, yellowfin, albacore, skipjack, and striped marlin). As a substantial part of the development work in 2013 related to population projections, the model operations performed in the testing framework were expanded to include stochastic and deterministic projections under a range of assumptions for recruitment in the projection period. This suite of data applications and model operations available for the testing of development versions enables a thorough evaluation of the effects of the developments.

MULTIFAN-CL Viewer

A development version of the MFCL viewer that can display the results of a multi-species or multi-sex application was updated as new output was added to the report files. 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: testing MFCL development versions prior to release; undertaking stock assessments that entail multiple model runs (e.g. sensitivity analyses), structural uncertainty 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 1.1.5.4 and this has been posted on the http://www.multifan-cl.org/ website.

New MFCL features

Stochastic population projections

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 of 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.

Significant developments were made to MFCL preceding and including version 1.1.5.4 to the features for model simulation runs that include projections into the future with stochastic recruitments. This made up a substantial component of the development work on MFCL during 2013. New features added in 2013 were:

a) improvements to the operations for stochastic simulation projections under zero fishing
b) running incremental simulations, e.g. to undertake Harvest Control Rule evaluations
c) constraint on the sum-product of regional recruitment proportions and the regional recruitment deviates to equal 1 in each model time period
d) stochastic recruitments applied as deviates to the predictions of the Beverton-Holt stock-recruitment relationship (BH-SRR) in each projection run
e) Application of deviates of BH-SRR estimated over a subset of the model time period (in progress).

Methods and Testing

MFCL currently incorporates uncertainty in the initial population state (i.e., terminal numbers at age from the main model period), 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 that the stochastic projection functionality operates according to the formulations, and includes the three sources of stochasticity.

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

a) Under zero-fishing during stochastic projections the assumed recruitment options were reviewed so as to take account of the BH-SRR predictions based upon the unfished spawning biomass. For models with multiple regions, the average recruitment distribution from the estimation model (under normal fishing) was applied to the predicted recruitment under zero-fishing in the projection period.

b) Harvest Control Rule (HCR) evaluations entail multiple iterations of each simulation projection so that the catch/effort strategies in the projection period may be adjusted according to the effects of the HCR on the population relative to the Reference Points. As such, this requires that each stochastic simulation projection must be repeated n times for each HCR event in the projection. The stochastic simulation feature in MFCL was amended so that single stochastic simulations may be run.

c) A conceptual algorithm for generating stochastic recruitments as deviates from predictions of the SRR in projection years was developed prior to the developer's workshop (Davies et al. 2012). The recruitment distributions from the product of a recruitment predictor and a set of log-normal deviates were examined and this focused attention on how these deviates are estimated and the method for applying them in generating future recruitment distributions. The regional recruitment deviates, $\gamma_{t,r}$, are the deviates on regional recruitment proportions with the criteria that $\prod_t \gamma_{t,r} = 1$ and $\sum_r \alpha_r \gamma_{t,r} = 1$. An example clearly illustrated this was not being satisfied, such that the sum of the product exceeded 1 for many time periods (Figure 1, left panel). 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 criteria to be satisfied.

A formulation was drafted with a new term rec_delta that normalises region_rec_diffs

$$\tilde{\gamma}_{t,r} = \gamma_{t,r} - \log\left(\sum_r \gamma_{t,r} \alpha_r\right)$$

This was coded conditional upon age_flags[178]in the routine get_initial_population() and a new penalty term was added to no_penalties(). This applied a new constraint on the estimation of the recruitment parameters. Tests of this constraint was run with this flag setting and resulted in a large improvement in the satisfaction of the constraint for the regional recruitment deviates (Figure 1, right panel). Temporal trends in total recruitment were expressed completely by the temporal recruitment deviates, rather than as previously in the regional recruitment deviates (Figure 2). Overall, there was no substantial impact due to applying the constraint upon the model estimates of total biomass (Figure 3).

Further testing of this feature was done in order to refine the scalar for the penalty term and to assess the impacts of this approach relative to that used for the current tuna assessments.
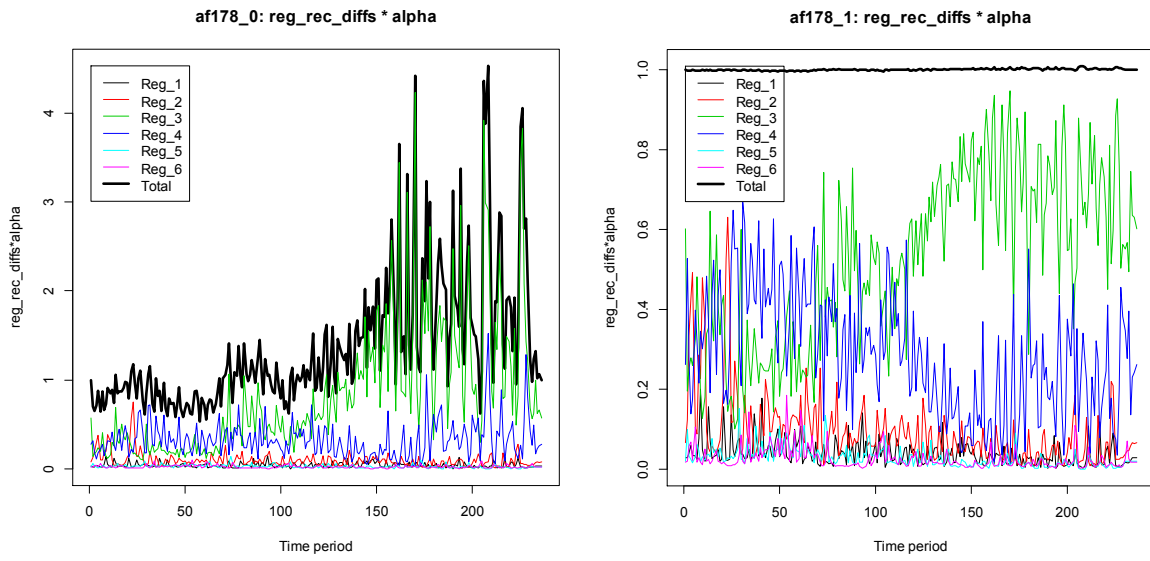
Figure 1. The product of $\gamma_{(t,r)}$ and α_r in each region with constraint (left panel), and without constraint (right panel), and with the sum over all regions (Total), in each time period.
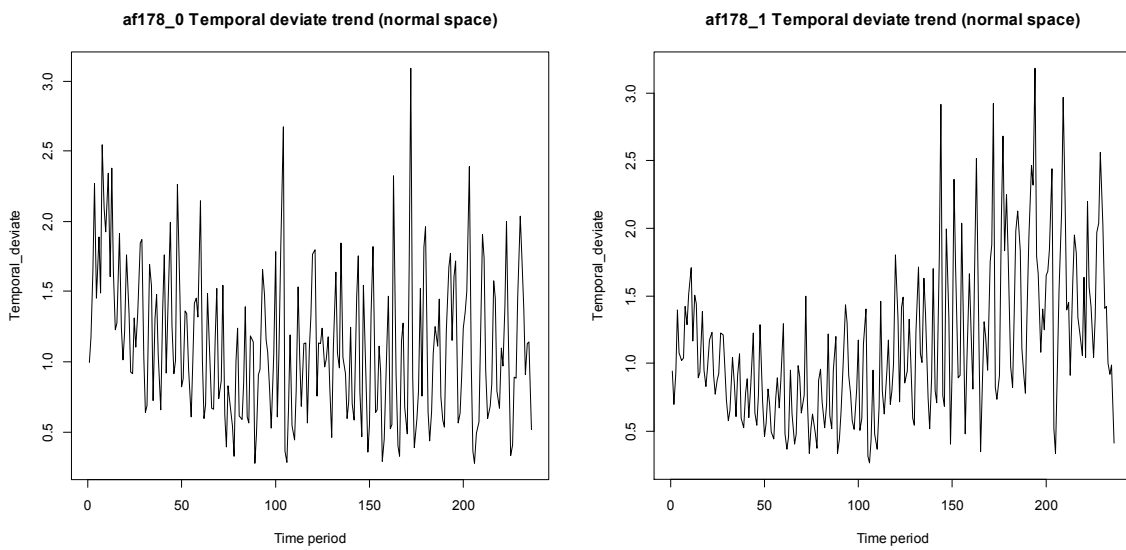

