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**DEVELOPMENTS IN THE MULTIFAN-CL SOFTWARE 2025-26**

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## EXECUTIVE SUMMARY

This paper summarises the developments made within the MULTIFAN-CL software project as carried out by the team at the Oceanic Fisheries Programme (OFP, The Pacific Community, Noumea, New Caledonia) from August 2025 to July 2026, and updates the report of Davies et al. (2025).

The current production version 2.2.7.7 has been benchmark-tested (Nov. 2025) and is available for wide distribution. Since then, the development version 2.2.7.9 has been tested for the specific developments made, has undergone abbreviated benchmark tests, and has been used by SPC-OFP for the 2026 bigeye and yellowfin tuna stock assessments.

During 2025-26, no significant mathematical innovations were implemented into the MULTIFAN-CL source code, which is consistent with the agreed 2025-26 workplan. Rather, the aim was to consolidate and enhance existing features to extend their implementation in stock assessment models, and for undertaking population projection analyses. However, a new feature was added to MULTIFAN-CL during 2025-26 being that prompted by a specific peer-review recommendation that revises the existing approach for imposing regional scaling upon the spatially-structured model. Its priority was raised during the SPC Pre-assessment Workshop, and was subsequently implemented in MULTIFAN-CL, and tested using the BET2023 assessment model example. The new feature adds a penalty function that is equivalent to putting a “prior” on the non-data quantity in respect of the presumed relativity in vulnerable abundance among the regions. It is demonstrated here to have achieved the recommendation’s aim of imposing regional scaling, but allowing for the estimation of index fishery-specific selectivities.

An independent investigation of the relative impacts of spatial heterogeneity in growth was required for the catch-at-age likelihood (an existing feature) to be upgraded from ‘prototype code’ to a production level. As such, the feature was re-instated, made operational, and provided the statistical model needed for the investigation.

Various other enhancements have allowed for more control over the estimation of particular parameters, and have improved the user’s operating environment. The user can now avoid unnecessarily long computation times for variance calculations of dependent variables, and can also tailor the required model run times during the exploratory stages of model development. These are important logistical considerations for the typically large and complex WCPO tuna assessment models.

Progressing towards the next generation of tuna stock assessment software became a priority project task during 2025-26 given the urgent transition required from MULTIFAN-CL to a new software framework. In addition to various contributions made by the MULTIFAN-CL project to the WCPFC Project 123 (“Scoping the Next Generation of Tuna Stock Assessment Software”), an independent development by Dr Kyuhan Kim greatly accelerated this progress by demonstrating that the **mfclrtmb** framework he has produced in RTMB, can match the performance and calculation accuracy of the native MULTIFAN-CL models. Parity tests among the two frameworks using several tuna assessment models indicate nearly identical results. As such, it provides a strong foundation for the future development of next-generation tuna stock assessment software. Useful future contributions from the MULTIFAN-CL project to this development will include: undertaking additional validation tests of model evaluations and minimisations between native MULTIFAN-CL and **mfclrtmb**; expanding automated benchmark testing and continuous integration workflows; and, assisting with whatever opportunities may exist for integrating the most effective aspects of both **mfclrtmb** and the native-RTMB project “opal”.

The focus of the 2026-27 workplan is a continuation of that for the past 3 years, i.e., to: consolidate and enhance existing features; act on peer-review recommendations; improve input processes and reporting; make any necessary corrections; and, keep user support documentation updated. No substantial new, or mathematically innovative, developments to the project are proposed in the coming year. Continued support to the next generation of tuna stock assessment software will remain a priority project task during 2026-27.

# 1 INTRODUCTION

MULTIFAN-CL 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 Dr David Fournier (Otter Research Ltd) and Dr John Hampton (The Pacific Community) for its initial application to South Pacific albacore tuna (Fournier et al. 1998). It has since provided the basis for undertaking stock assessments in the Western and Central Pacific Ocean.

The MULTIFAN-CL model is described in detail in the User's Guide (Davies et al. 2026). It is typically fitted to total catch, catch rate, size-frequency and tagging data stratified by fishery, region and time period. For example, recent tuna and billfish assessments (e.g., Teears et al. 2025, Kim et al. 2026, Magnusson et al. 2026) encompass long time periods, e.g., 1952 to 2024 in quarterly time steps, and model multiple separate fisheries occurring in up to 5 or 9 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), movement, 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 (integrated) likelihood comprised of the fits to the various data types, and penalized likelihood distributions for various parameters.

Each year the MULTIFAN-CL development team works to improve the model to accommodate changes in our understanding of the fisheries, to fix software errors, and to improve model features and usability. This document records changes made since August 2025 to the software and other components of the MULTIFAN-CL project, both for the current release version (2.2.7.8), and the current unreleased development version (2.2.7.9), and updates the report for the previous period, 2024-25 (Davies et al. 2025).

## 2 DEVELOPMENT OVERVIEW

### 2.1 Team

The senior developer of MULTIFAN-CL until December 2021 was Dr David Fournier, of Otter Research Ltd, (Canada), who has since retired. Development and testing are now undertaken by Mr Nick Davies. Other tasks include testing and debugging (ND, John Hampton, and Fabrice Bouyé (SPC)); documentation (ND); and planning and coordination (ND, Paul Hamer and JH). Related support project software is developed or managed by FB (MULTIFAN-CL Viewer, Condor, GitHub, Jenkins), Arni Magnusson, ND, and Robert Scott (R4MFCL, FLR4MFCL). More recently, related support project software includes various Shiny Apps (Kyuhan Kim), and the **mfclrtmb** framework that modernises MULTIFAN-CL within R/RTMB which is managed by Kyuhan Kim.

### 2.2 Calendar

As there is currently only one developer (ND), developer's workshops are no longer held, and the calendar year is less structured. However, broad periods may be identified, and include those for which more support is given to OFP stock assessment modelling.

August – November: Consolidating recent developments, benchmark testing, developments required for risk analyses

December – February: Code development, and testing

March – April: Training, stock assessment support, code development, and testing

May – July: Stock assessment support, code development, and testing

## 2.3 Collaboration and versioning

The repository and overall development are coordinated via the GitHub website on GitHub.com at <https://github.com/PacificCommunity/ofp-sam-mfcl> which is administered by Fabrice Bouye (fabriceb@spc.int) (section 2.4.7).

Problems with MULTIFAN-CL 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. A “master” branch exists for the MULTIFAN-CL source code from which release versions are posted. Development branches (“ongoing-dev”, “mac-dev”) have been created for holding development versions of the source undergoing development and testing. A formal testing procedure has been designed before source code is merged from the branch to the trunk, and a manual for the testing of new compilations, standardising the source code compilation procedure, and posting of executables is maintained.

## 2.4 Compilation framework and Source code repository

### 2.4.1 Compilation framework

A continuous integration facility allows for automatic nightly compilations of the MULTIFAN-CL source on the GitHub repository “master” branch. This automation is done using the software called Jenkins (<https://jenkins-ci.org/>), an Open-Source continuous integration tool that comes bundled with a web server used for administration. This software is now installed on a Linux Virtual Machine (VM) that is dedicated to MULTIFAN-CL development, and administers the compilations over the OFP network.

In this tool, we’ve added a custom scheduled task that automatically retrieves the MULTIFAN-CL source code out of the GitHub code repository (master branch); it also retrieves required libraries for the compilation. When done, our task compiles both debug and optimized versions of the software. We’ve also configured this task to produce code documentation out of the source code and to run some C++ code quality checking.

Doing a nightly compilation allows us to find out more quickly whether issues have been included in the source code repository without being solved by the developer. It also helps us identify issues in the makefile configurations that may prevent the compilation of MULTIFAN-CL on some more neutral environment (i.e. on a machine that is different from that of the developer’s).

During 2018-19 this facility was extended to support automated builds of the Windows (Visual Studio 2019) and the macOS release executables. The Windows10 VM used for undertaking the benchmark testing framework (see section 2.6) and the Mac Mini provides the platform for undertaking the routine compilation administered by Jenkins (see section 2.4.4). These automated builds were maintained throughout 2025-26.

It is also intended to add to the Jenkins tool the running of automated tests using example fish model data, and, in the future, unit tests for the software.

A directory structure on the dedicated VM mirrors that of all the developer’s platforms in respect of source code **Projects/**, associated libraries **libs/**, and **Testing/** directories. This ensures portability of source and makefiles among the developers and the automated build software.

### 2.4.2 Compilation of dependent libraries

For compilation of the dependent **OpenBLAS** library, the “dynamic architecture feature” is included to the routine compilations that builds several kernels for various processor types, and allows selection of the appropriate kernel at run-time. This may avoid the case where a MULTIFAN-CL executable that was compiled with OpenBLAS on a platform having a very recent processor, fails upon execution because function calls to the OpenBLAS library are attempted on platforms having relatively older processors. This compilation method results in a substantial increase (22 MB) in the executable size. However, it was noted that OpenBLAS libraries are important for the calculations used for the eigenvalues and eigenvectors of the Hessian matrix, and also aspects of the self-scaling size composition likelihood. This trade-off is therefore considered acceptable for the increased utility achieved.

In order for the MULTIFAN-CL project to be completely portable, three shell scripts automate the compilation of all the dependent libraries, before compiling MULTIFAN-CL. These scripts apply different options for OpenBLAS, QD and compilation flags for MULTIFAN-CL. The script “build\_openblas4mfcl.sh” builds 3 options of this library: "default", "generic", and "dynamic", where the "dynamic architecture feature" builds several kernels for various processor types, and allows them to be selected at run-time. Similarly, the script “build\_qd4mfcl.sh” builds 4 options of the QD library: "default", "O3", "O3fma", and "native". Given the various combinations of compilation options among the dependent libraries, ADMB and MULTIFAN-CL, compilations of 25 different executables may be produced. For a single option, it compiles in total: 49 minutes 5 seconds. This facilitates the portability of the entire MULTIFAN-CL compilation project including the dependent libraries, such that the complete project may be constructed and compiled with one step.

Note however, that for the automated compilation administered by Jenkins, compilation of the MULTIFAN-CL source code is undertaken using the independently pre-compiled dependent libraries QD and OpenBLAS.

#### 2.4.3 Compilation of Linux executable

The Linux version currently used for compilations is Ubuntu 22.04.5 LTS, with the gcc compiler version 11.4.0. No changes on account of compiler updates were required to the source code, and all compilations were stable during 2025-26.

#### 2.4.4 Compilation of Mac OS executable

During 2018-19, routine macOS compilations of the “master” and “development” branches were added to the compilation framework of the MULTIFAN-CL project. Compilations are done on the MULTIFAN-CL Testing PC (Mac Mini) that has the macOS Mojave installed (“macOS 10.14.6 Mojave”).

The Mac Mini PC has two compilation directories:

- Local compilation - stand-alone directory for testing development versions
- Jenkins compilation - for routine automated Jenkins compilations of the master branch (checked out from the repository, see section 2.4.1)

A Software ID certificate was assigned to the macOS compilation using an Apple Developer ID certificate for SPC. The macOS version is signed “Developer ID Application: The Pacific Community” issued by Apple. No differences were detected in the computations or performance among the signed and un-signed compilations.

No substantive problems with the macOS compilations were experienced during 2025-26, either with the operating system, compilation libraries, nor the C++ code.

Apple has now officially announced that they are ceasing production with Intel’s CPUs in favour of their own RISC ARM-based CPUs. The macOS compilation of MULTIFAN-CL will ultimately need to accommodate this change. A draft strategy for changing to the ARM-mac compilation for MULTIFAN-CL may entail:

- Following the 2021 Apple conference decide on a machine purchase to be made during 2022 (no machine has been purchased)
- Explore the potential for compiling on the existing Intel-mac with output target set to the new ARM-CPU using flags in the most up-to-date or the next version of XCode (the Apple dev tools/compiler)
- Maintain a careful watch of the capability of the Rosetta 2 emulator for running the MULTIFAN-CL executable (compiled for the Intel CPU) on an ARM-mac; this could offer a "breathing space" for our switch to the ARM-mac compilation
- Consider the merits of upgrading the mac Mini from Mojave to Catalina or Big Sur
- Potentially consider the lead developers purchasing an ARM-mac (external of SPC) for developing the compilation
- Aim for making the ultimate switch to the ARM-mac compilation for MULTIFAN-CL

The macOS x86 architecture is approaching its end point. If MULTIFAN-CL development is to continue with a macOS compilation, there will need to be some investment in both people and hardware to port to macOS AARCH64 instead.

#### 2.4.5 Visual Studio 2019 Windows compilation

Compiling the Windows executable is done using Visual Studio 2019 (VS2019), and all compilations were successfully completed during 2025-26 on the developer's workstation. No issues were encountered with the compilations as a result of updates to the VS2019 compiler.

#### 2.4.6 Development version

The development version is held in the development branches (usually "ongoing-dev") of the github repository. Upon completing benchmark testing of a development version, the source code in the development branch is merged to the master branch, and tagged with a release version number. At this point the development branch is created afresh for implementing any subsequent code developments, and a new compilation directory created. Other points where a new development version number is assigned is immediately following changes that may impact upon a minimised model solution, or alterations to the format of input/output files. These are then added to the development branch following preliminary testing, and tagged with the new version number. During 2025-26 a new development version was created following the benchmark testing of version 2.2.7.7.

A number of changes to the development version have been made since version 2.2.7.7 (Nov. 2025), and most of these were accompanied by abbreviated benchmark testing of the implications on the function evaluation and dependent variable estimates. These are described in sections 2.6.2 to **Error! Reference source not found.** While not fully benchmark tested, the detailed testing of the effects specific to each development, and the abbreviated testing, confirm no negative impacts on other existing features employed in the 2026 stock assessment models produced using the development version.

#### 2.4.7 Source code repository

The MULTIFAN-CL project is hosted on GitHub.com at:

- <https://github.com/PacificCommunity/ofp-sam-mfcl>

This site is only accessible to registered members of the OFP-SAM team. In order to better coordinate developments within components of the project, separate repositories were created for the:

- User's Guide: <https://github.com/PacificCommunity/ofp-sam-mfcl-manual>
- ADMB dependent library: <https://github.com/PacificCommunity/ofp-sam-admb>

The branches of the repository are managed such that following benchmark testing, the development version that has tested positive and held in either of the "mac-dev" or "ongoing-dev" branches, is then merged to the "master" branch. This creates a clear node in the "master" branch tagged as being the next release version. At that point a new development version is created in one of the "mac-dev" or "ongoing-dev" branches for undertaking the next phase of developments. This approach was followed for each of the versions during 2025-26, with the current development version being maintained in the "ongoing-dev" branch (version 2.2.7.9).

Between 9 Aug. 2025 and 8 Jul. 2026, a total of 27 source code commits were made to the master and development branches (29 source files have been modified, and 1 new source file added, see section 15), including a merge of the development branch to the master branch on: 3 Nov. 2025 for the distribution of version 2.2.7.7 to the Pacific Community. The current version in the "ongoing-dev" development branch is version 2.2.7.9.

During 2025-26, assistance was provided to the WCPFC Project 123: "Scoping the Next Generation of Tuna Stock Assessment Software". In one area, this assistance related to developing a public version of the MULTIFAN-CL github repository, see section 4.1.1.

### 2.5 **Developer's workshops**

As there is currently only one developer, no workshops were held during 2025-26. Since January 2022, Mr. Nick Davies has continued alone with the consolidation, enhancement and corrections to the existing features.

## 2.6 Benchmark testing during 2025-26

The benchmark testing framework is described in section 2.10.2, and one benchmark test, and several abbreviated tests, were undertaken in 2025-26. When relatively few changes have been made, the abbreviated tests explore their specific effects on example solutions obtained with the previous version. This is a precursor for undertaking the comprehensive benchmark test at a later date. A brief description of the tests, and the features tested, is provided in this section.