Figure 2. Temporal recruitment deviates without the regional recruitment deviate constraint (left panel) and with the constraint (right panel).
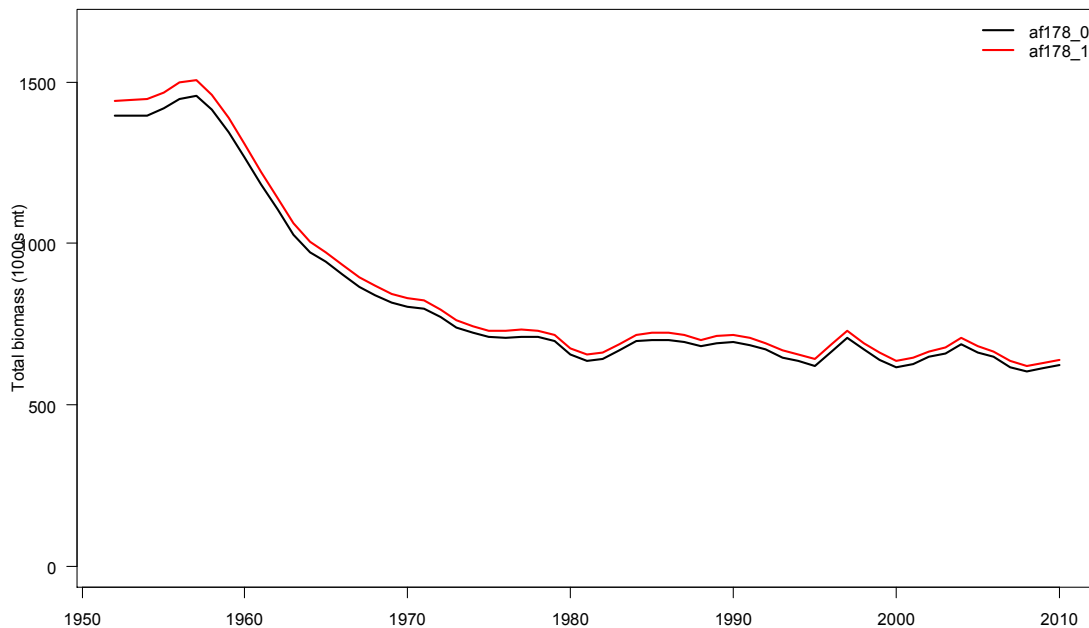
Figure 3. Total biomass for a model with the constraint upon regional recruitment deviates (red line), and without the constraint (black line).

d) Satisfying the constraint for the regional recruitment deviates results in all recruitment deviates being normally distributed in log-space and therefore stochastic recruitments may be generated by applying random samples of the deviates to the predictions of the BH-SRR in each projection run. Source code was drafted to apply the stochastic deviates as taken from the "simulated_numbers_at_age" file in the simulation projections. This entails calculating the spawning biomass in each year of the projection, deriving the associated BH-SRR prediction, and then adding the random deviate obtained from the stochastic sample of historically estimated recruitments. In this sense, the BH-SRR is considered in future scenarios.

Source code that assigns projection recruitments was modified to include the condition upon `parest_flags(239)` which results in the stochastic recruitments being translated into deviates which are applied to the BH-SRR in each year.

Under projections that assume future catch/effort scenarios that reduce spawning biomass, whereas using absolute stochastic recruitments the mean of the stochastic recruitments during the projection period remains reasonably constant (Figure 4), the effect of including the BH-SRR predictions produces a decline (Figure 5). The consequent effect of this is evident in the mean of the stochastic projection biomass with, and without conditioning upon the spawning biomass (Figure 6).

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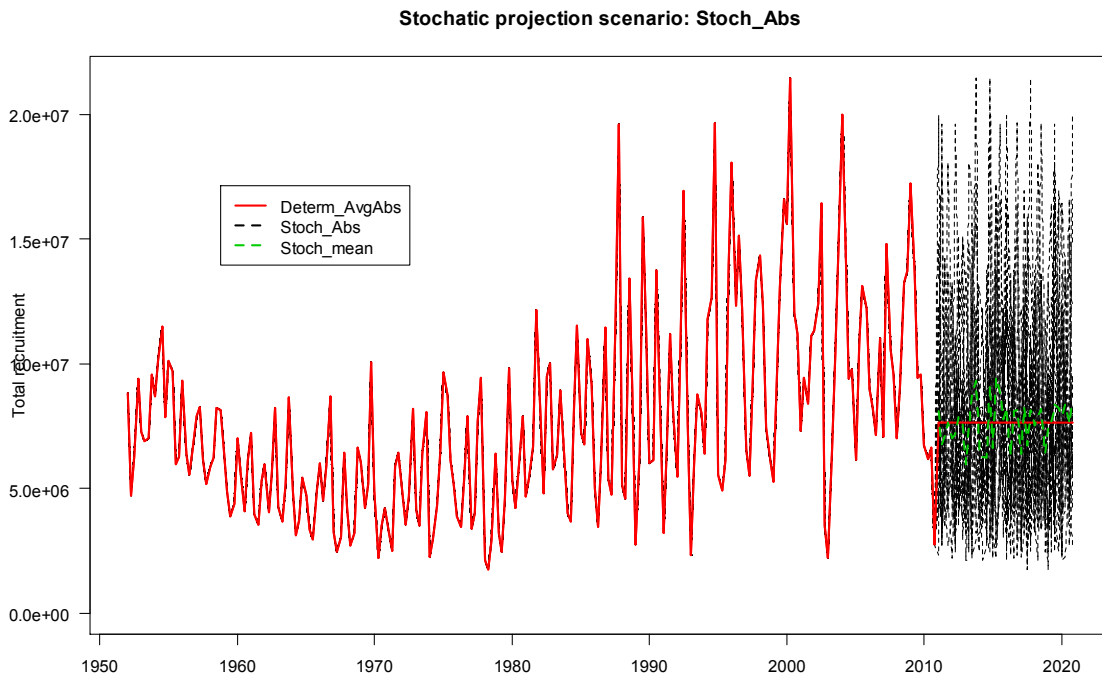**Stochatic projection scenario: Stoch_Abs**

Figure 4. Estimated recruitments (1952 – 2011) with recruitments for the projection period derived from: deterministic predictions using the average of historical absolute recruitments (Determ_AvgAbs), and 20 simulations with stochastic recruitments derived from random samples of the historical estimates (Stoch_Abs). The mean recruitment over all simulations in each projection period is shown (Stoch_mean).
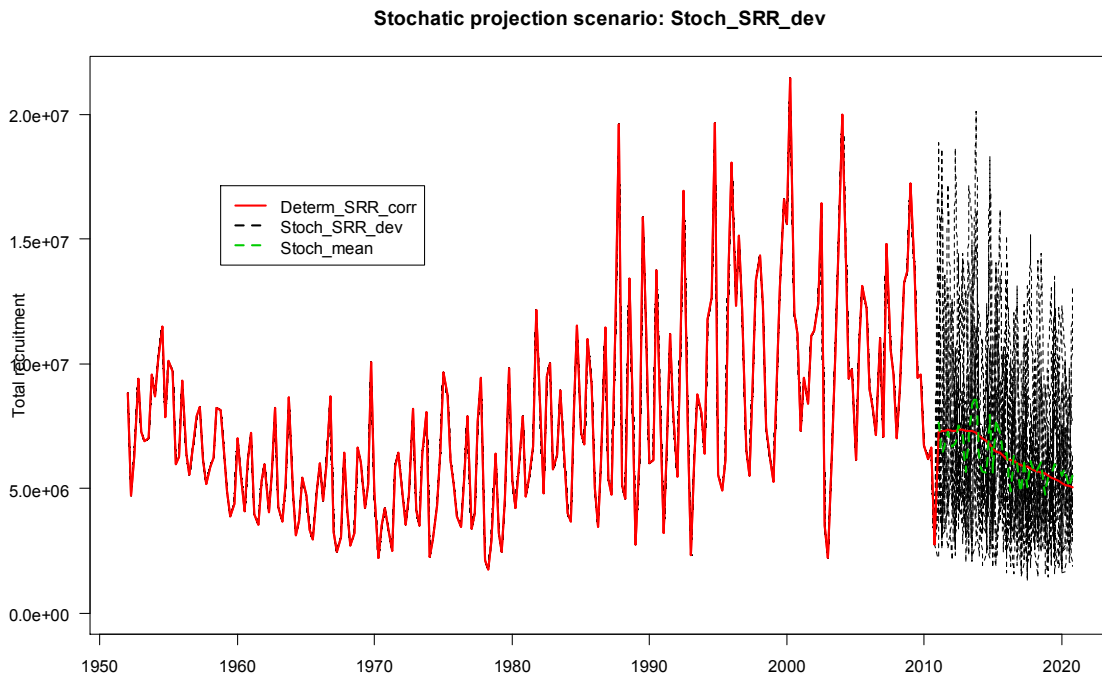
Figure 5. Estimated recruitments (1952 – 2011) with recruitments for the projection period derived from: deterministic BH-SRR predictions (with log-normal bias correction, Determ_SRR_corr), and 20 simulations with stochastic recruitments derived from random deviates from the BH-SRR predictions (Stoch_SRR_dev). The mean recruitment over all simulations in each projection period is shown (Stoch_mean).