### 2.6.1 Version 2.2.7.7

In September-October 2025, comprehensive benchmark testing was done between the MULTIFAN-CL development version, and the benchmark release version 2.2.7.3 previously tested in March 2025. A complete set of tests were undertaken, to examine the cumulative effect of a number of enhancements and corrections made to the development version source code since version 2.2.7.3, as described in section 6, and by Davies et al. (2025), primarily including:

- **Sex-structured model**
  - shared selectivity-at-length among sexes accommodates growth offsets
  - sex-specific Lorenzen natural mortality
  - sex-specific conditional age-length observations
  - Richards growth formulation implemented in multi-species and multi-sex models.
- **Estimation of the independent variables**
  - allow disabling of the tagging negative log-likelihood  $\tau$
  - increased diffusion coefficients upper bound
- **Length-based selectivity**
  - selectivity constraints applied for: non-decreasing; common selectivity above a specified age; zero selectivity above/below specified ages
- **Simulation projections of the catch-conditioned model**
  - capability for all projection fisheries to be effort-conditioned
- **Various enhancements and corrections**
  - corrected the Richards growth implementation of mean length-at-age
  - finer resolution for the initial equilibrium survival rate scalar.

**Note:** all the benchmark testing was done using the compilation of the development version for the “standard” 64-bit precision, as this ensures comparability with the benchmark version 2.2.7.3. The range of testing data sets was the same as for the previous benchmark test, comprising: 10 single-species sets; a multi-species set; a multi-sex set; a single-species deterministic projection set; and, a single-species stochastic projection set.

#### Issues identified during testing

Code changes made in the development version were identified that caused notable differences in the operation or results obtained versus those of **vsn2.2.7.3**.

- Multi-species mean length-at-age for size compositions and catch. The correction was made to the multi-species/sexes mean length-at-age calculation for the species/sexes greater than 1 meant that for multi-species/sexes models employing the Richards curve estimation, the solutions will differ from those obtained using earlier versions.
- Effect of changed estimation bound on diffusion coefficients. A difference among the versions in the total integrated likelihood is evident and is due to a change in the value of the penalty on the independent variables. This change is attributable to the increase in the upper bound of the diffusion coefficients (diff\_coffs) applied in version 2.2.7.7 that slightly reduces the reset penalty. The slight change in the reset penalty will alter the objective function and gradient values, producing a different

iteration step in the independent variables, hence also the minimisation path. This difference was evident in the single evaluation tests and resulted in different solutions from the doitall tests.

- Change in the assignment from flag input value – age\_flags(128). For vsn2.2.7.3, the flag setting was such that the natural mortality multiplier for specifying the initial equilibrium conditions is assigned as:  $\text{age\_flags}(128)/10$ . For the development version, the flag settings were such that the multiplier is assigned as:  $\text{age\_flags}(128)/100$ . It was therefore necessary to increase the flag setting by an order of magnitude for the model evaluations using vsn2.2.7.7.
- Orthogonal-polynomial recruitments – age\_flags(177) setting. A correction was made the development version relative to the operation of  $\text{age\_flags}(177)$  within the initial population calculations. In the instance of the orthogonal-polynomial recruitments parameterisation, this flag is redundant, and the correction recognises this case. Therefore, for the model evaluations using the development version, the  $\text{age\_flags}(177)$  was set = 0.

## Results

Minimised solutions of the model examples that estimate movement diffusion coefficients produced slightly different solutions due to the change in the diffusion coefficient bounds in vsn2.2.7.7. This change most likely accounts for the differences in the dependent variable estimates; that are generally around 1% or less. For the SWO examples having fixed coefficients, identical solutions were obtained among the versions.

Tests of the development version concluded that the results were consistent with respect to the benchmark version 2.2.7.3 as all existing features remain intact, therefore the development version was advanced to become the new MULTIFAN-CL release version, **2.2.7.7**.

### 2.6.2 Abbreviated test – version 2.2.7.8

On 12 April 2026, an abbreviated test was undertaken, to examine the effect of enhancements made to the development version source code described in section 6, largely relating to the re-instatement of the catch-at-age likelihood.

Single evaluations and doitall fits of two single species examples, BET2023 and YFT2023 (both are catch-conditioned) were undertaken by version 2.2.7.7 and the development version 2.2.7.8. Both operations revealed identical results among the versions, and for both examples.

This test of the development version concluded that the results were consistent with respect to the benchmark version 2.2.7.7 as all existing features remain intact.

### 2.6.3 Abbreviated test – version 2.2.7.8

On 22 May 2026, an abbreviated test was undertaken, to examine the effect of enhancements made to the development version source code described in section 6, largely relating to the implementation of the penalty on regional scaling.

Single evaluations and doitall fits of two single species examples, BET2023 and YFT2023 (both are catch-conditioned) were undertaken by version 2.2.7.7 and the development version 2.2.7.8. Both operations revealed identical results among the versions, and for both examples.

This test of the development version concluded that the results were consistent with respect to the benchmark version 2.2.7.7 as all existing features remain intact.

## **2.7 Postings to website**

There have been no postings of the MULTIFAN-CL release versions to the website since July 2020.

## **2.8 Independent Peer Review of the 2011 bigeye tuna 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 MULTIFAN-CL software. These aimed not only to improve the software's application in the context of the bigeye assessment specifically, but

also its stock assessment application more generally. These recommendations have been the basis of MULTIFAN-CL developments since the review, and an outline of the status in fulfilling these recommendations is provided.

At the beginning of 2025-26, of the thirteen recommendations, 12 had been implemented and tested, and 1 remained yet to be developed:

- Non-uniform size bins (recommendation "b")

No further progress was made on recommendation "b" during 2025-26, and it remains as an incomplete task on the work plan.

## 2.9 Yellowfin Tuna Independent Peer Review 2022

In 2022, an independent peer review was undertaken of the 2020 yellowfin tuna stock assessment model (Punt et al. 2023). The outcome included five recommendations for improvements to be made to MULTIFAN-CL relating to: the length-weight relationship variance; selectivity splines; age-reading error; CPUE overdispersion parameter; and, natural mortality at age. These recommendations have been included in the MULTIFAN-CL workplan, and are within the tasks proposed for 2026-27 (Table 7). One of the recommendations not directly related to MULTIFAN-CL, was however included in the developments reported here (see section 5.1).

## 2.10 Tool development

### 2.10.1 R4MFCL

The R scripts for working with MULTIFAN-CL, developed and maintained by OFP are on a GitHub repository (<https://github.com/PacificCommunity/ofp-sam-r4mfcl>) and have been partially updated to adapt to the recent MULTIFAN-CL release version file formats. These scripts are used to manipulate the input files, so that submitting model runs can be automated from R. Other scripts can be used to read in the output files, analyze the results, and generate plots and tables. No commits were made to the repository during 2025-26, indicating the low use or maintenance of this package, as it has now been surpassed by FLR4MFCL (<https://github.com/PacificCommunity/ofp-sam-flr4mfcl>) and the Shiny App.

### 2.10.2 Testing framework

The testing framework for MULTIFAN-CL compilations was first developed in 2011-12, and was applied during 2025-26 for the benchmark testing of versions 2.2.7.3, 2.2.7.7 and 2.2.7.8 (section 2.6). 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 directories. The testing criterion is based upon pair-wise comparisons of model run results obtained using an existing MULTIFAN-CL compilation (usually the current release version) versus those from a development version compilation. Tests are undertaken over multiple processor platforms (64-bit architecture only), with application to multiple input testing data sets, and with various options for the MULTIFAN-CL operation, viz. single or multiple model evaluations, or full do it all 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.

Since March 2013, the MULTIFAN-CL source code has undergone substantial developments, and those have been described in earlier reports (e.g., Davies et al. 2025), and the recent developments made in 2025-26 are described in Sections 5 and 6.

Following implementation of these new features to the development version it is regularly tested versus the release version to ensure the integrity of the existing operations preceding the developments. Known as "benchmark tests", those undertaken in 2025-26 are described in section 2.6. The development version was last tested in May 2026 versus the version 2.2.7.7 in abbreviated tests. The positive result of a comprehensive benchmark test of this development version will then define it as being the **benchmark** source code, and then posted as the **release version**. Subsequent development versions will then be tested relative to the benchmark

to establish their integrity, after which they may be defined as the new benchmark version. The testing framework entails two levels of tests:

1. Establish the accepted development version

The first level of testing ensures the integrity of existing model features by undertaking tests using a selection from a range of single-species data including: ALB2012, ALB2015, BET2011, BET2014, BET2017, BET2023, SKJ2011, STM2012, SWO2013, SWO2017, SWO2021, YFT2011, YFT2014, YFT2017, YFT2020, YFT2023, SKJ2014, SKJ2016, SKJ2022, and SKJ2023. The aim of the tests is to evaluate the similarity of single model evaluations and the fitted solutions obtained using the development version relative to that of the benchmark version. Identical or close similarity indicates the integrity of the development version for undertaking single-species model evaluations. Results are compared among the versions and operating systems, to confirm that the development and release versions produced identical, or very similar, solutions. When differences are found, which can be attributable to improvements in the development version, these are accepted.

Tests using multi-species and multi-sex data disaggregated among species are done which entails comparing the fitted solutions of the development version code versus those solutions obtained using the corresponding data for each species fitted individually. These tests concluded that the operations applying to each population in the disaggregated model have integrity and effectively emulate the solutions obtained when each population is modelled individually. Note that species-specific fisheries data were supplied to the models in the test data examples used. Testing was not conducted using test data for which all fisheries data were aggregated among species (or sexes).

Similarly, tests are done for deterministic and stochastic projections with the pair-wise comparisons among versions and operating systems being made.

A positive test result is when the benchmark tests conclude that the development version conserves the existing features, and so can either be advanced as the new release version, or accepted for the new benchmark development version.

2. Establishing integrity of new features, enhancements, and corrections

This second level of testing entails a detailed examination of new features. The inputs and model configuration are customized for the new features and the operation of the new algorithms are evaluated in respect of the original formulations. During 2025-26 this level of testing was done for the new feature (see section 5.1) and enhancements/corrections (see section 6), to ensure the correct calculations and the expected results.

### Review of Testing Framework

In January 2016 the testing framework was reviewed by project members with the following agreed tasks for improvements:

- a) Tidy up the testing framework functions and utilities so as to be as automated as possible and more user-friendly with a view to including other team members in running the tests.
- b) Upgrade testing framework functions and utilities for applicability to both single-sex and multi-sex file formats, with portability over condor.
- c) Integrate the testing framework functions and utilities into the R4MFCL package and ensure compatibility with all assessment modelling applications.
- d) Create a GitHub repository for the testing framework functions, utilities, and testing data.
- e) Consolidate the R4MFCL GitHub repository with Rob Scott as the lead developer, and add access levels to Nick Davies as a support developer.
- f) Construct a suite of routine tests for the R4MFCL package to be run following each revision to the repository, and load the updated R4MFCL package to the testing framework.
- g) Construct a single routine MULTIFAN-CL test operation (e.g., single-evaluation of a fitted test model solution) to be conducted daily and directly from the Jenkins compilation utility that returns an exit status value, with an email report sent to the project developers.

Little action has been taken on these tasks this year. It has been identified as a concern, and therefore that they be included in the 2026-27 work plan for the MULTIFAN-CL project.

The routine compilation and development of a macOS executable is fundamental to the project, and the testing framework includes the Mac Mini host platform, with the macOS executable used for tests within and among platforms and versions. The framework therefore has capacity for conducting tests upon all 3 platforms simultaneously over the Condor network. The analysis of the tests performs pair-wise comparisons among versions and over the three platforms: Linux, Windows, and macOS.

#### 2.10.3 Viewer

The MULTIFAN-CL Viewer provides a ready means of examining independent and dependent variables of model solutions by illustrations and plots. No substantive changes nor corrections were made during 2025-26, and the current version has not yet been placed on the MULTIFAN-CL website for public release.

#### 2.10.4 Condor parallel processing facility

The Condor ([www.condor.wisc.edu](http://www.condor.wisc.edu)) facility has been used routinely for managing multiple MULTIFAN-CL model runs on a grid currently numbering more than 78 computers; being Linux (72), Windows (5), or macOS (1) platforms. This grid enables parallel model runs for: benchmark testing MULTIFAN-CL development versions; undertaking stock assessments that entail multiple model runs (e.g. sensitivity analyses and structural uncertainty grid analyses), and for management strategy evaluations. During 2025-26, additional Linux Virtual Machines were added to the grid to increase the number of parallel runs possible using the Linux development version executable. All Linux machines were updated to Ubuntu 22.04 and HTCondor 24.

### 2.11 User's guide

During 2025-26, the MULTIFAN-CL User's Guide was regularly updated consistent with the new features, enhancements and corrections made to the software. However, a substantial revision was made for releasing the Guide on the public MULTIFAN-CL repository in September 2025 (see section 4.1.1). The revisions, plus those developments relating to versions (2.0.7.3 to 2.2.7.8) included:

- Update of "Recent developments" to be entitled "Version History" and to include the cumulative developments since version 2.2.7.2 up to 2.2.7.8, and re-ordered the listing to start with the most recent version
- Revised the copyright statement to be consistent with the public repository version
- Display the version number in title page
- Richards growth formulation in Technical Appendix-A
- Number of minimisation evaluations completed is reported to **.par** file – updated the **.par** description
- Derivatives and variance calculations of dependent variables and for the iTRP metrics
- Independent variables bounds check indicators in the **indepvar.rpt**
- Terminal recruitments constrained to mean value for a specified period
- Tagging recaptures-conditioned likelihood – added to Technical appendix a description of the likelihood formulation
- Penalty function on estimated relative regional abundance
- Included Dr Kyuhan Kim and Dr Arni Magnusson in the authors list

The updated User's Guide (Davies et al. 2026) has been committed to the MULTIFAN-CL github repository, and will be posted to the Website following the next set of comprehensive benchmark tests.

## 3 TRAINING WORKSHOP

No formal training tutorials were required during 2025-26, although regular training support and Q and A support was provided to SPC analysts, and Nick Davies attended most weekly meetings of the stock assessment team to contribute to the 2026 assessment model developments.

## 4 NEXT GENERATION SOFTWARE

In the past 2-3 years, firm initiatives have been taken towards transitioning from MULTIFAN-CL to a next generation of software for undertaking tuna stock assessments (Magnusson et al., 2025). This has been a priority since the retirement in 2021 of the lead developer of MULTIFAN-CL, Dr David Fournier, and the limited future of further development and maintenance of MULTIFAN-CL by the remaining developer, Nick Davies. A 3-year WCPFC Project 123 “Scoping the Next Generation of Tuna Stock Assessment Software”, is in progress that aims to examine and evaluate the alternative options for other, or new, software (Magnusson et al. 2025). During 2025-26 substantial progress was made towards this transition, with: the MULTIFAN-CL project making direct contributions to Project 123; a project for the development of a new RTMB modelling framework “opal” (Ducharme-Barth et al. 2026); and, an independent development that modernises the MULTIFAN-CL assessment workflows in R with the RTMB (Kristensen, 2024) framework.

### 4.1 Project 123 project – contributions

#### 4.1.1 Public repository

The creation of a public github repository for MULTIFAN-CL was completed in September 2025: <https://github.com/PacificCommunity/multifan-cl>. This entailed:

- Revised all error messages and inappropriate variable names
- Reviewed the license to simplified BSD 2-clause
- Copyright note inserted at the top of all source files, and removed copyright conflicts
- Removed redundant source code files
- Various code improvements for syntax and `#include` statements to local header files
- Removed unnecessary non-source related ancilliary files
- Compilations on all platforms (Linux, mac OS, Windows)
- README and RELEASE\_NOTES documentation; improved history paragraph and links
- Dependent library licenses – ensured usage conditions satisfied
- Complete update of the User’s Guide

To comply with license requirements for the release of the Windows compilation executable, all Windows .dll license conditions were reviewed to satisfy the copyright conditions for distribution with the MULTIFAN-CL public version executable.

#### 4.1.2 Presentation to mini-CAPAM 2025

During December 2025, a mini-CAPAM workshop was held for “Developing the next generation tuna stock assessment model”, with contributions from global agencies engaged in regional-scale fisheries stock assessments, to discuss pathways for future assessment software. The MULTIFAN-CL project was invited to contribute an item: “Model mis-specification of length-based processes among available model structures”.

The item provided an overview of model structures (age-, size-, and age-size-structured) that highlighted those aspects causing mis-specification of certain length-based processes, and identified the formulations developed in each that attempt to correctly specify or approximate them. The length-based processes considered were: individual, and inter-annual variability in growth; and, spatial heterogeneity in growth. A ranking of the mis-specification “level” was offered in respect of each model structure in terms of its caveats; with a recommendation given for that model structure having the least mis-specification. The potential for bias from these forms of mis-specification in the context of Western and Central Pacific Ocean tuna was illustrated, and include: high levels of both individual growth variability and fishing mortality; inter-annual environmental variation; and, large-scale movement. The workshop was urged to consider model structures that avoid these sources of mis-specification in developing the next generation software.

The recordings of both the presentations and discussions (and presentation slides) are at: <https://www.populationassessment.com/tuna/next-gen-model/workshop>

#### 4.1.3 Exploration of Gadget3

Gadget3 (<https://gadget-framework.github.io/gadget3/>) is an R framework that implements models consistent with the Gadget2 C++ software, but utilizes the TMB framework (Kristensen et al. 2016). Having an age-size-structured population dynamics model at its core, Gadget3 offers a model structure that avoids the mis-specification of length-based processes inherent in most other available assessment software. During 2025–26, preliminary steps were taken to explore Gadget3 as a potential option for undertaking WCPFC tuna stock assessment modelling. Contact with the Gadget3 developers was established, and the task was discussed online. A Gadget3 installation was set up locally, and the repository's relatively complex blue ling model example was run through to the stages of the iterative re-weighting and the MLE minimisation. Although less complex than a tropical tuna model, this test offered insight into the capability and performance of Gadget3.

Further progress on this task entails in-depth learning of the framework and the mfdb marine ecosystem data management tool, in order to fully develop a tuna model project in Gadget3. Unfortunately, the limited resources during 2025–26 prevented further advances in these two areas, but it remains as a priority task for 2026–27.

## 4.2 mfclrtmb – a package that modernises MULTIFAN-CL in RTMB

During 2025–26, Dr Kyuhan Kim independently made a substantial advance by progressing the MULTIFAN-CL modelling approach into the RTMB framework (Kim & Davies, 2026). The RTMB framework (Kristensen, 2024) is now widely regarded as one of the leading platforms for stock assessment software development due to its suite of desirable and essential modelling features, broad user base, and strong development support. Kim's achievement in implementing the MULTIFAN-CL modelling software in RTMB represents a significant step towards the development of next-generation software for tuna stock assessments.

The **mfclrtmb** framework modernises MULTIFAN-CL as a native-compatible, extensible R/RTMB stock assessment platform that can run, check, and extend MULTIFAN-CL stock assessment models. It preserves the native fixed-effect calculation pathway for existing assessment model inputs, while making the model easier to inspect, test, simulate, and extend through modular RTMB components.

The framework reads the existing set of MULTIFAN-CL inputs (the *.frq*, *.ini*, *.tag*, *.age\_length*, and *.par* files), together with the **doitall.sh** script used for managing minimisation phasing, thereby preserving compatibility with the existing assessment framework and facilitating direct comparison with native MULTIFAN-CL results. At the same time, inputs can also be represented in user-friendly R objects, making data inspection, manipulation, and model development substantially easier.

The framework evaluates or optimises fitted restart files using the native-compatible fixed-effect pathway by default. It can also optionally write MULTIFAN-CL-style outputs so that existing assessment, diagnostic, and plotting tools can continue to operate without modification. In addition, the framework exposes RTMB module hooks that allow users to introduce optional modifications to biological processes, likelihood components, penalties, random effects, and reporting structures.

Building on the RTMB framework, **mfclrtmb** also enables the relatively straightforward inclusion of random effects and Bayesian MCMC methods. Importantly, because the framework reproduces existing MULTIFAN-CL calculations and workflows, new methodologies can be introduced incrementally through modular components without disrupting existing assessment, diagnostic, and reporting workflows.

Due to the substantial compilation requirements of the native MULTIFAN-CL codebase, particularly for the tagging component, the package currently relies on TMB and Rcpp alongside RTMB to achieve practical compilation times and reduced memory requirements. This implementation can be further refined as computationally intensive components are reformulated or simplified in future developments, potentially enabling a transition towards a fully RTMB-based implementation while maintaining computational efficiency.

The GitHub repository for **mfclrtmb** includes complete assessment examples for BET, SKJ, and YFT stock assessments. These examples are benchmarked against the native MULTIFAN-CL objective function values and maximum-gradient diagnostics stored in restart *.par* files. Three benchmark tests were conducted to assess compatibility with the original MULTIFAN-CL software, and all tests confirmed near-identical results, with only negligible numerical differences attributable to numerical approximation methods.

While **mfclrtmb** has not yet been formally released as a public software package, documentation describing the framework, validation exercises, implementation status, and future development plans is available through the project website:

<https://pacificcommunity.github.io/ofp-sam-mfclrtmb/>

The website serves as a reference for the ongoing development of **mfclrtmb** and its role in supporting next-generation tuna stock assessment modelling.

The project website includes dedicated documentation covering:

- **User guide:** installation, input checks, *.par* evaluation, doital runs, outputs, self-tests, and MCMC.
- **Model structure:** state dynamics, catch-conditioned mortality, observation likelihoods, tagging processes, recruitment, and objective-function components.
- **MULTIFAN-CL flags:** active flag coverage for the bundled BET, SKJ, and YFT parity cases.
- **Developer guide:** module hooks, backend profiles, extension levels, compiled hotspot layouts, and parity-validation practices.
- **Reference:** exported functions grouped by workflow.

The **mfclrtmb** framework provides a compelling demonstration that RTMB is capable of supporting the memory and computational requirements of complex tuna population models while maintaining calculation accuracy and performance comparable to the native MULTIFAN-CL software. As such, it provides a strong foundation for the future development of next-generation tuna stock assessment software.

Plans for further development of **mfclrtmb** include:

- Undertaking additional validation tests of model evaluations and minimisations between native MULTIFAN-CL and **mfclrtmb**.
- Updating the framework to the latest native MULTIFAN-CL development version.
- Expanding automated benchmark testing and continuous integration workflows.
- Incorporating random effects to support time-varying quantities such as selectivity and recruitment.
- Testing Bayesian MCMC approaches for uncertainty estimation and inference.
- Exploring additional modular extensions and modern assessment approaches within the RTMB framework.

These, and other developments, are discussed in the context of Project 123 by Hamer et al. (2026).

## 5 NEW FEATURES

No significant mathematically innovative features were implemented into the MULTIFAN-CL source code during 2025-26. Rather, the existing features have been consolidated, enhanced, and extended for their implementation in single species, multi-species/sex models, and for undertaking population projections. The current development version is **2.2.7.9** which holds all the developments described in this section, and section 6 that relates to enhancements and corrections made to the existing features since July 2025. These will be merged to the next release version upon the completion of the forthcoming comprehensive benchmark testing.

During 2025-26 a new feature was added in respect of imposing prior information derived from relative abundances upon the estimation of relative regional abundances, i.e., regional scaling.

### 5.1 Penalty on regional scaling

The current approach employed for achieving a prior assumption regarding the regional distribution of total abundance, is to infer this from the statistical model relating to CPUE relative abundance indices in each region. The method assumes stationarity in fishery catchability among the index fisheries in each region, that is achieved by grouping the index fisheries for the CPUE likelihood calculation. The model predictions are fitted to the observations with respect to the mean CPUE index over all fisheries within the group, with assumed shared selectivity among all the index fisheries. The relative difference of the predictions in each region in respect of the grouped mean index provides inference of the regional scaling in vulnerable abundance.

Punt et al. (2023) reviewed an assessment that employed this approach (YFT2020), and made the recommendation: “Allow for some differences among regions in selectivity and catchability while maintaining similarities to keep information on regional scaling”. The basis for this recommendation was the “evidence of differences in length-at-age among regions, which might be best modelled using different selectivity patterns for each region”. To give effect to this recommendation, an alternative approach for achieving regional scaling has been developed, and is presented here with implementation using the BET2023 model as a case study.

### 5.1.1 Methods

As per the recommendation, the method aims to allow for: regional scaling from observed CPUE indices; and, the estimation of variable selectivity among the index fisheries. Given the current parameterisation in MULTIFAN-CL for catch-conditioned fishing mortality estimation, and the CPUE likelihood term, the most efficient method was to add a penalty function (denoted **pregb\_pen**) to the integrated likelihood in respect of the regional scaling derived from the observed CPUE indices. This is equivalent to putting a “prior” on this non-data quantity in respect of the presumed relative in vulnerable abundance among the regions. The prior means, or “targets”, could be assigned on the basis of a “global” CPUE standardisation model that provides relative mean indices (with precision and covariances) for each region and time period.

#### 5.1.1.1 Definition of variable – regional scaling

The **regional scaling** variable is defined as the mean of the ratio of: the regional relative abundance indices; and, the sum of the regional indices in each time step. It is a time-variant vector of potentially correlated ratios from which the mean of the ratios over all time periods is derived – this being the observed regional scaling.

The relative regional scaling vector for region  $r$  in time step  $t$  is externally estimated:

$$\vartheta_{r,t} = \frac{I_{r,t}}{\sum_{r=1}^R I_{r,t}}$$

where  $I_{r,t}$  is the CPUE index and  $R$  is the number of regions, and so that

$$\sum_{r=1}^R \vartheta_{r,t} = 1$$

Let

$$\hat{\boldsymbol{\vartheta}}_t = (\hat{\vartheta}_{1,t}, \dots, \hat{\vartheta}_{R,t})^T$$

be the CPUE-derived relative scaling vector at time step  $t$  and  $^T$  denotes transpose. The mean vector is estimated by averaging the externally estimated CPUE-derived regional scaling vectors over  $n_t$  time steps

$$\bar{\boldsymbol{\vartheta}}_r = \frac{1}{n_t} \sum_{t=1}^{n_t} \hat{\boldsymbol{\vartheta}}_{r,t}$$

The corresponding population model prediction of the relative regional vulnerable abundance is:

$$\varphi_{r,t} = \frac{\sum_j s_{f,j} N_{r,t,j} \bar{w}_j}{\sum_{r=1}^R (\sum_j s_{f,j} N_{r,t,j} \bar{w}_j)}$$

where  $N_{r,t,j}$  is the population numbers at age  $j$ ,  $s_{f,j}$  is the index fishery-specific selectivity at age for fishery  $f$ , and  $\bar{w}_j$  the mean weight at age (not required when CPUE indices are in respect of fish numbers). The mean predicted relative region-specific scalars over all model time periods is

$$\bar{p}_r = \frac{1}{n_t} \sum_{t=1}^{n_t} \varphi_{r,t}$$

To be considered, is an alternative for the indices for both  $\bar{\vartheta}_r$  and  $\bar{p}_r$  to be derived rather as the median of the vulnerable abundance in each region  $r$  over all time periods. This may better account for non-normality and outliers in the respective CPUE and population vectors.

#### 5.1.1.2 Multivariate normal prior

The distribution for the penalty function is the multivariate normal (MVN), that is advantageous because it may take account of the region-specific covariance in the externally estimated CPUE-derived vectors  $\hat{\vartheta}_t$ , and the predictions  $\varphi_t$ , such that

$$\hat{\vartheta}_t \sim \mathcal{N}_R(\mu_{\vartheta}, \hat{\Sigma}_{\text{CPUE}})$$

with the mean vector (as described above) as

$$\mu_{\vartheta} \approx \bar{\vartheta}$$

The empirical covariance matrix can be calculated from the time series of the relative scaling vectors

$$\hat{\Sigma}_{\text{CPUE}} = \text{Cov}_t(\hat{\vartheta}_t)$$

that is

$$\hat{\Sigma}_{\text{CPUE}} = \begin{bmatrix} \hat{\sigma}_1^2 & \cdots & \hat{\sigma}_{1R} \\ \vdots & \ddots & \vdots \\ \hat{\sigma}_{R1} & \cdots & \hat{\sigma}_R^2 \end{bmatrix}$$

Each element of this covariance matrix is calculated as

$$\hat{\sigma}_{r,s} = \frac{1}{n_t - 1} \sum_{t=1}^{n_t} (\hat{\vartheta}_{r,t} - \bar{\vartheta}_r) (\hat{\vartheta}_{s,t} - \bar{\vartheta}_s)$$

The diagonal elements,  $\hat{\sigma}_r^2 = \hat{\sigma}_{rr}$  are therefore the sample variances across time of the CPUE-derived relative scaling values for each region. The off-diagonal terms  $\hat{\sigma}_{rs}$  are the corresponding sample covariances across time between regions  $r$  and  $s$ . This covariance matrix is then used to define the multivariate normal penalty.

The population model predicted regional scaling (as shown above) is

$$\varphi = (\varphi_1, \dots, \varphi_R)^T$$

that provides the predicted mean regional scaling  $p_r$ . Because  $\mathbf{p}$  and  $\hat{\vartheta}$  both sum to one, the full covariance matrix may be singular. So, a simple way is to remove one reference region and work with  $R - 1$  dimensions.

Define

$$\mathbf{d} = \mathbf{p}_{-R} - \hat{\vartheta}_{-R}$$

Then the multivariant normal penalty is

$$P = \frac{w}{2} \mathbf{d}^T \hat{\Sigma}_{\text{CPUE}, -R}^{-1} \mathbf{d}$$

where  $w$  is the weight assigned to the penalty.

If the off-diagonal covariance terms are set to zero, the covariance matrix becomes diagonal:

$$\hat{\Sigma}_{\text{CPUE}, -R} = \text{diag}(\sigma_1^2, \dots, \sigma_{R-1}^2)$$

and the multivariate normal penalty becomes

$$P = \frac{w}{2} \sum_{r=1}^{R-1} \frac{(p_r - \hat{\vartheta}_r)^2}{\sigma_r^2}$$

which is the same form as the independent normal penalty. So, the independent normal version can be seen as the diagonal-covariance special case of the multivariate normal version.

For implementation, it may be better to avoid calculating the inverse covariance matrix ( $\hat{\Sigma}_{CPUE,-R}^{-1}$ ) directly. Instead, using the Cholesky decomposition,

$$\hat{\Sigma}_{CPUE,-R} = LL^T$$

we solve

$$Lz = d$$

Then the same penalty can be written as

$$P = \frac{w}{2} z^T z$$

which should be more numerically stable than using the inverse covariance matrix directly, and was the form used for the testing presented in this report. This penalty  $P$  is denoted **pregb\_pen** in the text.

#### 5.1.1.3 Implementation in MULTIFAN-CL

A set of 5 `parest_flags` were employed for this feature to activate, specify or assign values for its operation. Also, new input and output files were created. These operational details are documented in the MULTIFAN-CL User's Guide (Davies et al. 2026).

#### 5.1.2 Testing design

The aim of the testing, aside from ensuring the feature's correct implementation, was to demonstrate the effect of implementing the alternative approach that employs the penalty, compared to the current method for inferring relative regional abundance. The two methods were denoted:

- **CPUE\_scaling** – assumed stationarity in fishery catchability among the index fisheries (grouped for fitting to CPUE observations), and shared selectivity
- **Prior\_reg\_biomass** – index fisheries are not grouped for the CPUE likelihood calculation, selectivity estimated independently among index fisheries, **pregb\_pen** penalty applied in respect of target relative regional scaling

For the **CPUE\_scaling** example the BET2023 diagnostic case model was used

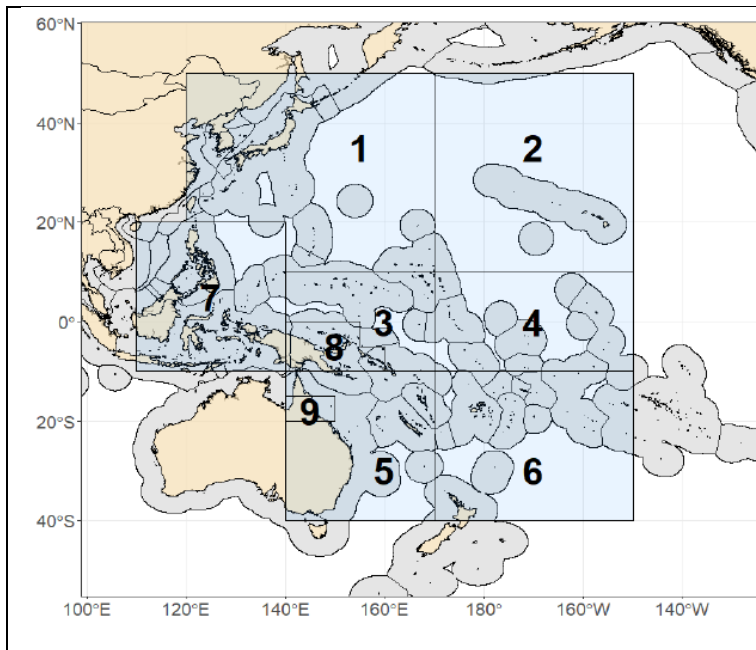
For the **Prior\_reg\_biomass** example four cases of the BET2023 model were considered having varying penalty weights, and denoted:

- **pregb\_mvn\_01** – CV $\approx$ 0.1
- **pregb\_mvn\_006** – CV $\approx$ 0.06
- **pregb\_mvn\_003** – CV $\approx$ 0.03
- **pregb\_mvn\_001** – CV $\approx$ 0.01

All the models were fit running the complete set of minimisation phases in the `doitall` script.