Stochatic projection scenario: Stoch_Abs

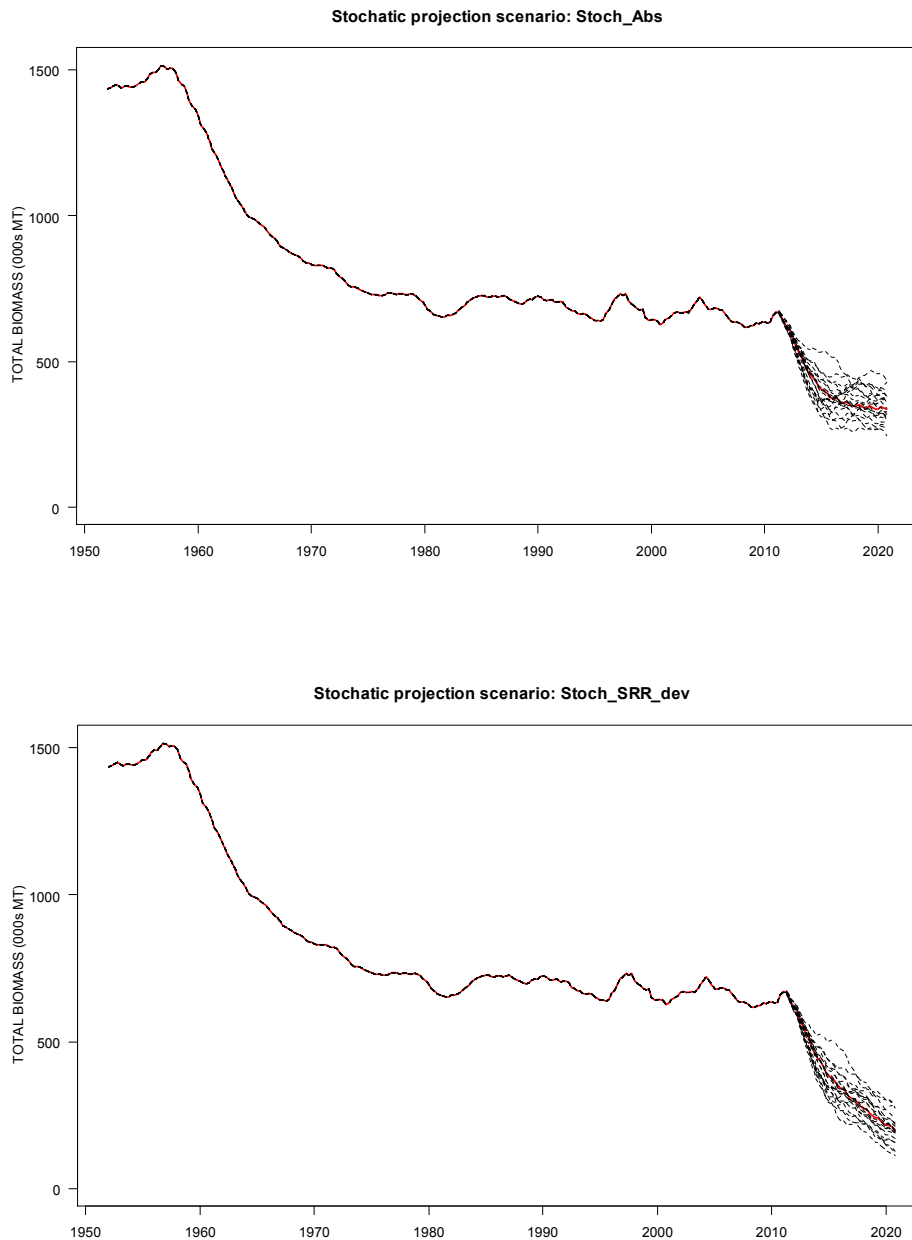**Stochatic projection scenario: Stoch_SRR_dev**

Figure 6. Estimated total biomass (1952 – 2011) with total biomass for the projection period derived assuming stochastic recruitments for 20 simulations sampled either from historical absolute estimates (top panel), or are conditioned upon the BH-SRR predictions (bottom panel).

e) For many stock assessments a temporal trend in recruitments may be estimated and a sub-set of the model calculation period may be defined that best describes the productivity of the stock (Figure 7). The BH-SRR may be estimated over this subset period rather than using the full set of estimated recruitments (Figure 8). The relationship estimated over the subset period may be used to condition stochastic recruitments in projections. This context simply requires that the flag settings applied when generating the stochastic recruitments are consistent with those for determining the sub-set period for estimating the BH-SRR. Running the projections is as for d) above.

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For the example used, the BH-SRR estimated over the entire model period predicted lower recruitments than that estimated over the sub-set period (Figure 8). The effect of conditioning stochastic recruitments upon either relationship is direct, such that the mean of stochastic recruitments declines less steeply over the projection period when the BH-SRR for the sub-set period is used (Figure 9). The higher variability in the recruitments over the sub-set period (Figure 7) is also reflected in the wider distribution of the stochastic recruitments generated using these deviates in the projection period (Figure 9). The consequent effect of this is evident in the mean of the stochastic projection biomass for each scenario, with less decline, but more variability for the scenario using the BH-SRR estimated over the sub-set period to condition stochastic recruitments (Figure 10).
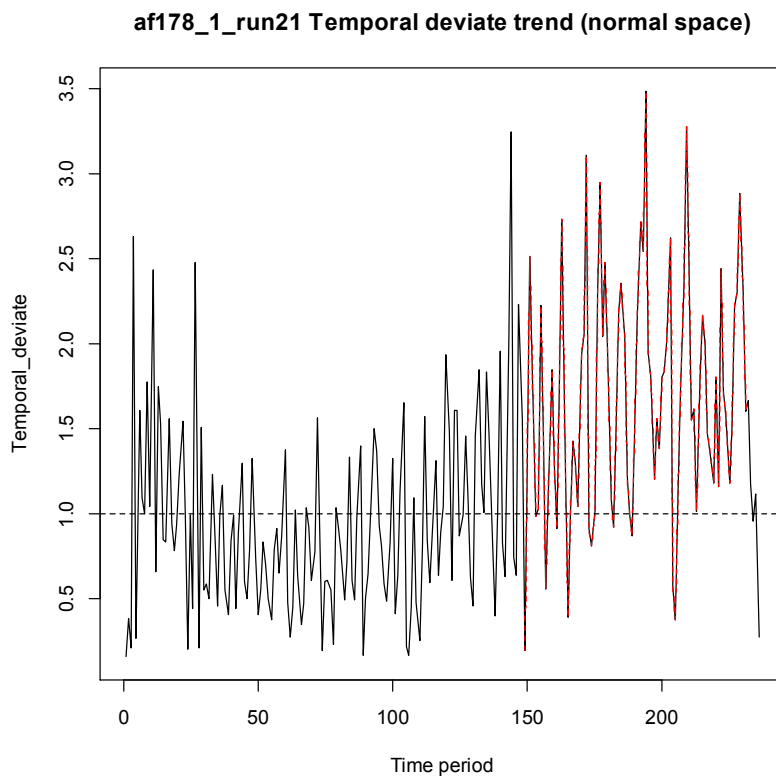