The region-specific CPUE indices input to the BET2023 model are presented in **Error! Reference source not found.**, illustrating clear and consistent differences among regional catch rates. These are expressed as the mean of the relative proportions of CPUE in each region over all time periods, and are shown in **Error! Reference source not found.**, illustrating that highest abundances are in regions 2, 4, and 7.

The mean region-specific proportions as derived from the CPUE indices for each of the BET2023 geographic regions were as follows:



| Region | $\bar{\theta}_r$ |
|--------|------------------|
| 1      | 0.127            |
| 2      | 0.262            |
| 3      | 0.094            |
| 4      | 0.219            |
| 5      | 0.048            |
| 6      | 0.098            |
| 7      | 0.130            |
| 8      | 0.018            |
| 9      | 0.004            |

To consider the effect of the penalty upon how well-determined is the model solution, Hessian diagnostics were carried out on the testing example **pregb\_mvn\_01** to determine if a positive definite Hessian (PDH) solution was obtained.

### 5.1.3 Results

The results are described in terms of the comparison between: the four **Prior\_reg\_biomass** models; and, the **CPUE\_scaling** model; and specifically in terms of the differences in respect of the **Prior\_reg\_biomass** models.

The **pregb\_pen** penalty terms are relatively small (<100, mostly <5 points) with respect to the other data types of the integrated likelihood (Table 1). The model fit was improved for the data types: CPUE, tagging, weight frequencies, and the overall total likelihood was improved for all of the **Prior\_reg\_biomass** model options; despite the addition of the **pregb\_pen** penalty term. The model fit worsened, albeit only slightly, for the data types: age-length; and, length frequencies (Table 1, shaded).

While the overall fit to the CPUE data type was improved, it deteriorated in regions 1 to 3 (Table 2). Similarly, the overall fit to the weight frequency data type was improved, but it deteriorated in regions 6 and 9 (Table 3).

For all of the **Prior\_reg\_biomass** model options, the temporal trend in the estimated abundance in region 1 was initially higher, and the decline was steeper during the initial model periods compared to that of the **CPUE\_scaling** model (Figure 3).

The penalty targets differ from that of the estimated regional scaling of the **CPUE\_scaling** model for region 2, and slightly for regions 4, 6 and 7 (Figure 4). This is probably attributable to the relative goodness of fit to the region-specific CPUE time series as estimated for the **CPUE\_scaling** model, that may result in the model-predicted values deviating from the arithmetic mean of the observed indices. The **Prior\_reg\_biomass** model estimates of regional scaling compared to the penalty targets and the **CPUE\_scaling** model (Figure 4) indicate:

- the region 1 biomass is consistently higher than the target;
- the region 6 biomass is consistently lower than the target;
- models with a penalty weight higher than CV=0.1 are closer to the regional targets; and,
- they are broadly consistent with the regional scaling of the **CPUE\_scaling** model.

The **Prior\_reg\_biomass** model estimates of the index fishery selectivity-at-age differ markedly from that of the shared estimated selectivity-at-age of the **CPUE\_scaling** model (Figure 5). Specifically, they:

- are nearly asymptotic for regions 2, 5, and 7;
- have reduced selectivity for the older ages (dome-shaped) for all other regions;
- have spurious values for age = 1 in region 6; and,
- for those models having  $CV < 0.1$ , appear spurious in region 9 (Figure 5).

The **Prior\_reg\_biomass** model estimates of absolute recruitments are generally higher, but particularly in the first half of the model periods (Figure 6). This is reflected in the mean total biomass being between 28 - 36% higher than **CPUE\_scaling** model, but having a similar temporal trend in adult biomass (Figure 7). The effect is for adult biomass to be around 8% less depleted ( $SB_{current}/SB_{F=0} \sim 0.44$ ) compared to the **CPUE\_scaling** model estimates (Figure 8). The **Prior\_reg\_biomass** model growth estimates also contribute to these differences in abundance, with the asymptotic length-at-age ( $L_{Amax}$ ) being estimated slightly higher (Figure 9).

The general effects of using the **pregb\_pen** penalty to impose regional scaling upon the model fit, rather than the existing method (**CPUE\_scaling**), has been to:

- change the regional abundances in regions 1, 2, and 6;
- increase stock productivity (recruitment, growth);
- improve the fits to CPUE, tags, WF data; and,
- improve the total integrated likelihood, despite the added penalty term value.

These changes are most likely related to the effects of removing the assumption of shared selectivity among the survey index fisheries, which improves the relative fit among the WF and CPUE data. Noting that the penalty does not achieve a close fit to the regional scaling targets in some regions (1, 2 and 6). This is therefore, a consequence of the relative importance among the data types in the integrated likelihood which is altered by the approach that employs the penalty function, and variable selectivity for the index fisheries.

#### 5.1.4 Hessian diagnostics

The solution for the testing example **pregb\_mvn\_01** was run for an additional 5000 function evaluations to achieve a more converged solution, that had a maximum gradient =  $4.3807e-04$ , and an improved total likelihood by 0.01687 absolute points. For the estimated Hessian matrix there were no negative eigenvalues calculated with this solution (the smallest value was  $1.8751e-08$ ), and it was therefore a positive definite Hessian (PDH) solution. This suggests that, for this particular testing example, the approach using the **pregb\_pen** penalty for regional scaling did not impact upon whether the model was ill-determined or not.

## 6 ENHANCEMENTS AND BUG FIXES

An overview of the enhancements and corrections made to existing features in MULTIFAN-CL during 2025-26 (up to March 2026) was provided to the pre-assessment workshop (Hamer, 2026). Those, and other developments made subsequent to that meeting to July 2026, are described in more detail in this section.

### 6.1 Catch-at-age likelihood

Implementation in MULTIFAN-CL for fitting models to the catch-at-age data type was largely completed in prototype form before 2008, but had not yet been fully completed, tested, nor applied for any production stock assessment. While reviewing and instating this feature was not in the project workplan item, it became significant for the purposes of an investigation into the effects of spatial heterogeneity in growth upon the bigeye stock assessment (Hampton et al. 2026). This study sought to approximate region-specific growth using a model fitted to region-specific catch-at-age data simulated from individual regional models. Hence, the need for a catch-at-age likelihood within the integrated statistical model became a priority task.

### 6.1.1 Code Implementation

The prototype code was reviewed and tested using a BET2023 model example to ensure the data input, variable assignments, and likelihood calculations were working correctly. Several corrections were needed: to the allocate/deallocate of the `age_freq` variable during the input procedure; and, to the composition data dimension assignments. Otherwise, the prototype code for the core tasks was mostly intact. New code implementation was required for: adding the Dirichlet-Multinomial likelihood effective sample size parameter to the independent variables report; employing a `parest_flag` for specifying the likelihood penalty weight; reporting the predicted catch-at-age for each fishing incident having an observation; developing a new routine `print_pred_age_frequencies()` to report observed/predicted values of the estimated likelihood; and, reporting the fishery-specific likelihood components to the detailed likelihood report “**test\_plot\_output**”.

### 6.1.2 Data input and flag settings

Details of the input data configuration and flag settings are described in the User’s Guide (Davies et al. 2026), but some aspects are mentioned here.

Catch-at-age data is input simply as another form of fishery-specific composition data, and as such is appended to each fishing incident row of the fishery data in the input `.frq` file, as an additional vector after the length- and weight-frequency sections. Several flag settings in the `.frq` file are required to activate the input of these data, for selecting the likelihood form for the statistical fit: log-normal or Dirichlet-Multinomial, and to implement the feature.

### 6.1.3 Testing

Preliminary testing of the feature was performed using proxy input data simply to validate the likelihood calculation, and the observed and predicted variables entering the calculation, and also, to develop the reports of the fit to the observations. A large part of the testing was performed in applying the feature to the BET2023 example (Day et al. 2023), in an evaluation of regional variation in growth by Hampton et al. (2026), that entailed fitting to very large simulated region-specific observation data sets. Using self-test simulations, the log-normal catch-at-age likelihood appeared to perform well in replicating the operating model population estimates. However, the Dirichlet-Multinomial likelihood formulation as developed in the prototype code appeared to be incomplete, and different to that currently applied to the size composition data in MULTIFAN-CL. A task has been added to the 2026-27 work plan to generalise the Dirichlet-Multinomial likelihood formulation for size composition data, to also accommodate age-composition data (see section 8 and Table 7).

For comprehensive examples of implementing this feature, please refer to Hampton et al. (2026).

At this point, the feature is available for implementation in production stock assessments while using only the log-normal likelihood formulation.

## 6.2 **Recaptures-conditioned tagging data likelihood**

### 6.2.1 Rationale

Ianelli et al. (2012) made recommendation “d”: *An option which allows the tagging data to inform movement only rather than movement and mortality*. Recent focus on spatial stock assessments, has identified a strong requirement for assessments using tagging data to explore solutions with the tagging likelihood in “recapture-conditioned” mode, as an alternative to solutions fitted to the negative-binomial likelihood for which total mortality is implicit. This alternative approach is sometimes loosely termed as using tagging data to “inform” the model in respect of movement only.

The differences among the two tagging statistical models are evident between:

- using the probabilities of caught tagged fish being caught in a particular year (can be independent of the total mortality in the population); and,
- using the probability of live tagged fish from a specific release event being caught in particular year (is therefore dependent upon total mortality).

The second approach (total mortality-conditioned) is sounder, and consistent with the assumptions of the tagging experiment, while the first approach (recaptures-conditioned) is implemented by conditioning the

tag likelihood in respect of the relative recapture rate for all releases made at a single time event. This methodology uses a modified Dirichlet-Multinomial likelihood conditioned in respect of recaptures only within each time period (Davies et al. 2026). It differs from the second approach, that uses a negative-binomial likelihood in respect of each tagging group over all time periods, and therefore includes the temporal effects of fishing mortality. The intent of the first approach is to fit tagging data conditioned in respect of recaptures only within each time period, i.e. so that the observations “inform” movement processes only.

Code implementation for this feature was developed at workshops between 2015 and 2018, first implemented for the single-species model, but then extended for the multi-species case, for grouped recaptures, and for tags being pooled into an aggregate tag group after a specified number of time periods at liberty. It was only tested preliminarily using the SKJ2016 model with tags pooled and grouped, with comparisons to solutions obtained using the standard negative-binomial tagging likelihood. The results appeared promising and plausible. While only preliminary, the feature was reported to SC15 as being available for modelling applications, but in prototype form (Davies et al. 2019).

During 2025-26, the task was to complete the testing of the feature, to review the code implementation, and to demonstrate its application with a recent tuna model example.

#### 6.2.2 Methods and Testing

The methods of fitting to tagging data were compared using two models, denoted as:

- **fmort\_cond** – using the standard total mortality-conditioned likelihood form
- **recaps\_cond** – using the recaptures-conditioned likelihood form

Using the BET2023 model having nine specified regions, with tags pooled and grouped, the **recaps\_cond** option was applied, and compared with respect to the standard **fmort\_cond** option that uses the negative-binomial tagging likelihood.

#### 6.2.3 Results

A minimisation of the **recaps\_cond** model starting from initial parameter values, produced an implausible solution, with implausibly high abundance. This indicated a lack of statistical inference relating to population abundance in the absence of predicted tag recaptures being conditioned in respect of total mortality. An alternative minimisation of the **recaps\_cond** model was attempted, starting from the solution obtained for the **fmort\_cond** model, switching to the recaptures-conditioned likelihood form, and then undertaking the minimisation for a large number of evaluations until convergence. This approach was successful, and ensured the model was in a plausible parameter space at the outset of the minimisation.

Aspects of the **recaps\_cond** estimates were plausible and comparable to the **fmort\_cond** model, with some moderate differences visible in the estimated movement (Figure 10). The comparison is in respect of the distribution of regional biomass through the fish’s lifetime by source region as derived from a simulation using the estimated movement coefficients. It indicates the proportion of biomass within a region that is sourced from recruitment within that region and from other regions. The main difference among the two models relates to the movement from region 6 (the plotted purple component, Figure 10). Movement from region 6 into only regions 5 and 9 was estimated for the **fmort\_cond** model. Whereas, movement from region 6 into all other regions was estimated in the **recaps\_cond** model. However, it is noted that almost no tagged fish were released in region 6, and consequently almost no movement observations for this region exist (Day et al. 2023). It is therefore likely that this difference among the models is due to the recaptures-conditioned likelihood not penalising model predictions for this instance to a similar extent as in the mortality-conditioned likelihood. The **recaps\_cond** model movement coefficients for region 6 are probably largely estimated in respect of the assumed prior.

The estimated reporting rates were broadly similar among the models, with differences in only several of the recapture groups.

The main difference among the two models related to absolute abundance estimates. The **recaps\_cond** model absolute biomass was substantially higher, with current spawning biomass more than 100% higher than the **fmort\_cond** model (Figure 11). While age-specific natural mortality was estimated to be slightly higher for young age classes (Figure 12), the major cause of this difference in absolute abundance was due to the higher

estimated recruitments of the **recaps\_cond** model. This reflects how different is the statistical inference taken from tagging data among the two approaches, that affects model abundance estimates. The mortality-conditioned likelihood ensures a reasonable fit of recaptures in respect of the period at liberty (Figure 13), while a substantially worse fit was obtained for the recaptures-conditioned approach. This may be expected given that only movement is inferred from the recaptures, irrespective of estimated mortality over time. However, for this particular example, the disparity in abundance estimates illustrates how important the tagging data are for estimating total mortality, and that other data types, e.g., CPUE, may be less “informative”. For the **recaps\_cond** model, improved fits were obtained to most other data types including CPUE, and the Dirichlet-Multinomial term for the tagging data had a lower absolute magnitude. This may indicate the effect of data conflict in this model example when the mortality-conditioned tagging likelihood approach is employed, producing slightly worse fits to other data types, and a lower estimated abundance. The relative effect of the recaptures-conditioned tagging likelihood is therefore likely to be case-specific, and dependent upon the relative importance among data types in the integrated likelihood.

## 6.3 Growth – testing the estimation of the Richards parameter

### 6.3.1 Rationale

The feature for estimating the Richards growth curve was completed with a final correction made in 2024-25 (Davies et al. 2025). The task remained to evaluate the feature’s implementation in a production stock assessment model context, and this was undertaken during 2025-26 using the SKJ2025 model as a testing example.

### 6.3.2 Testing and results

Two models were estimated using the SKJ2025 example, and the minimisation methods are described:

- **vonB**: von Bertalanffy growth as estimated for the skipjack 2025 [diagnostic case](#); doitall completed to 13.par with only 1000 evals in final phase; an additional phase 14 with 20K evals
- **richards**: doitall fit as per the vonB model, without growth offsets being estimated, with the estimated Richards growth parameter  $\gamma$

The **richards** model obtained a somewhat better likelihood solution (by 21.8 absolute points), however, the growth parameter  $\gamma$  was estimated at the upper bound value of 0.4, and is therefore not the optimal solution. The greatest improvement in the model fit was in respect of the CPUE data type.

A substantial difference in the estimate growth was obtained for the **richards** model, with a substantially lower asymptotic length-at-age (Figure 14). This resulted in higher historical adult biomass, but relatively similar estimates in the final model periods (Figure 15). The model fits to the size composition data were slightly improved, as well as for the CPUE data, but were worse for the tagging data.