Figure 7. Temporal deviates in annual recruitment estimates, with a sub-set period defined for deriving a recruitment relationship (dashed red line).
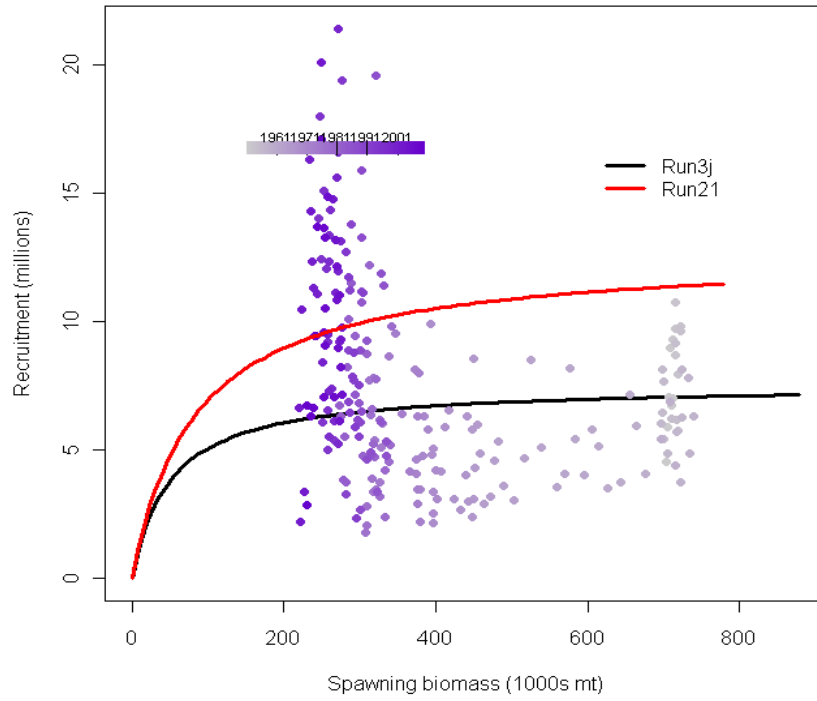
Figure 8. Comparison of the BH-SRR when estimated over the entire model time period (Run3j), with that when a subset time period is used (Run21).
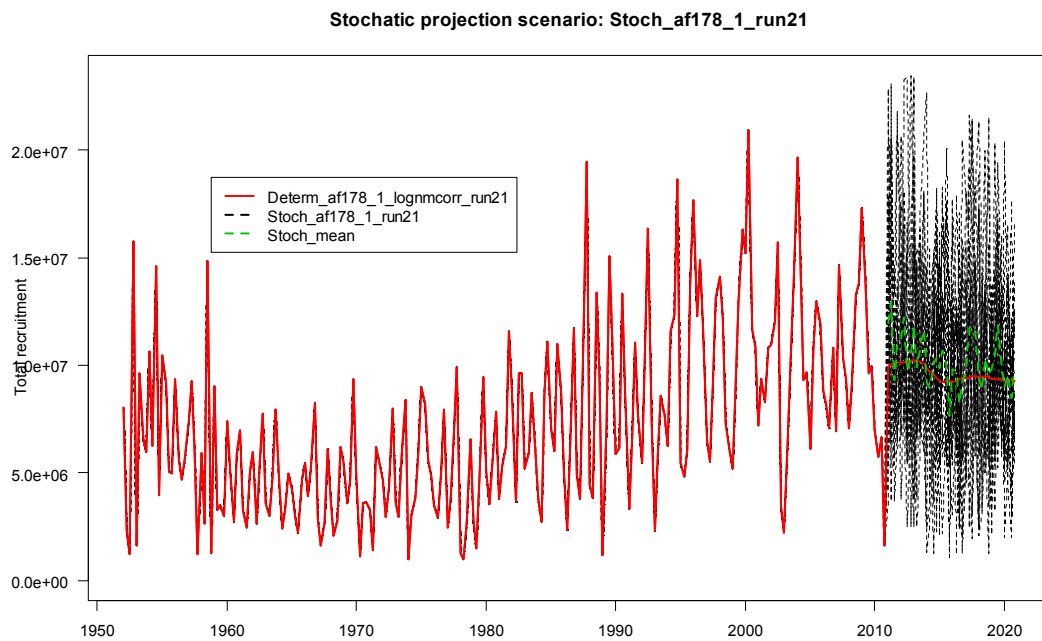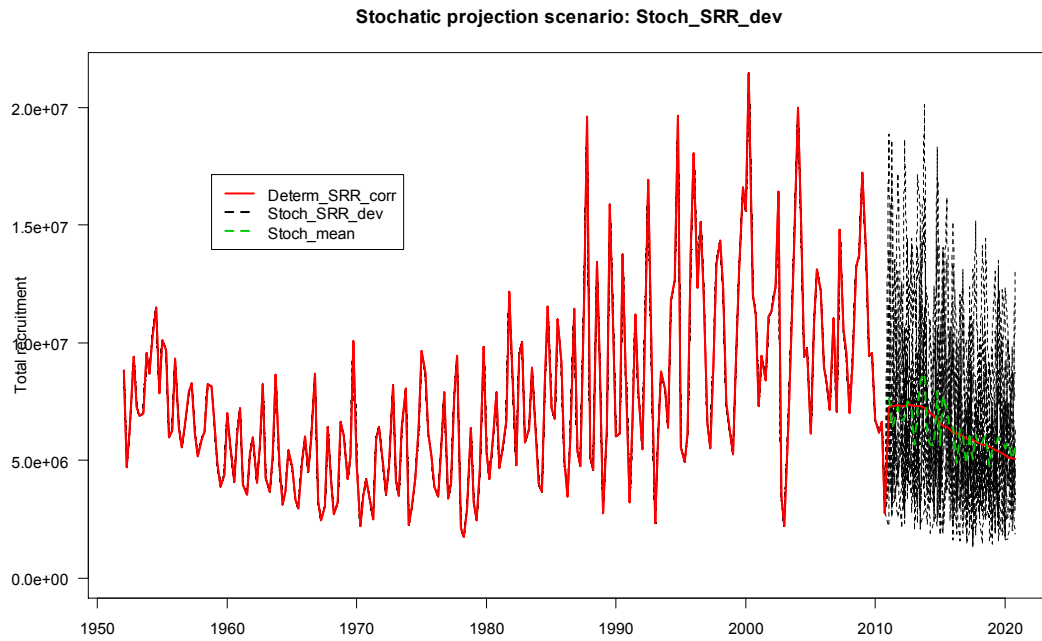
Figure 9. Estimated recruitments (1952 – 2011) with recruitments for the projection period derived from: deterministic BH-SRR predictions (with log-normal bias correction, Determ_SRR_corr), and 20 simulations with stochastic recruitments derived from random deviates from the BH-SRR predictions estimated over the entire model period (Stoch_SRR_dev, top panel), and also those estimated over a subset of the model period (Stoch_af178_1_run21, bottom panel). The mean recruitment over all simulations in each projection period is shown (Stoch_mean).

Stochatic projection scenario: Stoch_SRR_dev

Stochatic projection scenario: Stoch_af178_1_run21

Figure 10. Estimated total biomass (1952 – 2011) with total biomass for the projection period derived assuming stochastic recrui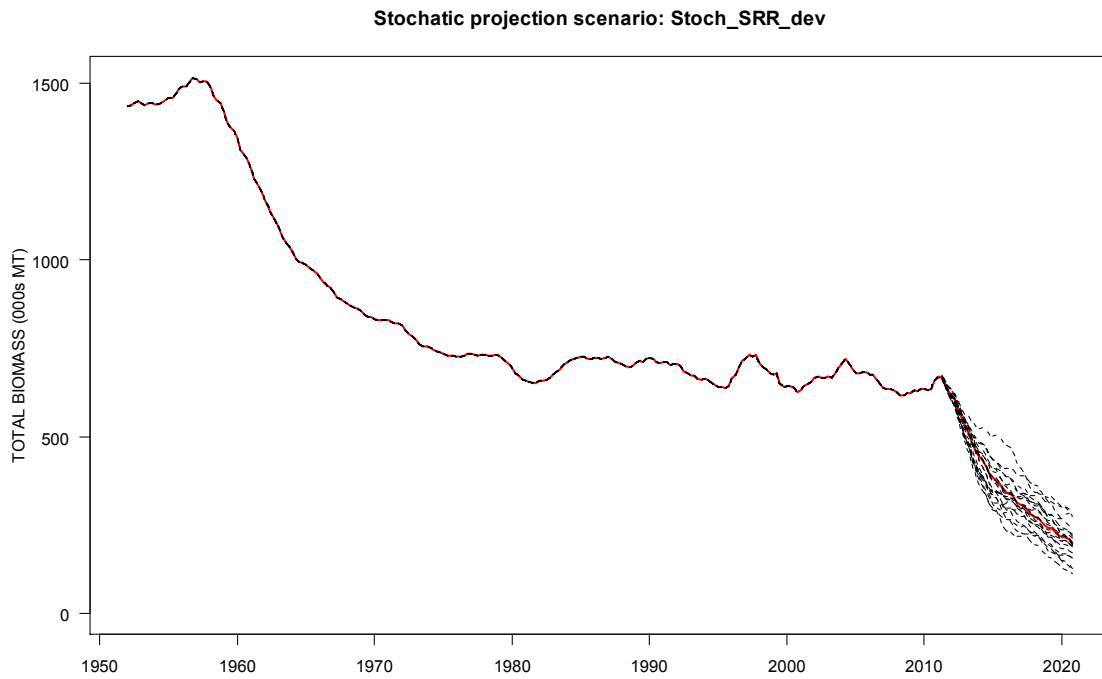tments for 20 simulations upon the predictions of a BH-SRR estimated over the entire model calculation period (top panel) or a subset period (bottom panel).

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. As mentioned above, this development is the highest priority recommendation from the independent review panel of the 2011 bigeye stock assessment (Ianelli et al. 2012), and entails a fundamental and large scale modification to MFCL. Consequently, it has been 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 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 October 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, and to extend the development for a multi-sex application.

Multi-species application

The source development branch that facilitates multi-species analysis has been tested by examining the convergence of a model fit to multi-species data towards the solutions obtained using the identical single-species data. Outstanding differences between the two solutions were examined that required changes to the source code in: xml.cpp (a bad derivative); and wfast96.cpp (extension for using multi-species wmid).

Equilibrium yield calculations for the multi-species solution were developed that required source code developments in numerous routines including: stock_recruit_bh_steep(), yield_analysis_bh(), yield_analysis_bh_steep(),yield_analysis_bh_penalty(), and get_yield_at_multiplier2(). Further development was required to accommodate multi-species fishing mortality, i.e. to extend F_age_year to be multi-species by modifying the routine get_fishing_mortality_by_age_by_year().

Multi-sex application

The multi-species development branch source code was then extended for application to multi-sex data by firstly sharing the recruitment parameters among sexes; i.e. making the

assumption that the sex ratios at age 0 are equal (50%:50%). Annual recruitments are formulated as follows:

$$\acute{N}_{1,t,r} = \bar{R} e^{\tau_t} \alpha_r \gamma_{t,r}$$
           Eq.1

(Equation A.1, Appendix A, Kleiber et al. 2012)

where:

$\bar{R}$ is average annual recruitment, (totpop)

α_r is the proportion of annual recruitment assigned to region r, (pop_delta)

τ_t is the annual deviate of spatially aggregated recruitments from $\bar{R}$, (recr)

$\gamma_{t,r}$ is the deviate on regional recruitment proportions (region_rec_diffs)

Sharing of these four parameters among the sexes was implemented with changes to source code in rnaux2.cpp and setcomm.cpp for routines set_value(), set_value_inv() and size_count() to group these parameters when assigning them to the X vector. This feature was conditional upon a set of newly-defined region_flags[3] (for sharing region_rec_diffs and pop_delta), and species_flags[1] (for sharing recr). Consequently a new version for the input of the .par was created to denote the presence of these new flags.