The test indicated that the Richards growth estimation feature as applied to this example may produce markedly different estimates to that of the standard von Bertalanffy function, but that the estimation bounds may need revising to allow for a well-determined estimate of the Richards growth parameter  $\gamma$ .

## 6.4 Abbreviated derivatives and variance calculations of selected dependent variables

### 6.4.1 Rationale

Two tasks were added to the MULTIFAN-CL work plan in respect of calculating the variances of dependent variables, with each having separate objectives to:

- Optimize the variance calculation for selected ranges of dependent variables that may rationalise the computational performance; and,
- Add a new set of dependent variables, the interim target reference points (iTRP), as they are required for developing management advice.

#### 6.4.2 Method

The first task implements three options for the variance calculations that undertake either: the complete set of all dependent variables; an intermediate set (certain time-series variables and reference points); or, only the small set of stock status reference points. The options are controlled via **parest\_flags(37)** in respect of the assigned values: 0, 2, and 1, respectively. The first option (no abbreviation) requires up to 15 hours of computation time for some large and complex models, while the third option (full abbreviation) requires only a matter of minutes. The intermediate abbreviated option was implemented in the code, that includes the time series of total recruitment and spawning biomass, in addition to the small set of stock status reference points. Also implemented, was to include the population numbers at age by region for the final model year. The latter would enable sampling from the joint distribution of the terminal population numbers to propagate the estimation uncertainty into model projections. While including these additional dependent variables will increase the computational time relative to the full abbreviated option, it would nevertheless remain very tractable and useful for reporting diagnostic case variance estimates.

The second task adds to the set of dependent variables, the iTRP metrics as developed for the South Pacific albacore (SPA) assessment model in 2024-25. This reference point is central to the management strategy evaluations (MSE) conducted by SPC-OFP, and therefore estimating its uncertainty is critical to assessing the relative performance of candidate management strategies. The metrics are formulated as a ratio of: the latest or current stock status; and, the iTRP statistic. Both these factors entail predictions of the model under zero fishing mortality.

An important caveat must be stated in respect of the iTRP metrics implemented in the code: they are unique to the South Pacific Albacore (SPA) tuna stock assessment model. As such, the metrics are not generic for all tuna assessment models, and are not intended to be. The implementation is specific only to the SPA context and are labelled as such in the variances output file.

##### 6.4.2.1 Intermediate abbreviated calculation option

Under the **full-abbreviated** calculation option for the derivatives and variances of dependent variables, only the following stock status reference points are included:  $F_{recent}/F_{MSY}$ ,  $SB_{recent}/SB_{MSY}$ ,  $SB_{latest}/SB_{F=0}$  and  $SB_{recent}/SB_{F=0}$

To establish the intermediate abbreviated option, to this set, the following dependent variables were added:

- Total adult biomass over all model regions in each model year (year-quarter or year)

$$SB_{yr} = \sum_{ir} SB_{yr,ir}$$

where  $SB$  is the adult (spawning) biomass,  $ir$  is the region, and  $yr$  is the model year.

- Total recruitment (number of 1 year-old fish at the start of the model year) over all model regions in each model year

$$R_{yr} = \sum_{ir} R_{yr,ir}$$

where  $R$  is the recruitment.

- The population numbers at age by region for the terminal model year,  $nyr$ :  $N_{nyr,ir,age}$
- The ratio of fished:unfished total adult biomass over all model regions in each model year,  $SB_{yr}/SB_{yr,F=0}$

##### 6.4.2.2 iTRP metrics

The interim South Pacific albacore target reference point, iTRP, developed for the albacore tuna management strategy evaluations is:

$$iTRP = 0.96 * \text{mean} \left[ \frac{SB_{nyr-5}}{\overline{SB}_{nyr-15:6, F=0}}, \frac{SB_{nyr-4}}{\overline{SB}_{nyr-14:5, F=0}}, \frac{SB_{nyr-3}}{\overline{SB}_{nyr-13:4, F=0}} \right]$$

where *nyr* is the final model year (for the ALB2024 example it is fixed at 2022, i.e. the years for the calculation are 2017 to 2019).

The iTRP metrics in respect of latest and recent status are formulated relative to the adult biomass stock status. Adult biomass for the “recent” period is defined as that for the last 4 calendar years including the latest; i.e.,  $\text{mean}(SB)$  for the years (*nyr*-3) to (*nyr*). The “latest” period is defined as the most recent year (*nyr*).

The reference unfished adult biomass,  $SB_{F=0}$ , over a specified period is the average spawning biomass predicted to occur in the absence of fishing over a 10-year period preceding the most recent year less 1; i.e.,  $\text{mean}(SB_{F=0})$  for the years (*nyr*-10) to (*nyr*-1). Hence, the reference points for the adult biomass stock status are:

$SB_{\text{recent}}/SB_{F=0}$  - the average spawning biomass for a “recent” period (defined as above); relative to the reference unfished adult biomass

$SB_{\text{latest}}/SB_{F=0}$  - the spawning biomass for the most recent year; relative to the reference unfished adult biomass

The iTRP metrics employ these two reference points for adult biomass status in respect of the iTRP:

$$iTRP_{\text{recent}} = \frac{SB_{\text{recent}}/SB_{F=0}}{iTRP}$$

$$iTRP_{\text{latest}} = \frac{SB_{\text{latest}}/SB_{F=0}}{iTRP}$$

### Variance formulation

The variances of the iTRP metrics are therefore:

$$\text{var}(iTPR_{\text{recent}}) = \text{var} \left( \frac{SB_{\text{recent}}/SB_{F=0}}{iTRP} \right)$$

$$\text{var}(iTPR_{\text{latest}}) = \text{var} \left( \frac{SB_{\text{latest}}/SB_{F=0}}{iTRP} \right)$$

The variance calculation is achieved using the delta method by firstly calculating the ratio derivatives of  $SB_{\text{recent}}/SB_{F=0}$  and  $SB_{\text{latest}}/SB_{F=0}$ , and the derivative for the iTRP.

The derivatives and variances of the South Pacific albacore iTRP metrics are produced by default for each of the three dependent variable calculation options (no abbreviation, intermediate-, and full-abbreviation).

### 6.4.3 Testing and Results

#### 6.4.3.1 Abbreviated calculation options

Using the SKJ2025 example, the three abbreviated calculation options were compared in respect of the number of dependent variables and the computational performance on a stand-alone linux machine (Table 4). The intermediate option required only 5% of the calculation time of the no-abbreviation option (18 minutes), which is very tractable in a production stock assessment model context, and yet provides the main quantities of management interest.

The entries in the variances report file (\*.var) for the full abbreviation option include:

adult\_rbio(212):  $SB_{\text{latest}}$  (where “212” is the index for the model final year)

adult\_rbio(recent):  $SB_{\text{recent}}$

adult\_rbio(itrp\_6 to itrp\_4): numerators of the three component iTRP terms

average\_F/Fmsy(recent):  $F_{\text{recent}}/F_{\text{MSY}}$ ,

average\_SB/SBmsy(recent):  $SB_{recent}/SB_{MSY}$   
 adult\_rbio(nyr) - average\_adult\_rbio\_noeff(40\_periods):  $SB_{latest}/SB_{F=0}$   
 adult\_rbio(recent) - average\_adult\_rbio\_noeff(40\_periods):  $SB_{recent}/SB_{F=0}$   
 adult\_rbio(itrp\_6) - average\_adult\_rbio\_noeff(itrp\_6):  $\frac{SB_{nyr-5}}{\overline{SB}_{nyr-15:6,F=0}}$   
 adult\_rbio(itrp\_5) - average\_adult\_rbio\_noeff(itrp\_5):  $\frac{SB_{nyr-4}}{\overline{SB}_{nyr-14:5,F=0}}$   
 adult\_rbio(itrp\_4) - average\_adult\_rbio\_noeff(itrp\_4):  $\frac{SB_{nyr-3}}{\overline{SB}_{nyr-13:4,F=0}}$   
 adult\_rbio(nyr) - average\_adult\_rbio\_noeff(40\_periods) - iTRP:  $iTRP_{latest}$   
 adult\_rbio(recent) - average\_adult\_rbio\_noeff(40\_periods):  $iTPR_{recent}$

In addition to those above, the entries in the \*.var file for the intermediate abbreviation option also include:

adult\_rbio(1 to nyr):  $\log(SB_{yr})$   
 ln\_abs\_recr(1 to nyr):  $\log(R_{yr})$   
 ln\_abs\_N\_term\_age(1,1):  $N_{nyr,ir,age}$  where the numbers in parentheses are *ir* and *age*  
 adult\_rbio(1) - adult\_rbio\_noeff(1):  $SB_{yr}/SB_{yr,F=0}$  where the number in parentheses is *yr*

The \*.var file for the no abbreviation option includes the above entries for the intermediate abbreviation, as well as the many other dependent variables in the default calculation.

#### 6.4.3.2 iTRP dependent variables

Using the SKJ2025 example, the component terms for the South Pacific albacore *iTRP* were calculated (Table 5). Given that the adult biomass stock status reference points, latest and recent, were both close to 0.5 and the *iTRP* statistic was less than that value, the two *iTRP* metrics are both > 1.0, indicating the stock status is higher than the *iTRP*.

As is typical of ratio estimates, especially those having component terms being averages, the estimated variances for the two *iTRP* metrics were low, having CVs on the normal scale of 0.041 and 0.039, for the recent and latest metrics, respectively (Table 5).

## 6.5 Specifying the period for deriving the mean recruitments that are fixed for the terminal time periods

### 6.5.1 Rationale

Terminal recruitments are typically poorly estimated, and so an existing feature allows for recruitments to be fixed for a defined set of terminal time periods to a mean value. When **parest\_flags(400)** is set > 0, the flag value *n* specifies those *n* terminal time periods to have a temporal recruitment deviate = 0, i.e. no deviate is applied to the recruitment, effectively setting the log-recruitment at the level of the total population scalar (totpop), i.e. mean recruitment. This is essentially the mean of the log-recruitment, for which the absolute recruitments in normal-space will usually be lower than the arithmetic mean of the absolute recruitments in normal-space. Therefore, the existing feature also allows the option to fix the terminal recruitments to the arithmetic mean of the absolute recruitments in normal-space by setting **parest\_flags(398)=1**.

Both the above two options employ a mean of the historical recruitment estimates (either in log- or normal-space) calculated over the entire time period of the model (excluding the specified terminal periods). It may be desirable instead, to specify a subset of the model time periods for this calculation. Therefore, an additional option was developed for specifying the range of time periods for calculating the mean value to which

the terminal recruitments are constrained to. The method for this option is described, with the subset range being specified by **parest\_flags(364 and 365)**.

### 6.5.2 Method

Absolute recruitments in normal space in time  $t$  and region  $r$  for age class  $a = 1$ , are:

$$N_{a=1,t,r} = \bar{R} e^{\varphi_t} \alpha_r \gamma_{t,r}$$

Where:

- $\bar{R}$ , is the temporal average of spatially aggregated recruitment
- $\varphi_t$  determines the multiplicative deviation  $e^{\varphi_t}$  at time  $t$  of  $\bar{R}$ , with constraint that  $\sum_t \varphi_t = 0$ .
- $\alpha_r$  is the average proportion of  $\bar{R}$  in region  $r$ , and
- $\gamma_{t,r}$  is an additional region-specific deviation at time  $t$  and region  $r$ .

The implementation for the existing two options for fixed terminal recruitments are:

1. Mean of log(recruitments) – **parest\_flags(398) == 0**

The set of consecutive terminal recruitments are fixed at the default value for the temporal deviates being 0 on the log-scale,

$$\varphi_{t=terminal} = 0$$

2. Mean of absolute recruitments in normal space – **parest\_flags(398) == 1**

The arithmetic mean of the multiplicative deviates  $e^{\varphi_t}$  is assigned to the terminal temporal deviates:

$$\varphi_{t=terminal} = \log\left(\frac{\sum_t e^{\varphi_t}}{n}\right)$$

Where  $n$  is the total number of model time periods, excluding the terminal periods specified by **parest\_flags(400)**. This calculation assigns the log(mean of the deviates in normal space) to  $\varphi_t$ .

The new option for specifying the range of time periods for calculating the mean value to which the terminal recruitments are constrained to entails

$$\varphi_{t=terminal} = \log\left(\frac{\sum_{t=s}^{t=f} e^{\varphi_t}}{(f - s) + 1}\right)$$

where  $s$  and  $f$  are the first and last periods, respectively, of the subset of the model time periods specified for calculating the mean deviate assumed for the terminal time periods.

### 6.5.3 Testing and results

The SKJ2022 assessment model example was used to test and illustrate the new option because the estimated recruitments exhibit a clear temporal trend (Figure 16), that may produce contrast among models employing the new option with variations of  $s$  and  $f$ . In this example, recruitments were fixed at a mean level for the last two model time periods. Three models were tested, all using the existing option for terminal recruitments fixed to the mean of absolute recruitments in normal space, i.e., **parest\_flags(398) = 1**. The models differed only in respect of the time periods (excluding the terminal periods) there were included in the mean calculation:

- **mean** – all model time periods
- **low** – only the first 41 periods
- **high** – only the last 69 periods

such that the models **low** and **high** assumed: low and high recruitments, relative to the **mean** value, respectively (Figure 16). A single evaluation (deterministic) was performed for each model maintaining the identical independent variables for each. The terminal recruitments and dependent variables (total biomass) were compared among the models. As expected, the terminal absolute recruitments in normal space reflect the

difference in the low, mean and high values for the mean recruitment deviates applied in each model (Figure 17, top panel). The effect of this difference upon model total biomass in the terminal periods is slight, given that recruiting fish contribute relatively little to overall biomass, however, the relative effects among the mean values remains evident (Figure 17, bottom panel).

## 6.6 Increased upper estimation bound for diffusion coefficients

### 6.6.1 Rationale

This enhancement was not a task within the 2025-26 workplan, but exploratory model development for the 2025 SKJ stock assessments identified that a small number of the diffusion coefficients were estimated at the specified upper bound. These independent variables were also identified as contributing to the negative Hessian eigenvalues for the solutions that were not positive definite Hessians. It was therefore a priority to adjust the upper bound for this independent variable.

### 6.6.2 Method and Results

The code implementation that passes the independent variables to the minimisation procedure was modified such that the upper bound was increased from 3.0 to 4.0, without adjusting the penalty value. A SKJ2025 exploratory model was re-fitted with this enhancement active, and which had a positive effect, such that it achieved a PDH solution.

It was noted during subsequent benchmark testing (see section 2.6.1) that solutions obtained using the development version (that included this enhancement), differed with respect to the benchmark release version. The enhancement slightly altered the estimation penalty and the maximum values of the diffusion coefficients, and hence, the minimisation path taken; producing very slightly different solutions. This has implications for the replication of previous assessments when using the most recent version of MULTIFAN-CL.

## 6.7 Tagging negative binomial tau – option to disable estimation

### 6.7.1 Rationale

This enhancement was not a task within the 2025-26 workplan, but it was deemed desirable for calculating the likelihood profile of a solution to retain fixed the maximum likelihood estimate (MLE) value for the negative binomial tagging likelihood dispersion parameter  $\tau$ .

### 6.7.2 Method

The existing options for estimating  $\tau$  included:

- bounds: -50.0 and 50.0
- bounds specified by **parest\_flags(306)**
- only an upper bound specified by **parest\_flags(358)**

A new option was added such that estimation of  $\tau$  was completely de-activated, and was fixed at the value from the input solution **.par** file.

## 6.8 Report grouped survey index fishery-specific CPUE likelihood components

### 6.8.1 Rationale

This enhancement was not a task within the 2025-26 workplan, but it may be important to identify individual fishery-specific components of the CPUE likelihood when the survey index fisheries are grouped. For the purpose of imposing regional scaling on a model (when not employing the new feature described in section 5.1), stationary catchability among the survey fisheries of each region may be assumed, and this requires assigning all the fisheries to a single group for the CPUE likelihood calculation. In the detailed likelihood report (**test\_plot\_output**), the CPUE likelihood estimate was reported for the sum total of the group, and not for the individual fisheries comprising the group.