In order that a single Beverton-Holt stock-recruitment relationship (BH-SRR) is estimated for both sexes, the call to stock_recruit_bh_steep() was made conditional upon the new species_flags[2] that identifies which of the two sexes is the females, and for which the spawning biomass will be used in deriving the relationship.

This functionality was tested using the prototype multi-species input data as a proxy for two sexes, and to ensure that the recruitment and BH-SRR parameters were that for that species denoted as being the female sex in species_flags[2].

The existing multi-species functionality for maturity-at-age, growth, length-weight relationships, and natural mortality were considered sufficient for describing sexual dimorphism and sex-specific natural mortality. Similarly, the sharing of fishery-specific mortality and catchability among species would be adequate for the fisheries defined as acting upon both sexes equally.

An algorithm was developed for calculating the equilibrium yield combined over both sexes that entails calling routine get_yield_at_multiplier2() once for each sex and summing the equilibrium catch which is used in deriving F_{MSY} and MSY. This algorithm will be discussed with other developers before implementing the coding required to implement it.

Observations for combined catches and tags for species/sexes

A necessary extension of the multi-species/sex development is to allow for the input of observations for catches and size composition data that don't differentiate the species or sex, i.e. aggregated data. These data are common in fisheries for which the species composition is not determined or for which sex-ratios are not estimated.

The format of the multi-species .frq file (version 7) was adapted to a new version (8) that includes new columns to denote which of the species/sexes are included in a row of fisheries data. These columns populate the fisheries header record (fhr.fisn) and a new pointer was created (pmsd->reg_in_catch) to identify observations as aggregated or not. The robust-normal length-frequency likelihood was adapted in routine square_fita( ) to accommodate

aggregated observations by aggregating the corresponding predictions for each species/sex. This prototype code was tested and found to be working satisfactorily.

Further development of this functionality to include aggregated catches, weight-frequency, and tagging data, is now the focus for the immediate developments of MULTIFAN-CL.

Testing

The integrity of the model fit to the multi-species data was achieved during the developer's workshop. A single model evaluation using multi-species data produced excellent correspondence to that using single-species data, indicating the differences in the likelihood contributions and gradient calculations had been resolved. A doitall fit to the multi-species data was undertaken and produced solutions sufficiently converged to conclude a positive test result; i.e. almost the same solution is obtained when fitting to the multi-species data as would be obtained when fitting to the single species data. Model quantities were very similar in terms of biomass (Figure 11), recruitment (Figure 12), equilibrium yield (Figure 13), and growth (Figure 14). These developments confirmed the very similar equilibrium yield estimates being output from the single model evaluation using multi-species data. The slight differences in the estimates can be attributed to differences in the order of the derivative calculations that will result in a different minimization "track", and the cut-down data sets being used.

At this point it was concluded that, within the context of the prototype multi-species model assumptions, the source code generated solutions that had integrity with respect to the results obtained from that using single species data. The functionality needed for the multi-species application was operating without apparent error. This development branch source code could then be used as the basis for extension to other similar applications, e.g. multiple sexes.

Figure 11. Comparison of biomass estimates for two species derived from a fit to single-species data (Single-spp model), and from a fit to multi-species data (Multi-spp model).

SRR curve and pred.Recrs for single/multi-spp models: species 1

SRR curve and pred.Recrs for single/multi-spp models: species 2

Figure 12. Comparison of recruitment and BH-SRR estimates for two species derived from a fit to single-species data (Single-spp model), and from a fit to multi-species data (Multi-spp model).

Figure 13. Comparison of equilibrium yield estimates for two species derived from a fit to single-species data (Single-spp model), and from a fit to multi-species data (Multi-spp model).

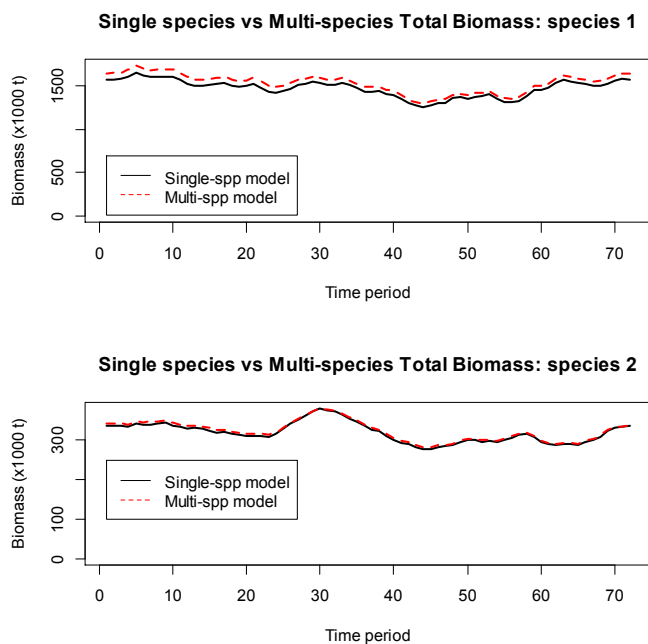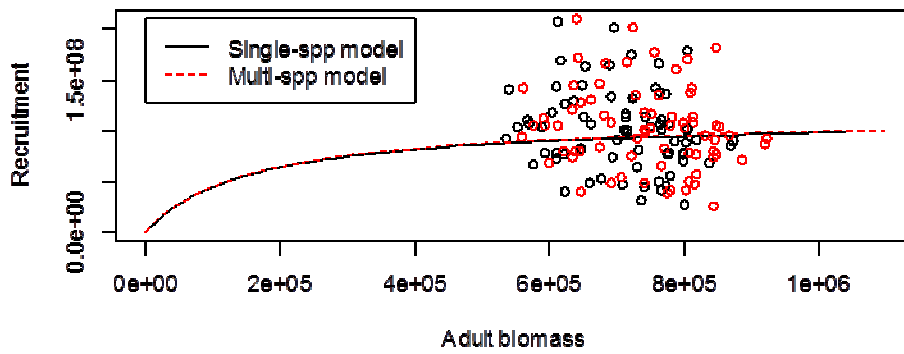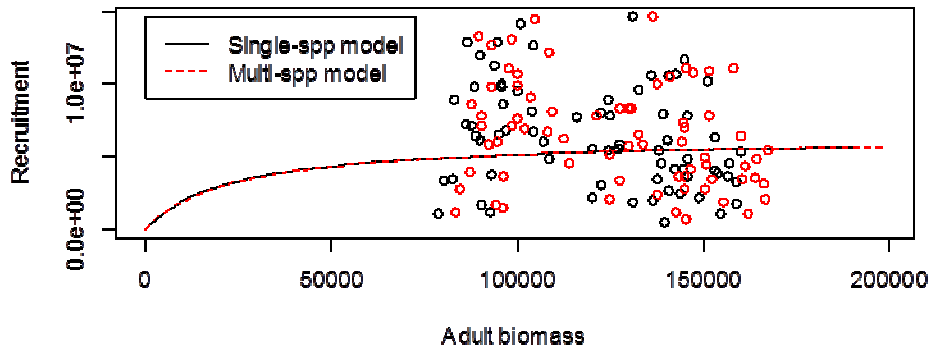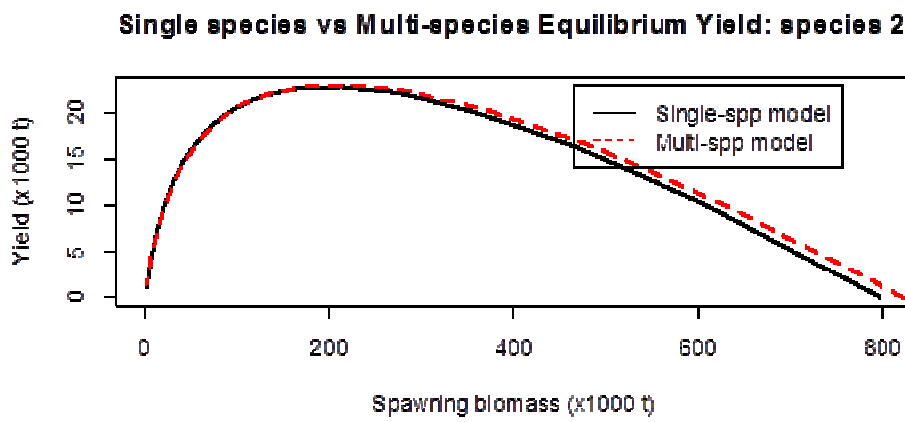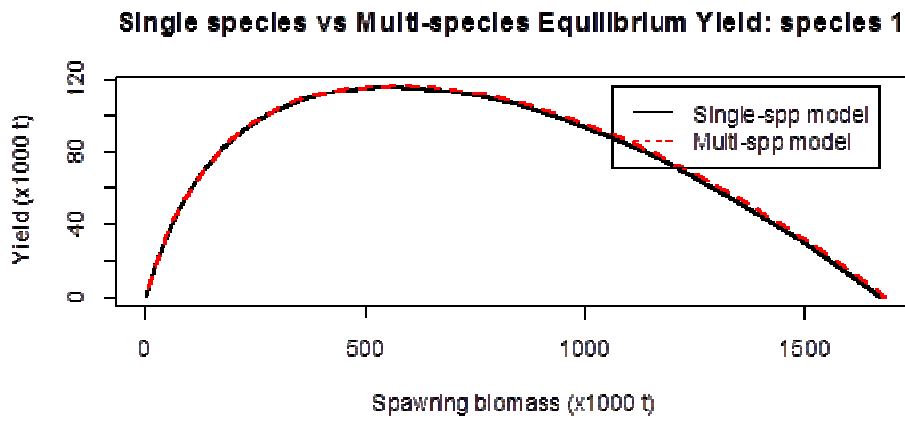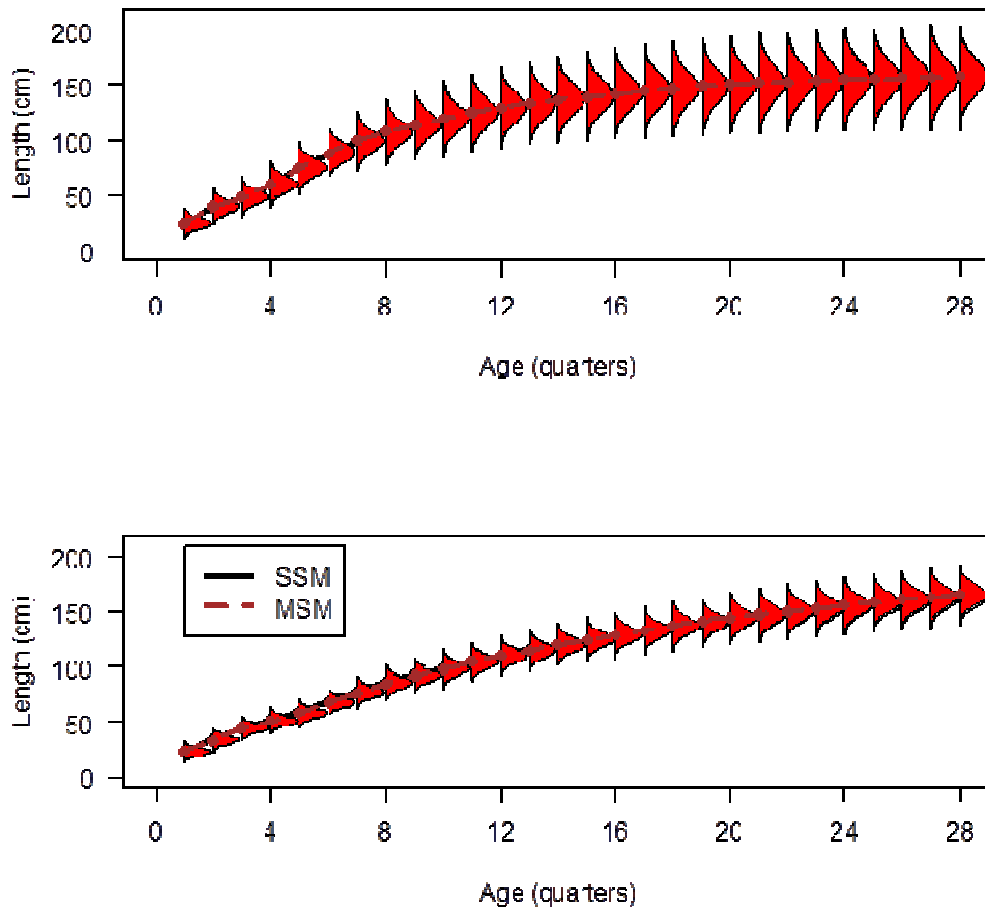**Figure 14. Comparison of growth estimates for two species derived from a fit to single-species data (SSM), and from a fit to multi-species data (MSM). Each panel is a different species.**