### 6.8.2 Method

The algorithm for the grouped CPUE calculation required substantial modifications to subset the individual fishery-specific components. It was also necessary to apply this generically to all cases of the CPUE likelihood in respect of: the concentrated/non-concentrated formulation; index in numbers/biomass; and, constant penalty weight over-ride/no over-ride. Consequently, the algorithm in the code implementation was completely revised to be more efficient by assigning the predicted index variable in respect of numbers or biomass to a generic vector preceding the calculations for all the options for the grouped case. A substantial improvement in the code structure became evident, that removed about 400 lines and simplified code to be easier to understand and read.

The subset survey index fishery-specific CPUE likelihood components are now reported in the detailed likelihood report (*test\_plot\_output*), together with the grouped value.

## 6.9 Independent variable estimates – bounds check indicators

### 6.9.1 Rationale

This enhancement was not a task within the 2025-26 workplan, but it is useful to have a ready indicator of independent variables being estimated at, or very close to, the specified bounds. This condition often occurs for ill-determined parameters, or when the minimisation is unstable.

### 6.9.2 Method

A detailed report of the independent variables (*indepvars.rpt*) was added to MULTIFAN-CL version 2.2.7.0 (Davies et al. 2024), listing the estimates and bounds for each. The enhancement was made to evaluate each estimate relative to a threshold of the estimate being within 0.1% of either bound's value. If true, a character string "\*\*\*\*\*" is appended to the end of the row for that independent variable in the report. This offers a clearly visible, or digitally locatable, identifier of the variable's bound being reached during estimation.

## 6.10 Number of evaluations and iterations added to \*.par file

### 6.10.1 Rationale

This enhancement was not a task within the 2025-26 workplan, but was added because of the utility of having a record of how many model evaluations and minimisation iterations were required to achieve a model solution. This is particularly useful when designing the logistics of large-scale parallel minimisations or "grids" of models for factorial uncertainty estimation.

### 6.10.2 Method

While the maximum number of evaluations is specified by the analyst when submitting a model for minimization, and this is stored as a flag setting, no record is kept of the actual number that were performed when either: the convergence criterion was achieved; or, the minimization terminated; before the maximum number of evaluations was reached.

During the minimisation procedure routine that evaluates the maximum gradient relative to the convergence criterion, the current evaluation and iteration number were assigned to global variables, which upon termination were written to the *.par* file, e.g., as:

```
...
# Objective function value
  3.21159787957713e+05
# The number of parameters
  1498
# The number of evaluations
  15566
# The number of iterations
  7333
# Likelihood component for tags 2.13061452632088e+04
```

...

## 6.11 Exit error screen notice: input tag event mixing period error

### 6.11.1 Rationale

This enhancement was not a task within the 2025-26 workplan, but was identified as being essential in the instance of retrospective analyses that successively remove tagging data. In such cases, it is possible for the retrospective removal of these data, together with the shortening of the model calculation period, to result in tagging events having specified mixing periods that coincide with, or include, the final model period. This produces an implausible tagging event, such that no recaptures are available for the likelihood, and produces bound exception errors.

### 6.11.2 Method

An error exception was implemented for: those tag release events having data such that the release date is greater than or equal to: the terminal period minus the number of mixing periods. These are implausible release events and also, the Newton-Raphson tagging mortalities are not calculated for the mixing period that coincides with the terminal model period. These release events should not be included in the tagging data input to the model.

A sanity check was drafted to catch these instances prior to entering the fitting procedure, to prevent an evaluation termination occurring. A screen report is issued upon terminating the evaluation, with details on how to amend the tagging data. This exit error was made robust to the **-makepar** operation, such that the sanity check is only performed when the **tag\_flags** are populated, i.e., in phase 1, or greater, of the minimisation.

## 6.12 Bug fixes

### 6.12.1 Correction: insert conditional routine call to get equilibrium structure for yield

A routine call required when undertaking the equilibrium yield calculations was made conditional upon the estimation of the Beverton-Holt stock-recruitment relationship (BH-SRR) being estimated. This was necessary if the solution being reported to the output **plot.rep** file was implausible, and without an estimated BH-SRR.

### 6.12.2 Correction: assignment of the Richards growth parameter for multi-species/sexes

In undertaking the testing of the feature for estimating the Richards growth curve (see section 6.3), it was evident that the assignment of the estimated Richards growth parameter  $\gamma$  from the independent variable minimisation vector was incorrect for the case of the species or sex index  $> 1$ . The assignment was corrected.

### 6.12.3 Correction: added the weight frequency Dirichlet-Multinomial parameters to the independent variables report

While the estimated parameters of the Dirichlet-Multinomial size composition likelihood for length frequency data were included in the detailed independent variables report, those estimated for the corresponding weight frequency likelihood were missing from the report. They were duly added to the detailed report "indepvar.rpt", with the text string identifiers:

```
fish_pars(24)_weight_dirichlet_mult_var_mult_coff  
fish_pars(25)_weight_dirichlet_mult_var_mult_covariate
```

with the number of rows for each parameter corresponding to the number of fisheries grouped, or ungrouped, for its estimation.

## 7 APPLICATION OF FEATURES

### 7.1 Stock assessments for SC22

The 2026 bigeye and yellowfin stock assessment models (Kim et al. 2026, and Magnusson et al. 2026) were undertaken with implementation of selections of the above-mentioned enhancements in the updated development version 2.2.7.8 of MULTIFAN-CL.

### 7.2 Investigation of the impacts of spatial growth heterogeneity

The catch-at-age likelihood development was initially prompted, and subsequently used by Hampton et al. (2026) in investigating the relative impacts of spatial heterogeneity in growth. The log-normal catch-at-age likelihood formulation was employed in fitting to region-specific catch-at-age compositions having inherently different growth patterns. The feature proved useful for the purposes of this study.

## 8 FUTURE WORK

A listing of the status of the work that was originally proposed, that is pending, in progress, or completed during 2025-26 is provided in Table 6. While a proportion of what was proposed, as well as unforeseen tasks subsequently added, were completed, a number of tasks were not.

The proposed future work plan for the development of MULTIFAN-CL in 2026-27 is presented in Table 7. Those tasks not completed in 2025-26 have been carried over into this workplan. As was the case for the 2025-26 workplan, no new developments that require substantive mathematical innovation are proposed for the 2026-27 workplan. Rather, resources will be directed to: consolidating aspects of existing features that are incomplete; enhancements of existing features; and to MULTIFAN-CL support documentation. The general approach for the future workplan is the same as that of 2025-26, and includes:

- Testing the implementation of examples that employ all the new features and refine the I/O and diagnostic reports.
- The code for existing features will be reviewed and refined; a backlog of bug fixes will be completed; outstanding tasks from the bigeye and yellowfin tuna independent review panel recommendations will be addressed; and any "small-scale" requests in the tasks list.
- Provide training and support for OFP stock assessment scientists.
- Provide support for WCPFC Project 123 to scope the next generation tuna model and the succession beyond MULTIFAN-CL.
- Providing support for MSE requirements and improvements.
- Maintaining the documentation required for the MULTIFAN-CL User's Guide.

Some of the items in Table 7 (tasks rolled over from 2025-26) have been retained, but will be fit within the context of the 2026-27 workplan, and others have been set aside for the years that follow.

## 9 DISCUSSION

No mathematically innovative or structurally new features were implemented into the MULTIFAN-CL source code during 2025-26. Rather, as for 2024-25, the approach set out in the 2025-26 work plan was followed for the existing features to be consolidated, enhanced, and extended for their implementation in developing stock assessment models, and for undertaking population projections for MSE and TRP analyses.

However, a new feature was added to MULTIFAN-CL during 2025-26 being that prompted by a specific peer-review recommendation (Punt et al. 2023) to revise the existing approach for imposing regional scaling upon the spatially-structured model. While not a direct recommendation for the MULTIFAN-CL software, it did necessitate sizeable source code implementation and testing. Instead of making the strong assumptions of stationary catchability and shared selectivity among the survey index fisheries, this feature imposes a penalty function (multivariate normal) having specified regional scaling target values, and completely relaxes the assumption of shared selectivities. Tests of this approach using the bigeye tuna model revealed large differences

in the index fishery selectivity estimates relative to those obtained using the existing approach, and improved the model fits overall. This result seems to justify the impetus of the peer-review panel's recommendation that: differences in region-specific size compositions most likely reflect spatial heterogeneity in growth, for which the estimated selectivity may proxy. This indeed seemed to be the case, with dome-shaped selectivity-at-age being estimated for one of the northern regions that is consistent with the slower growth believed to occur in this region, and with a substantial improvement in the fit to the observed CPUE indices.

Other developments made during 2025-26 related to enhancements of existing features, however, re-instating the catch-at-age likelihood entailed upgrading the existing feature from a state of prototype code, to a production level. Corrections and new code implementations were needed to make it operational, with the generation of new output diagnostic reports. This development was prompted by the investigation by Hampton et al. (2026) of the relative impacts of spatial heterogeneity in growth, and proved useful for the purposes of this study.

The various other enhancements to MULTIFAN-CL fall into three broad categories:

- reviewing and testing existing features (using tagging data to “inform” movement only, Richards growth curve estimation);
- adjustments to parameter estimation (altering the estimation bounds, disabling parameter estimation, defining terminal recruitments); and,
- improvements of the user's operating environment (control of variance estimation, adding management advice metrics, number of evaluations).

The first category provided tractable demonstrations of the existing features using the recent stock assessment models for bigeye and skipjack tuna (2023 and 2025, respectively). These were not only demonstrations that the feature has been implemented as intended, but also showed the significant effect of the alternative parameterisation for each example. While case-specific, each parameterisation produced markedly different model solutions compared to the “standard” diagnostic cases, and offered insights into the parameterisation's effects. The result using the recaptures-conditioned tagging likelihood, clearly shows the importance of this data type for estimating absolute abundance, while the movement patterns were not drastically different, apart from one of the regions for which there was almost no data. The result using the Richards growth estimation shows that as a consequence of the large difference in estimated growth, particularly the asymptotic length, there was a change in the quality of fit among the data types. These tests have demonstrated the utility of the features for at least exploring alternative model parameterisation options at the outset of developing stock assessment models.

The second category allows for more control over particular parameter estimation, (having been implemented at the request from model analysts), while the third category aims to streamline the user's work environment. A significant reduction is now possible in the calculation time required for the variances of dependent variables by selecting the intermediate abbreviation option; by up to 95% (around only 18 minutes for the example tested). This facilitates these calculations to be performed over the large grid of models that is typical in current tuna assessments. Similarly, having both the number of evaluations and minimization iterations are now reported to the solution *.par* file, the analyst may tailor the computation times of model runs to be done on the basis of the number of evaluations required to achieve a pre-determined gradient level. Thus, the user can avoid unnecessary model run times during the exploratory stages of model development. This is an important consideration for the WCP0 tuna assessment models that typically require between 5 to 24 hours to achieve a converged solution.

The new features and enhancements were tested in detail using tuna stock assessment model examples, with the outcomes and implications reported to SPC-0FP in feature-specific reports. Where these developments were isolated from other existing features, i.e., essentially adding a new module to the MULTIFAN-CL framework, only abbreviated benchmark testing was undertaken to economise on resources. In these instances, the comparative test results were identical as expected.

A substantial change to the 2025-26 MULTIFAN-CL project workplan related to sizeable contributions being made to the WCPFC Project 123 “Scoping the Next Generation of Tuna Stock Assessment Software” (Magnusson et al., 2025). This change was a priority due to the urgent transition needed to a new software

framework for undertaking tuna stock assessments. The contributions included: completing the public github repository for MULTIFAN-CL (as an essential reference and source code resource for contributors); delivering a presentation to the 2025 mini-CAPAM workshop (as part of the global discussion on the best software development directions); and, undertaking a preliminary exploration of the Gadget3 modelling framework for its potential application in tuna assessments (because it employs the age-size population structure). In addition to these, the independent development by Dr Kyuhan Kim achieved a significant advance towards the next generation software, by extending the MULTIFAN-CL modelling approach into the RTMB framework. Called the **mfclrtmb** framework, it demonstrates in practice that the memory and computational requirements of complex tuna population models are possible within RTMB, while maintaining the calculation accuracy and performance comparable to the native MULTIFAN-CL software. It has satisfied a fundamental requirement regarding RTMB as a framework suitable for spatially-structured tuna models, that it is as good as or better than the current MULTIFAN-CL software. The next steps will most likely be technical in nature, beginning with examining the role that the Rcpp has in **mfclrtmb**, in that it avoids typical R computational bottlenecks that C++ can address. Alongside RTMB, it achieves practical compilation times and reduced memory requirements. This implementation may be further refined as computationally intensive components in **mfclrtmb** are reformulated, or simplified, in future developments, potentially enabling a transition towards a fully RTMB-based implementation, while maintaining computational efficiency. Opportunities may exist for integrating the most effective aspects of both **mfclrtmb** and the native-RTMB project "Opal" (Ducharme-Barth et al. 2026) in the next steps of developing the software.

A number of tasks set out in the initial 2025-26 workplan were replaced by several smaller, but high priority or more important tasks introduced during the year as were required for completing the 2026 stock assessments. This flexibility in implementing the workplan is typically necessary for ensuring that the production version of MULTIFAN-CL is capable of producing stock assessment models having specific assumptions and parameter configurations, and is able to obtain well-determined solutions. Consequently, those lower priority, incomplete tasks for 2025-26 have been carried over to the 2026-27 workplan, which will most likely also continue to include a considerable contribution towards the next generation software developments.

## 10 DECLARATION OF GENERATIVE AI AND AI-ASSISTED TECHNOLOGIES IN THE SC PAPER PREPARATION PROCESS

Generative AI tool: GitHub Copilot (Microsoft) was used for development support to assist with the code development, refactoring, and documentation of the **mfclrtmb** package (see section 4.2). No AI technologies were used in all other parts of this document, the analyses presented herein, nor in the drafting and editing of text in this document. The methodology, model implementations, interpretations, and the scientific conclusions are the responsibility of the authors.

## 11 ACKNOWLEDGEMENTS

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## 13 TABLES

**Table 1. Total integrated likelihood components by data type, and maximum gradient, for the BET2023 model options as described in the text. Shaded cells indicate those options with a worse fit relative to the CPUE\_scaling model option.**

| Likelihood component | CPUE_scaling | pregb_mvn_01 | pregb_mvn_006 | pregb_mvn_003 | pregb_mvn_001 |
|----------------------|--------------|--------------|---------------|---------------|---------------|
| pregb_pen            | -            | 72.07        | 3.897         | 1.239         | 0.214         |
| Length frequency     | -74469.375   | -74423.246   | -74425.797    | -74445.478    | -74428.579    |
| Weight frequency     | -962161.076  | -962554.368  | -962430.599   | -962379.369   | -962393.965   |
| Tagging data         | 6308.667     | 6144.528     | 6161.169      | 6120.582      | 6120.21       |
| CPUE survey index    | -2393.623    | -2553.278    | -2563.169     | -2570.408     | -2569.411     |
| Age-length data      | 1569.897     | 1573.193     | 1572.955      | 1576.725      | 1591.011      |
| Total                | -1030851.398 | -1031442.993 | -1031380.337  | -1031393.898  | -1031379.589  |
| Gradient             | 8.1588e-06   | 8.3146e-04   | 6.5106e-03    | 2.7944e-03    | 2.6780e-03    |

**Table 2. CPUE likelihood components specific to each of the survey index fisheries among the BET2023 model options as described in the text. Shaded cells indicate those options with a worse fit relative to the CPUE\_scaling model option.**

|          | CPUE_scaling | pregb_mvn_01 | pregb_mvn_006 | pregb_mvn_003 | pregb_mvn_001 |
|----------|--------------|--------------|---------------|---------------|---------------|
| Fshry_33 | -298.154     | -291.259     | -292.773      | -292.888      | -291.893      |
| Fshry_34 | -225.244     | -211.744     | -210.939      | -217.658      | -217.018      |
| Fshry_35 | -333.908     | -331.826     | -328.374      | -330.837      | -330.906      |
| Fshry_36 | -297.428     | -314.666     | -313.627      | -311.937      | -311.857      |
| Fshry_37 | -285.919     | -289.218     | -289.262      | -288.533      | -288.427      |
| Fshry_38 | -324.586     | -363.365     | -392.092      | -392.29       | -392.111      |
| Fshry_39 | -342.684     | -353.533     | -349.81       | -353.886      | -354.709      |
| Fshry_40 | -229.081     | -303.673     | -322.728      | -318.259      | -318.589      |
| Fshry_41 | -56.619      | -93.992      | -63.564       | -64.119       | -63.902       |
| Total    | -2393.623    | -2553.278    | -2563.169     | -2570.408     | -2569.411     |

**Table 3. Weight-frequency likelihood components specific to each of the survey index fisheries among the BET2023 model options as described in the text. Shaded cells indicate those options with a worse fit relative to the CPUE\_scaling model option.**

|          | CPUE_scaling       | pregb_mvn_01 | pregb_mvn_006 | pregb_mvn_003 | pregb_mvn_001 |
|----------|--------------------|--------------|---------------|---------------|---------------|
| Fshry_33 | -87487.754         | -87601.302   | -87597.484    | -87589.392    | -87594.01     |
| Fshry_34 | -58251.238         | -58280.527   | -58273.2      | -58270.321    | -58268.723    |
| Fshry_35 | -89726.426         | -89777.478   | -89779.214    | -89777.251    | -89777.903    |
| Fshry_36 | -58991.376         | -59014.345   | -59012.971    | -59014.864    | -59014.477    |
| Fshry_37 | -19094.435         | -19098.573   | -19098.025    | -19097.243    | -19097.111    |
| Fshry_38 | -15210.278         | -15203.355   | -15197.457    | -15197.595    | -15197.518    |
| Fshry_39 | -34628.254         | -34642.239   | -34640.603    | -34640.116    | -34640.135    |
| Fshry_40 | -17263.303         | -17275.044   | -17275.902    | -17276.657    | -17277.014    |
| Fshry_41 | -1115.416          | -1114.55     | -1105.398     | -1105.096     | -1104.928     |
| Total    | <b>-381768.481</b> | -382007.414  | -381980.253   | -381968.534   | -381971.818   |

**Table 4. Number of dependent variables and calculation times (derivatives and variances) for each of the three options available in MULTIFAN-CL using the SKJ2025 model example.**

| Abbreviation option | Norm_eval no. dep_vars | F0eval no. dep_vars | Total no. dep_vars | Calculation time |
|---------------------|------------------------|---------------------|--------------------|------------------|
| None                | 10,692                 | 3,823               | 14,515             | 5 hr 38 min      |
| Intermediate        | 562                    | 219                 | 781                | 18 min           |
| Full                | 10                     | 7                   | 17                 | ~1 min           |

Table 5. iTRP component terms and metrics as calculated for the SKJ2025 model example.

| Numerator  | $SB$       | Denominator                                  | $\overline{SB}_{F=0}$ | Ratio    |
|------------|------------|----------------------------------------------|-----------------------|----------|
| $nyr - 5$  | 3530198438 | $nyr - 15:6$<br>$nyr - 14:5$<br>$nyr - 13:4$ | 6347792043            | 0.55613  |
| $nyr - 4$  | 3250591594 |                                              | 6437442045            | 0.50495  |
| $nyr - 3$  | 3122422046 |                                              | 6460117133            | 0.48333  |
|            |            |                                              |                       |          |
| Mean ratio |            |                                              |                       | 0.514806 |
| $iTRP$     |            |                                              |                       | 0.494214 |

$SB_{latest}/SB_{F=0}$                       0.520

$SB_{recent}/SB_{F=0}$                       0.507

|                 | Log_scale | Normal_scale | sd (log-scale) | $CI_{lower}$<br>(normal-scale) | $CI_{upper}$<br>(normal-scale) |
|-----------------|-----------|--------------|----------------|--------------------------------|--------------------------------|
| $iTRP_{latest}$ | 0.050942  | 1.05226      | 0.04035        | 1.01065                        | 1.09559                        |
| $iTRP_{recent}$ | 0.025102  | 1.02542      | 0.03823        | 0.98695                        | 1.06539                        |

**Table 6. The workplan for 2025-26 indicating the modifications to MULTIFAN-CL with respect to their state of completion as of July 2025. Shaded cells indicate tasks completed.**

| <b>2011 Bigeye Tuna Peer review recommendations</b>                                 |                                                                                                                                                                                        |                                |
|-------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------|
| Task                                                                                | Description                                                                                                                                                                            | Status of completion           |
| b. Non-uniform size bins                                                            | Allow the length bins to be of different widths. One might, for example, want many narrow length bins for the smaller lengths, but fewer but wider length bins for the larger lengths. | Development 0%                 |
| d. Tags inform movement                                                             | Include an option which allows the tagging data to inform movement only rather than movement and mortality.                                                                            | Development 100%; Testing 100% |
| <b>Other developments (* indicates those added to the workplan after July 2025)</b> |                                                                                                                                                                                        |                                |
| Task                                                                                | Description                                                                                                                                                                            | Status of completion           |
| Dependent variables derivatives calculation and variance estimation                 | Option for intermediate abbreviation that includes selected time series and terminal numbers at age<br>Add iTRP metrics                                                                | Development 100%; Testing 100% |
| Prior on regional relative abundance                                                | Allow a penalty on regional scaling, that relaxes the assumption for stationary catchability, and estimate index fishery-specific selectivities                                        | Development 100%; Testing 100% |
| * Independent variables report                                                      | Display an identifier to attract attention at the end of any record where the estimated independent variable is at the estimation bound                                                | Development 100%; Testing 100% |
| Terminal recruitments constraint                                                    | Option for specifying the range of years for calculating the mean value to which the terminal recruitments are constrained to                                                          | Development 100%; Testing 100% |
| Catch-at-age likelihood                                                             | Test and complete the existing partial implementation in MULTIFAN-CL for the catch-at-age likelihood formulation                                                                       | Development 80%; Testing 80%   |
| Growth estimation                                                                   | Implement the linear relationship for standard deviation of mean length-at-age and length for the Richards parameterisation, and for multi-species/sex instances                       | Development 100%; Testing 100% |
| * Likelihood components report                                                      | Add the fishery-specific CPUE likelihoods for grouped survey index fisheries                                                                                                           | Development 100%; Testing 100% |
| Repository                                                                          | Complete development of a public version of the MULTIFAN-CL github repository.                                                                                                         | Development 100%; Testing 100% |
| Input of independent variable bounds                                                | Allow for input of specified independent variable bounds via the *.ini file, with clear reporting of the bounds used in the minimisation in the *.par file                             | Development 0%; Testing 0%     |
| Operating space of independent variables                                            | New report file of the input and operating space of each independent variable as applied in MULTIFAN-CL, whether it is in either normal- or log-space                                  | Development 0%; Testing 0%     |
| Constrain deviates                                                                  | Apply constraints on the recruitment deviates such that the $\bar{x} = 0$ . Apply also to the effort deviates for fisheries with missing effort data for the complete time series.     | Development 10%; Testing 0%    |
| Outstanding testing of existing features                                            | Multi-sex model projections                                                                                                                                                            | Testing 0%                     |
| Catch-conditioned method                                                            | Enable the estimation of selectivity deviate coefficients sel_dev_coffs                                                                                                                | Development 10%; Testing 0%    |

|                                     |                                                                                                                                                                                                                                                                                                                                                                                             |                            |
|-------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------|
| Tags inform growth                  | Development of a feature that incorporates size data from tag recaptures to inform growth estimation.                                                                                                                                                                                                                                                                                       | Development 0%; Testing 0% |
| OM size comps                       | Generate a report of the OM size compositions for projection period without error at the end of the projection period as required for deriving economics-based indicators.                                                                                                                                                                                                                  | Development 0%; Testing 0% |
| Turing test                         | <p>Ensure the quality of pseudo-observations to be made more realistic by:</p> <ul style="list-style-type: none"> <li>• Including the sel_dev_coffs and eff_devs estimates in applying process error in projection size compositions and effort</li> <li>• Including over-dispersion error in tagging data</li> </ul>                                                                       | Development 0%; Testing 0% |
| Stochastic projection functionality | <ul style="list-style-type: none"> <li>• Implement process error in future recruitments with application of the derived autocorrelation coefficient in historical recruitment estimates</li> <li>• Fix a bug in generating inputs for stochasticity in <math>N_{\text{terminal}}</math> (more stable method is to use terminal year less 5 as the period for obtaining variance)</li> </ul> | Development 0%; Testing 0% |

**Table 7. Proposed workplan for MULTIFAN-CL in 2026-27 and subsequent years.**

| <b>Peer review recommendations</b>                                      |                                                                                                                                                                                                                                                             |                |
|-------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------|
| Task                                                                    | Description                                                                                                                                                                                                                                                 | Implementation |
| b. Non-uniform size bins                                                | Allow the length bins to be of different widths. One might, for example, want many narrow length bins for the smaller lengths, but fewer but wider length bins for the larger lengths.                                                                      | 2025-26        |
| <b>Tasks from the Yellowfin Tuna Independent Peer Review Panel 2022</b> |                                                                                                                                                                                                                                                             |                |
| Length-weight variance                                                  | Extend MULTIFAN-CL so that variability in weight-at-length can be taken into account                                                                                                                                                                        | 2026-27        |
| Selectivity splines                                                     | Extend MULTIFAN-CL so that it is possible to specify the number of spline knots when defining selectivity and where they are located with respect to age (length) as the current approach means that the selectivity for some knots is constrained to zero. | 2026-27        |
| Age-reading error                                                       | Extend MULTIFAN-CL so that account can be taken of age-reading error when fitting to conditional age-at-length data.                                                                                                                                        | 2026-27        |
| CPUE overdispersion                                                     | Add the ability to specify overdispersion in CPUE as an additive rather than multiplicative factor.                                                                                                                                                         | 2026-27        |
| Natural mortality at age                                                | Integrate the calculation of M-at-age from the sex-ratio data into MULTIFAN-CL unless a sex-specific assessment is used.                                                                                                                                    | 2026-27        |
| <b>Developments carried over from 2025-26</b>                           |                                                                                                                                                                                                                                                             |                |
| Task                                                                    | Description                                                                                                                                                                                                                                                 | Implementation |
| Catch-conditioned method                                                | Allow the fml_effort_rltshp penalty calculation to be conditional on a fish_flags(fi) that facilitates it being disabled, or specified, only for particular fisheries.                                                                                      | 2026-27        |
|                                                                         | Enable the estimation of selectivity deviate coefficients sel_dev_coffs                                                                                                                                                                                     | 2026-27        |
|                                                                         | Review the operation of existing control phase routines undertaken in Phase 1 in respect of their suitability for a catch-conditioned model, and draft a new control phase specific to the catch-conditioned model as needed.                               | 2026-27        |
| Catch-at-age likelihood                                                 | Translate the Dirichlet-Multinomial size composition likelihood implementation from the catch-at-age likelihood                                                                                                                                             | 2026-27        |
| Constrain deviates                                                      | Apply constraints on the recruitment deviates such that the $\bar{x} = 0$ . Apply also to the effort deviates for fisheries with missing effort data for the complete time series.                                                                          | 2026-27        |
| Tags inform growth                                                      | Development of a feature that incorporates size data from tag recaptures to inform growth estimation.                                                                                                                                                       | 2026-27        |
| CPUE likelihood                                                         | Review the formulation of the concentrated log-normal likelihood formulation as used in CASAL (Bull et al. 2012) for its suitability for implementation in MULTIFAN-CL.                                                                                     | 2026-27        |
| Outstanding testing of existing features                                | Multi-sex model projections                                                                                                                                                                                                                                 | 2026-27        |
| Input of independent variable bounds                                    | Allow for input of specified independent variable bounds via the *.ini file, with clear reporting of the bounds used in the minimisation in the *.par file                                                                                                  | 2026-27        |
| Operating space of independent variables                                | New report file of the input and operating space of each independent variable as applied in MULTIFAN-CL, whether it is in either normal- or log-space                                                                                                       | 2026-27        |
| Time-variant selectivity                                                | Allow constraint for setting of zero selectivity-at-age for the number of young age classes                                                                                                                                                                 | 2026-27        |
| Transmuting recruitment trend                                           | Implement a penalty on non-linear trends in temporal recruitment deviates                                                                                                                                                                                   | 2026-27        |
| BH-SRR                                                                  | Ensure robustness when steepness approaches a value = 1                                                                                                                                                                                                     | 2026-27        |

|                                              |                                                                                                                                                                                                                                                                                                                                            |              |
|----------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------|
| EM fits only projection parameters           | For the “assessment” estimation model (EM) embedded in a management procedure, only fit parameters relating to the “new” data provided for the projection time periods, i.e., for effort devs, catchability devs, recruitment devs, while holding all other parameters fixed at the initial values.                                        | post-2026-27 |
| OM size comps                                | Generate a report of the OM size compositions for projection period without error at the end of the projection period as required for deriving economics-based indicators.                                                                                                                                                                 | post-2026-27 |
| Stochastic projection functionality          | <ul style="list-style-type: none"> <li>- implement process error in future recruitments with application of the derived autocorrelation coefficient in historical recruitment estimates</li> <li>- stochastic variability in terminal numbers at age</li> <li>- consolidate the generation of stochasticity in effort_dev_coffs</li> </ul> | post-2026-27 |
| Turing test                                  | <p>Ensure the quality of pseudo-observations to be made more realistic by:</p> <ul style="list-style-type: none"> <li>- Including the sel_dev_coffs and effort_dev_coffs estimates in applying process error in projection size compositions and effort</li> <li>- Including over-dispersion error in tagging data</li> </ul>              | post-2026-27 |
| Recruitment random effects                   | Report on the feasibility of its implementation in MULTIFAN-CL.                                                                                                                                                                                                                                                                            | post-2026-27 |
| Length-based selectivity                     | Resolve the anomalies that produce undesirable discrepancies in predicted weight frequency compositions.                                                                                                                                                                                                                                   | post-2026-27 |
| Self-scaling multinomial with random effects | Complete draft paper for peer review.                                                                                                                                                                                                                                                                                                      | post-2026-27 |
| Recruitment correlates                       | Region-specific environmental recruitment correlates estimated within the orthogonal polynomial parameterisation for recruitments                                                                                                                                                                                                          | post-2026-27 |
| Movement correlates                          | Add a time-series structure (e.g., random walk, time blocks or using environmental correlates) to movement coefficients                                                                                                                                                                                                                    | post-2026-27 |
| Recruitment deviate penalties                | Allow for time-variant penalties on recruitment deviate estimates (that apply to specified subset periods)                                                                                                                                                                                                                                 | post-2026-27 |
| Tagging multi-sex                            | Account for instances of differences between size composition the tag releases and the sex-specific populations                                                                                                                                                                                                                            | post-2026-27 |
| Region specific SRR                          | Allow that region-specific spawning biomass is responsible for recruitment within that region. This is consistent with the assumption that stocks may not be truly panmictic. This would estimate region-specific SRRs.                                                                                                                    | post-2026-27 |
| Report comments                              | Add comment descriptions of the selectivity parameter configurations in the output .par and .rep reports                                                                                                                                                                                                                                   | post-2026-27 |
|                                              |                                                                                                                                                                                                                                                                                                                                            |              |
| <b>Tasks newly added</b>                     |                                                                                                                                                                                                                                                                                                                                            |              |
| PDH diagnostics                              | Refine and describe the algorithm of positive definite Hessian (PDH) diagnostics to be done for an assessment; add a unique identifier to the Hessian file, therefore its parallelised components, and possibly to the *.par, to ensure continuity among them when stitching parallel *.hes files.                                         | post-2026-27 |
| Simulation pseudo-observations               | Correction required to the generation of simulation pseudo-observations of tagging data when employing the catch-conditioned model                                                                                                                                                                                                         | post-2026-27 |
| Variance report                              | Resolve the discrepancy between $F_{recent}/F_{msy}$ in the dependent variables variance report and the $F_{mult}$ in the plot.rep report                                                                                                                                                                                                  | post-2026-27 |
|                                              |                                                                                                                                                                                                                                                                                                                                            |              |
| <b>Other Tasks</b>                           |                                                                                                                                                                                                                                                                                                                                            |              |
| Pre-Assessment Workshop                      | Attend and deliver an item on MULTIFAN-CL updates                                                                                                                                                                                                                                                                                          | 2026-27      |
| Scientific Committee                         | Submit an Information Paper on MULTIFAN-CL updates to SC23                                                                                                                                                                                                                                                                                 | 2026-27      |

|                          |                                                                                                                                |         |
|--------------------------|--------------------------------------------------------------------------------------------------------------------------------|---------|
| User's Guide             | Maintain the User's Guide to be up to date with respect to the new features, enhancements and corrections added during 2026-27 | 2026-27 |
| Next Generation Software | Contribute to Project 123 in respect of the developing the Opal and mfcIrtmb modelling frameworks                              | 2026-27 |