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.

Multi-threading

MFCL facilitates large and complex population modelling, with the current WCPO tuna assessments being among the most complex having up to 148 fisheries, 6 model regions, 40 age classes, 95 length intervals, 200 weight intervals, 236 time periods and estimating 6178 parameters. Obtaining a solution can require over 24 hours of computation time on the most power of processors. Substantial gains in model development and diagnostics would be made by reducing the computation time for obtaining a solution by increasing the scope for exploring alternative model assumptions during the preparation of a stock assessment. Improved computation efficiency is obtained by performing independent operations in parallel within a single processor by assigning them to multiple threads; known a multi-threading. Once completed, the calculations from each thread are then "collected" and the

model computation can continue. The time required for the task when undertaken on parallel threads is therefore reduced by the multiple of the threads employed.

The first step in exploring the potential for this development in MFCL was to apply a proof of concept code for multi-threading the automatic differentiation model builder (ADMB) gradient calculation, which is performed with each evaluation of MFCL towards obtaining a model solution. A project was created (`new_sim_thread4.cpp`) created that employed 24 slaves and was run on "sterne", a linux 64-bit super-calculator at the Oceanic Fisheries Programme. The multi-threaded application achieved an approximately 9-fold improvement in speed.

Having demonstrated the benefits and the coding structure required for multi-threading the MFCL C++ code, the approach was applied to the tagged population catch calculations which may be undertaken independently, and therefore in parallel, in respect of the tag release groups. A development branch of the MFCL repository was created, 9 existing source code files were modified, and 15 new source code files were written for the memory management to, and from, the three slave processors. The multi-threaded application was activated by a new `parest_flags`. The improvement in speed was trialed on "sterne" with a real time reduction due to multi-threading being (3m0.022s - 1m41.482s) / 3m0.022s = 43.6%.

This level of increased performance is substantial and offers great potential for species with large amounts of tag-recapture data, e.g. skipjack with 196 release groups. The branch source code has been positively tested over the testing framework versus the trunk source code using single-species data (no differences detected), and will therefore be merged following completion of this development and further testing.

Compilation for Mac OS X

Numerous enquiries have been submitted to the project for a Mac OS X compatible MFCL executable, particularly from users of the TUMAS application released by the Oceanic Fisheries Programme (OFP). A Mac OS X (Snow leopard) virtual machine was built in Virtual Box and Xcode was installed so as to compile C++. The ADMB libraries required for MFCL (in compilation folder "admb07") were compiled successfully and subsequently the development branch for the multi-species/sex source code was compiled. This Mac OS X 64-bit executable was then tested on the VMs at the October 2012 developer's workshop and at OFP in Nouméa, and produced identical solutions to that of the corresponding linux 64-bit compilation. The capacity to produce a Mac OS X executable has significance for the distribution of MULTIFAN-CL to a wider range of users, and is of value to the TUMAS project that has notable demand from Mac users.

Fixes

Several fixes were made to the formulations in MFCL in 2012-13.

Maximum projection fishing mortality

A specific problem was examined where a segmentation fault occurred during a stochastic projection of the SKJ model when more than 1.75 times the status quo effort is assumed for the future. This was isolated in the Newton-Raphson calculation for fisheries catch while a non-zero population exists. The problem was resolved by increasing the maximum fishing mortality value (`rmax`) for this option to 5.0, which facilitates very high catches despite low population abundance.

Examining this scenario closer revealed exceptionally low population abundance in one of the regions due to the projection fisheries data applied, resulting in extremely low catches most likely due to the high "observed" catch assumed for the future. It was recommended that analysts apply a routine diagnostic to projection reports that compares "observed" and predicted catches over the projection period to consider the integrity of the harvest scenarios being explored.

Penalty on deviates from the BH-SRR

Source code for translating `age_flags(145)` into a penalty weight was modified so as to enable the application of extremely low values as follows:

```
double pen_wt;
  if (fsh.age_flags(145)>0) pen_wt=fsh.age_flags(145);
  if (fsh.age_flags(145)<0) pen_wt=pow(10.0,fsh.age_flags(145));
```

This allows for a negative value, e.g. -3, being interpreted as a penalty weight of 0.001. This modification was made on the basis of a recommendation from the independent review panel of the 2011 bigeye stock assessment (Ianelli et al. 2012).

BH-SRR predictions in projections under zero fishing

Fixes were required in lesmatrix.cpp for the BH-SRR calculation for projection biomass under zero fishing. Firstly, the call to `get_average_recruitment()` required modification to pass the formal argument `N_q0` so as to use the unfished population in deriving the average proportion of recruitment to the model regions. Secondly, the call to `get_bh_alpha_and_beta()` was modified to send the formal argument `Nsave` to the routine `calculate_the_biomass()` when deriving the BH-SRR parameters under zero fishing. These fixes ensured the correct recruitment calculations in deterministic and stochastic projections when using the BH-SRR.

Application of new features

Several of the recent developments described above have been used in stock assessment and management advice papers submitted to the 9th meeting of the scientific subcommittee of the WCPFC (SC9). The general nature of the application is described and the significance of its utility for the management of tuna and billfish outlined.

Hampton et al. 2013. Analysis of the implementation and effectiveness of key management measures for tropical tunas. WCPFC-SC9-2013/SA-WP-05

- Deterministic projections using the average of absolute recruitments taken from part of historical period (10 years)

Davies et al. 2013. Stock assessment of swordfish in the southwest Pacific Ocean. WCPFC-SC9-2013/SA-WP-05

- Constraint on regional recruitment deviates, log-normal bias-correction on BH-SRR predictions

Berger et al. 2013. Determination of appropriate time-windows for calculation of depletion-based limit reference points. WCPFC-SC9-2013/MI-WP-xx

- Constraint on regional recruitment deviates, log-normal bias-correction on BH-SRR predictions, adjustment for BH-SRR multiplier in zero-fishing runs

Berger et al. 2013. Proposed F-based limit reference points for bigeye, yellowfin, and south Pacific albacore tuna. WCPFC-SC9-2013/MI-WP-xx

- Constraint on regional recruitment deviates, log-normal bias-correction on BH-SRR predictions, stochastic projections with resampled recruitments applied as deviates to BH-SRR predictions, adjustment for BH-SRR multiplier in zero fishing runs in each stochastic projection.

Berger et al. 2013. Determination of an MEY for south Pacific albacore. WCPFC-SC9-2013/MI-WP-xx

- Constraint on regional recruitment deviates, log-normal bias-correction on BH-SRR predictions, stochastic projections with resampled recruitments applied as deviates to BH-SRR predictions, adjustment for BH-SRR multiplier in zero fishing runs in each stochastic projection.

This extensive use of these new developments illustrates their importance and relevance to the scientific advice being considered by SC9 for developing management advice for the WCPFC.

Future work

The current and future work plan for MFCL is outlined in Table 1 with those having high priority being assigned a priority identification of 5. Tasks of immediate priority are discussed in the following section.

Discussion

Substantial developments and improvements have been made to MFCL during 2012-13, with most relating to the multi-sex development and to stochastic simulation functionality.

Excellent progress has been made on the multi-sex application, and it is anticipated to be completed on schedule. A critical point of this development was achieved in 2013 when the multi-species application was tested using the testing framework for consistency with the calculations using single-species data for all the tuna and billfish assessments undertaken by OFP. The positive result obtained for all species confirmed the integrity of the development branch, and therefore it was committed to the MFCL repository trunk. The existing branch of this multi-species source code is now being used for developing the remaining functionality that is to include the combined equilibrium yield calculation over both sexes, and the model fitting to tagging data combined over both sexes. This work will be the focus of the next developer's workshop to be held in September 2013.

The developments for stochastic projections completed to date have addressed almost all of the current requirements for undertaking the Biological Reference Point work prepared by OFP for the WCPFC, in particular, those relating to risk-based and zero-fishing reference points. This was one of the highest priorities for the MFCL developments in 2012-13.

Multi-threading of the tagged population catch calculation is a promising new development made during 2013 which offers great potential for MFCL applications that are computationally intensive. Indeed, the application of highest priority in the project currently,

a multi-sex model, effectively entails a doubling of the model computations. Sex disaggregation will therefore halve the analytical time available for exploratory analyses and estimating structural uncertainty for an assessment model using this structure. For highly complex population models, the 43% reduction in processing time gained by multi-threading will offset the computational increase to an extent, making it feasible and practical. Another application that will benefit is structural uncertainty analysis. If sufficient gains in computation time are made, it may even be possible for Monte Carlo Markov Chains to be calculated for less complex models.

The developments that address the five recommendations of the independent peer review panel of the 2011 bigeye stock assessment has the highest priority for 2013 because of their significance for improving the forthcoming assessment. While good progress has been made on the multi-sex development, immediate attention will be given to the other four recommendations at the developer's workshop in September 2013. The recommendations of highest priority relate to time-varying selectivities and adding conditional age-length data in the likelihood.

A fundamental component of the MFCL project is the testing of new developments. The testing framework has increased the rate and the range of data and applications over which they are tested. While ensuring software integrity, this has permitted a relatively large number of new developments to be included in new postings of MFCL in 2012-13. However, considerable further work is required to clear the back-log of model developments made in the past, including: release group-specific tag reporting rates, tag-fishery-specific reporting rates, the fit to tags during the mixing period, the catch-conditioned model, and length-based fishery selectivities. This is a high priority task for 2013-2014, 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, in particular the MULTIFAN-CL viewer. An example of a multi-sex population model will be constructed as part of completing this development, most likely using swordfish data because sexually disaggregated size data are available for some fisheries and sex-specific growth rates have been published. Using the MULTIFAN-CL viewer, the model output quantities and diagnostics may be interrogated with ease and will assist greatly in this development.

Table 1. 2013-2014 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
1. BET Peer Review tasks					
f.	Sex-structure	Extend MFCL to allow gender to be explicitly represented. This will allow the impacts of differences in growth and natural mortality between the sexes to be represented. The current approach to modeling, for example, length-specific natural mortality (e.g. WCPFC-SC4-2008/ ME-WP-1) seems unnecessarily complicated given the lack of gender-structure in the model.	5	Nick/Dave	Almost complete
g.	Likelihood components	Create an output table which lists all of the likelihood components by fleet and automates the process of computing effective samples sizes (and other summary statistics related to model fit). 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		
j.	Multinomial likelihood	Add an option which allows the analyst to assume a multinomial likelihood for the compositional data in the first phases and only transition to the robust normal likelihood in the later phases.			Algorithm available, and draft code prepared
l.	Tagging likelihood weighting	An option to add a likelihood weight to the tagging data component should be added.			

e.	Age-at-length likelihood term	Allow conditional age-at-length data to be included in the likelihood function. This will allow the ageing data from current sampling (e.g. WCPFC-SC6-2010/GN IP-04) to be formally included in the assessment.			
i.	"Tail compression" option	Include a "tail compression" option, which would pool all length- and weight-data for large and small sizes based on a specified percentage (e.g. all lengths would be pooled so that the "plus" length-class contained 0.1% of the length-frequency).			
k.	Maturity-at-length	When maturity data are based on length, converting to ages should be done within the model. Presently, the maturity-at-age is based on a fixed age-length relationship.			
m.	Annual recruits for BH-SRR	Consider fitting the stock-recruitment relationship to the annual rather than seasonal recruitments.	5	Nick/Dave	
2. Development of new functionality					
40	Multi-species/stock/sex dimensionality	o merge Dave's Multi-spp. version of the source with the OFP assessment version (2012-11-15) and create this in the repository trunk branch o set up new development branch; with regular testing at each new step o maintain mirror copy of Dave's source locally o continue with supporting Dave's developments o control the output formats for MFCL_viewer	5	Dave/Nick	Bullets 1 to 3 complete.
25	Stochastic projections	o stochastic deviates about the BH-SRR predictions; incl. "run21" scenario o testing of numbers-at-age in yrproj_1 stochasticity;	5	Nick/Dave	Bullet 1 is complete

		decoupled from those in final estimation model period o Test effort deviates stochasticity			
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	Nick/Dave	Region-specific yield calculations are already an option in MFCL. (section in code called"Daves_folly"). Anything else to do?
22	Seasonally varying selectivity coefficients	Implement a scheme to estimate seasonal variability in selectivity coefficients	4	Dave	Needed for ALB assessment and might be useful for others
	Shark stock-recruitment relationship	Development and testing of a stock-recruitment relationship function for sharks	4	Dave	
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	
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	2	Dave	
	Tagging informs movement only	Implement a method for allowing tagging data to inform movement only, rather than movement and mortality.	2	Dave	Structure is already available

	Tag loss parameters	Implement a scheme to allow for the specification of short- and long-term tag loss parameters.			
26	Biological parameters in respect of 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.	2	Dave	
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	Dave	
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 24 when the new tagging data is incorporated.	3		Some structure there now but we probably want something more flexible.
37	Hyperstability	Implement fishery-specific hyperstability, as a relationship between vulnerable biomass and catchability	3		
Add	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	This will facilitate quicker operation.

30

Add	Calibrate model over-parameterisation	o Design a survey of model runs with alternative penalty weights on catch devs and recruitments to attempt to reduce over-parameterisation and reduce variance o 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. o 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 justuiied 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. o There is also the orthogonal recruitment code (perhaps that applying to seasonal recruitment indices with deviates), which needs to be checked and tested.	3	Nick	Essential for evaluating the utility of simpler models.
Add	Stochastic projections - eff_devs; N_yr1	o Check why the stochastic effort deviates don't work o Create option for numbers-at-age stochasticity that is independent of the Hessian variance estimates	2		If these sources of error prove to be important
Add	Dynamic MSY	• 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. Output formats for MFCL_viewer (Fabrice)	2		

Add	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		
3. Testing					
Add	Testing framework	Refine and maintain Testing Framework o standard suite of tests for compilation (all species assessments) o Draft a manual for undertaking the testing o Post on website	5	Nick	Mostly complete. Input template, manual and posting still needed.
Add	Cut-down models	Revise the cut-down models for their operation and utility for testing all the possible operations.	5	Nick	Add
Add	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	
42	Outstanding testing of existing features	o Release group-specific tag reporting rates; any changes to format may entail new output formats for MFCL_viewer (Fabrice) o 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. o Fit to tags during the mixing period - test alternative parameterisations (remove observed, estimated + scaled by reporting rates) o Catch-conditioned model (see Appendix B) o Length-based selectivity o Structured recruitment estimates - seasonal	5 but first test the things we use now	Nick	In progress

		recruitments +annual deviates; find out if this is the orthogonal recruitment feature; test to see if this works			
Add	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	Not yet started
Add	Cut-down report for dependent variables	Design a new dependent variables report that is a cutdown version and excludes all those (time-consuming) not immediately required for the assessment.	3	Pierre	Not yet started
Add	SRR over T1T2 for eqm_yield calcs	Flexibility in SRR period used in equilibrium yield estimates: discuss newbh.cpp code with John regarding the subtleties of the term norm2(tmpdif)used as it may be applied in other parts of the code	2	Nick	
Add	Fishery-specific projection catches mixed	Projection period fishery data to have flexibility to be transferred from catch in numbers to catch in weight within a given fishery.	2	Dave/Nick	
Add	Fishing mortalities calculation - Eq.A5	Attempt to regenerate the output F from Eq A.5 in the MULTIFAN-CL User's Guide using the outputs in plot.rep	2	Nick	
Add	Fixed selectivities	You set fish_flags(i,16)=2, and fish_flags(i,3) to the age from which you want the selectivity to be zero. However, this was done quickly, and the penalty weight is too large and is currently hard-wired in alldevpn.cpp. The statement is: double xpen=1.e+6 at line 435. This needs to have a lower default value (e.g. 100) and an age_flag setting to allow the user to specify what it should be. In general, if you are starting from a fit where the selectivity for the	2	Nick	

		fishery in question is high, you want to start with a lower penalty and progressively increase it as needed to get it close enough to zero. Once it is close to zero you can have the penalty large to keep it there.			
Add	Confirm Hessian precision	Check Hessian off-diagonals for the 2-pt and 4-pt approximation by taking the difference of the off-diagonals given matrix symmetry.	2		
4. Bug fixes					
Add	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/Dave	Complete
Add	Projection problem	SKJ model crash under FMSY harvest strategy	5	Nick	Complete
Add	Memory management	o mfcl.cfg file settings cannot be obtained that run the BET and YFT models (only about 1.7 GB) on the 32-bit exec, but instead has to use the 64-bit exec. Determine why this is the case and attempt to modify to allow running on 32-bit. o Implications of this change upon the model running within TUMAS (Fabrice)	3	Dave	Not yet started
Add	Phase 1 fit crash	In the 2011 BET assessment win64 runs were crashing part-way in phase1. Debug the cause.	3	Nick	
Add	Corruption of catch.rep	Contents of catch.rep get corrupted after running the hessian, all values are v.low (-13)	2	Nick	
Add	Remove simulation run error message	Inappropriate error message (or potentially an unspecified flag): Check context of "Error -- incorrect number of	2	Nick	

		simulated recruitments…..."; This is routinely generated when doing a standard single evaluation model run (not in fitting) but is not produced when doing a simulation run.			
Add	Newton-Raphson fishing mortality maximum	o Modify nrcatch3.cpp so that alternative default values are used for the estimation/projection periods. Current default rmax = 5.0 which can create problems with model estimation unless age_flag(116) is set to lower value, e.g. 0.7. A high value doesn't matter for the single evaluation projection calculations. o Document the rmax adjustment in the code; ascertain if this will not cause the population to become implausible when doing estimations; draft new code that can check if the current fcomp is being used in a projection or not.	2	Nick	Mostly complete
Add	Hidden numbers	Numbers hidden in header record of output files: report all parameter and variable values on separate lines from the header records starting with #, e.g. BH-SRR alpha and beta	2	Nick	
5. SOFTWARE PROJECT MANAGEMENT					
Add	Update compilations	o Compilation of release version that includes age_flag(178) and stochastic projection with BH-SRR predictions developments since 2012-11-15 compilation o Post on website	5	Nick	Complete
Add	Repository management	Following merging of code create multi-spp development branch. Need help from Fabrice	5	Nick/Fabrice	Complete

Add	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	
Add	Compilation for MAC OS X	Replicate Dave's compilation of MFCL for MAC OS. Need help from Fabrice	3	Nick/Fabrice	Partly complete
Add	Synching to Dave	Cross-check of source code that Dave is using in ./mymfcl and synchronise it with the latest version	3	Nick	
Add	Communications within project	Develop and maintain communication procedures among MFCL project developers that facilitates transparency in code development	3	Nick	Ongoing
Add	VS2010 + SP1	Confirm and test VS2010 with SP1 is an appropriate platform and the implications for static linking. Has been tested (see devnotes) and checked that it works fine. Need help from Fabrice	3	Nick/Fabrice	
Add	ADMB compilations	o Specify 32-bit or 64-bit names for the ADMB library objects placed in the sub-folder temporary library folders, e.g. adsqd32.lib and adsqd64.lib; ensure these are referenced correctly in the MFCL makefiles for 32-bit and 64-bit. o The linux makefile for ADMB does not include compilation of the df1b2-separable folder which is compiled under the Windows version. To ensure that the Linux and the Windows compilations of ADMB are identical, the Linux makefile should be reconciled. Action – contact Dave and check our Linux makefile against his. Need help from Fabrice	3	Nick/Fabrice	

Add	Makefile improvements	• Update and improve all windows makefiles: o Add "clean" to makefiles o Confirm that checkdiskdir is working properly o Add .rsp and .obms to suffixes for the linux scheduled chmod and granting of permissions on skulls • Need help from Fabrice	3	Nick/Fabrice	
Add	Lapacke compilation	Include Lapack library for single value decomposition in Windows compilation	3	Nick/Dave	Useful if genuinely a diagnostic. But would need to make it clear how to use it, so the effort isn't wasted.
6. DOCUMENTATION					
Add	User's guide update	General objective: maintain the MFCL User's Guide and repository documentation; and draft a Programmer's and Compilation Manual by Dec 2011 o Update the User's Guide to include all developments done since the 2011-07-10 compilation o VB deviates flag settings: Add to the User's Guide that parest_flag(184) must be set >0 if you are wanting to estimate the VB deviates for the 1st X age classes. Parest_flag(173) specifies X and parest_flag(182) determines the penalty weight for the deviations. If you forget to set pf(184), then the model will use whatever values are set in the .ini file if pf(173) is set.	3/5	Nick/Pierre	Mostly complete
Add	Flag listing	Update all flag listings in Appendix B of User's Guide	3	Nick/Pierre	
Add	Programmer's	o Summarise flow diagrams and structure document; collate all notes	3	Nick/Fabrice	

	guide	o Explore utility of dOxygen for create manual. Need help from Fabrice			
7. WEBSITE					
Add	Storage of mfcl.exe	Create linked-page for storage of MFCL versions used for historical assessments (permitting repeatability) Need help from Fabrice	3	Nick/Fabrice	
Add	User notification	Notify all MFCL users of the new website and latest compilation	3	Nick	
Add	Make a bulletin brd	Design a bulletin for monitoring the posting of messages, and if possible convert this facility to an email list for all enquiries to be directed to the Development Team Need help from Fabrice	2	Nick/Manu	
Add	Registration summary	Summarise existing Registrations, prepare mail out notice of commencement of the email list and an update of new MFCL feature. Need help from Fabrice	2	Nick/Fabrice	
Add	Enable google_analytics	Enable google_analytics to website that counts the hits. Need help from Fabrice, Manu, Sylvain	2	Nick/Manu/Sylvain/Fabrice	
8. MULTIFAN-CL Viewer developments					
Add	Change to plot.rep	o # Recruitment block - shift from within the block: # Absolute biomass by region (across) and year (down), into a separate block of its own o Represent the results in the sections #length-sample/weight-sample components of likelihood by fishery (unhide)	3	Nick/Fabrice	

9. R4MFCL					
Add	Parallel Hessian calculation	o Get the Rscript that runs this working properly; test o load functions to R4MFCL	3	Nick/Pierre	Partly complete - script is working but not generic
Add	Update flaglist.csv	Update I:/assessments/Pop dy modeling/MFCL/flaglist.csv with new flags	3	Nick	
Add	Create gforge repository	Design the most suitable repository, possibly on GFORGE that Pierre can access.	3	Pierre/Fabrice	
Add	Redesign read.par	Fill out the *.rem section to be in discrete objects. With help from Pierre	3	Nick/Pierre	Partly complete - in progress
Add	Upload to google	Upload new R4MFCL to google code website "code.google.com/p/r4mfcl/"	3	?	
Add	Documentation	Document changes and start a manual	3	?	

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., Fournier, D., Hampton, J., Kleiber, P., Hoyle, S., Bouyé, F., and Harley, S. 2012. Recent developments in the MULTIFAN-CL stock assessment software. WCPFC-SC8-2012/SA -IP-01

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., Sisior, K., and Williams, A. 2011. Bigeye tuna age, growthm and reproductive biology (project 35). WCPFC-SC7-2011/SA-WP-01