14 FIGURES

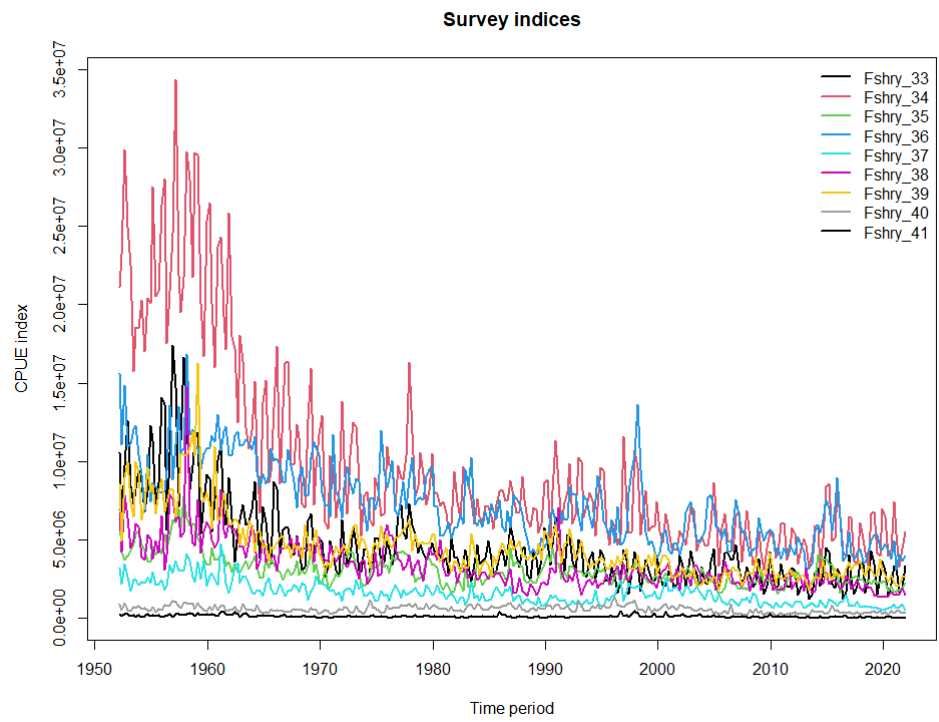


Figure 1. Region-specific CPUE indices input to the BET2023 model.

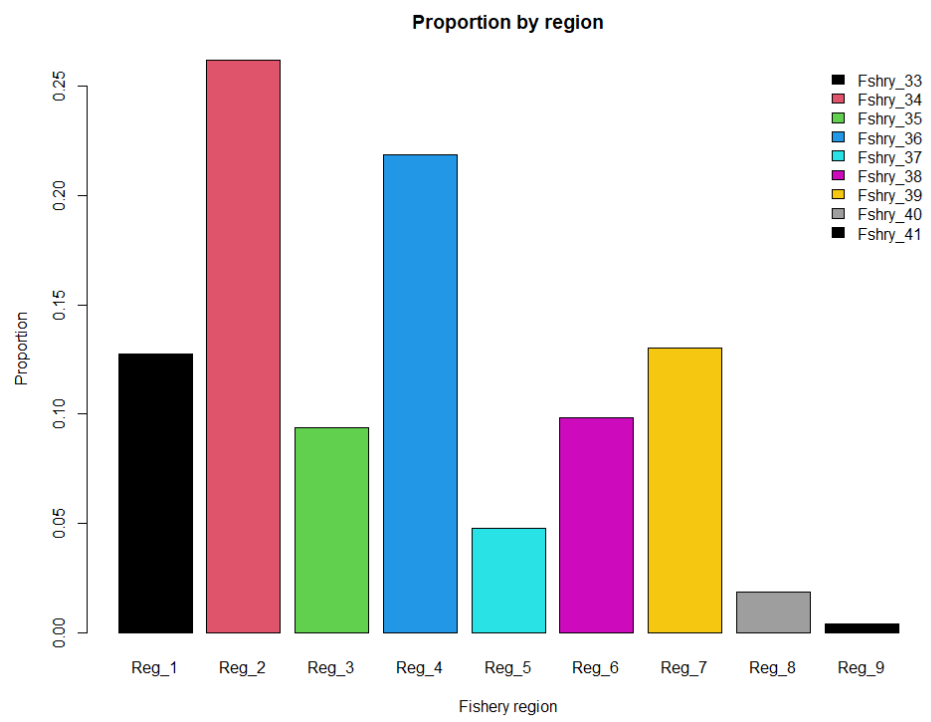
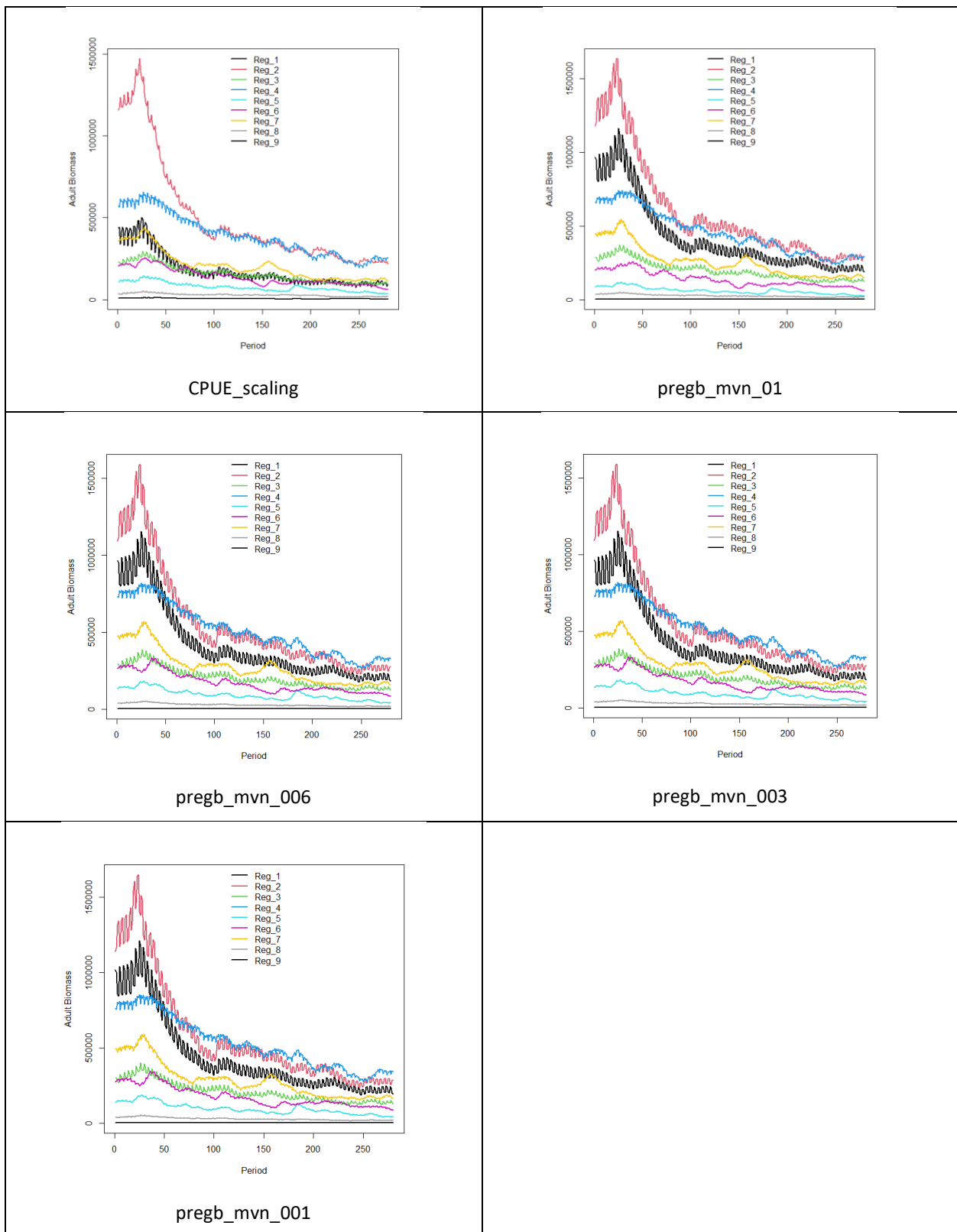


Figure 2. Mean region-specific CPUE expressed as regional relative proportion of 1, i.e., the regional scaling.



**Figure 3.** Comparison of the estimated region-specific spawning biomass for the BET2023 model options as described in the text.

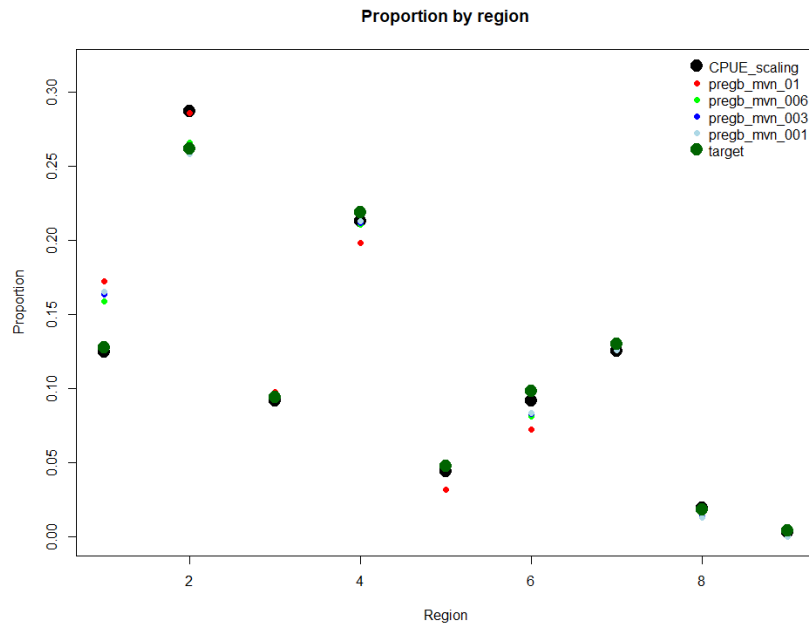


Figure 4. Comparison of the estimated regional scaling for the BET2023 model options as described in the text, and with respect to the `pregb_pen` target values for each region (target).

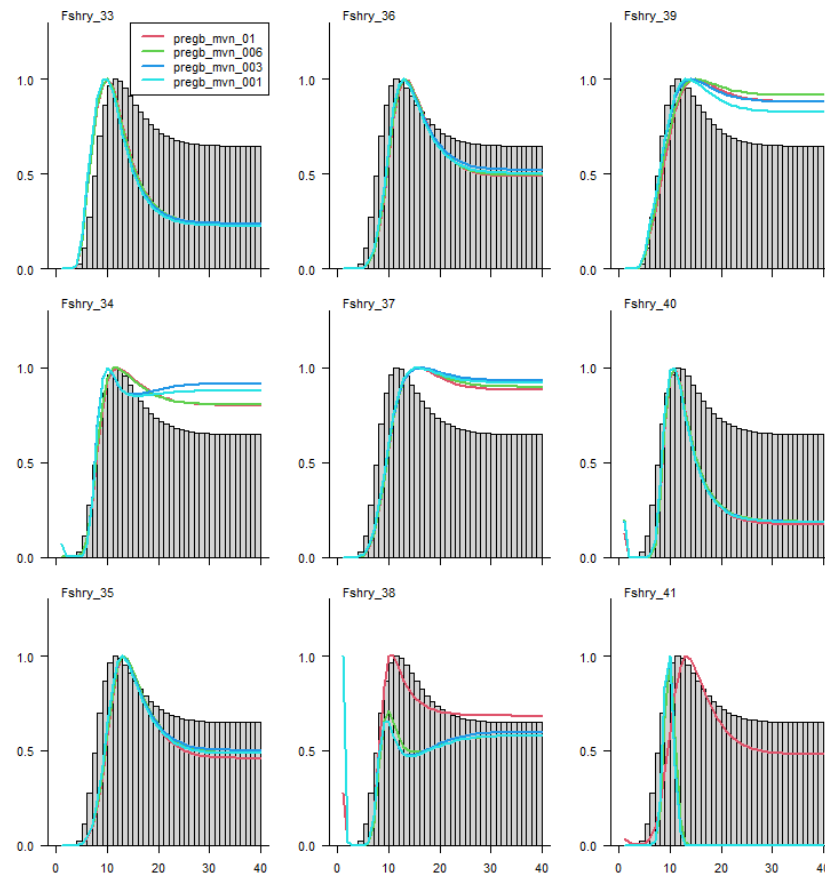


Figure 5. Estimated selectivity-at-age for the CPUE survey-index fisheries of the BET2023 model options as described in the text, with that of the `CPUE_scaling` option displayed as histograms.

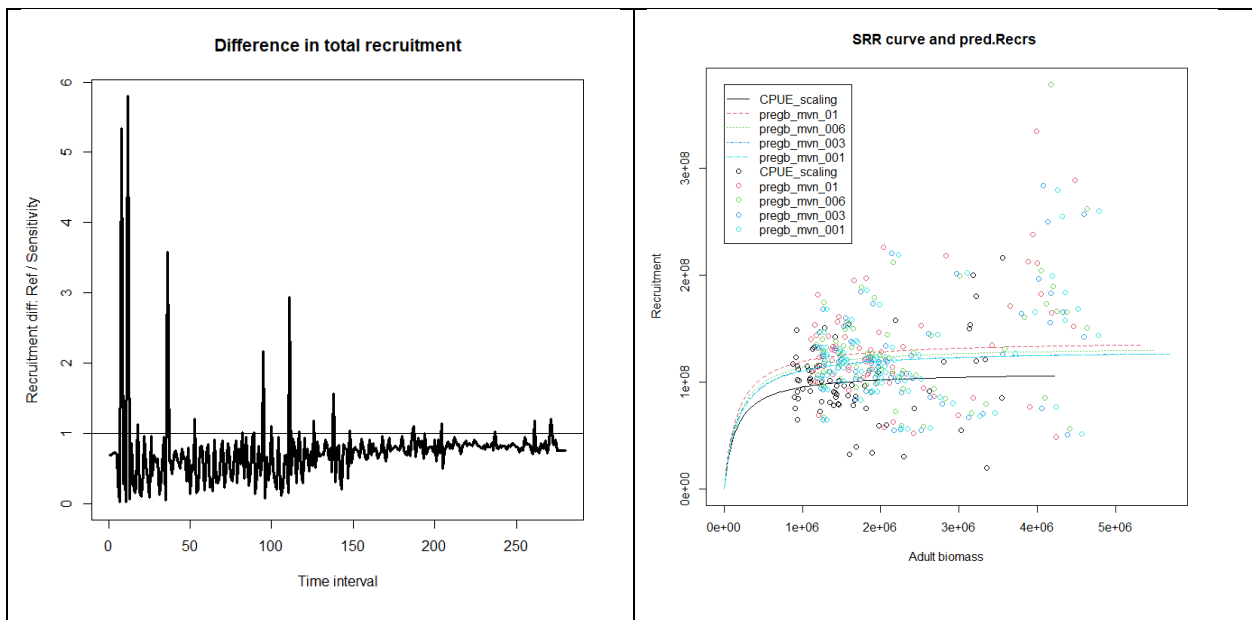


Figure 6. Comparison of the estimated recruitments for the BET2023 models defined in the text showing: relative difference between the CPUE\_scaling and pregb\_mvn\_01 models (left panel); and, absolute recruitments with the estimated BH-SRR (right panel).

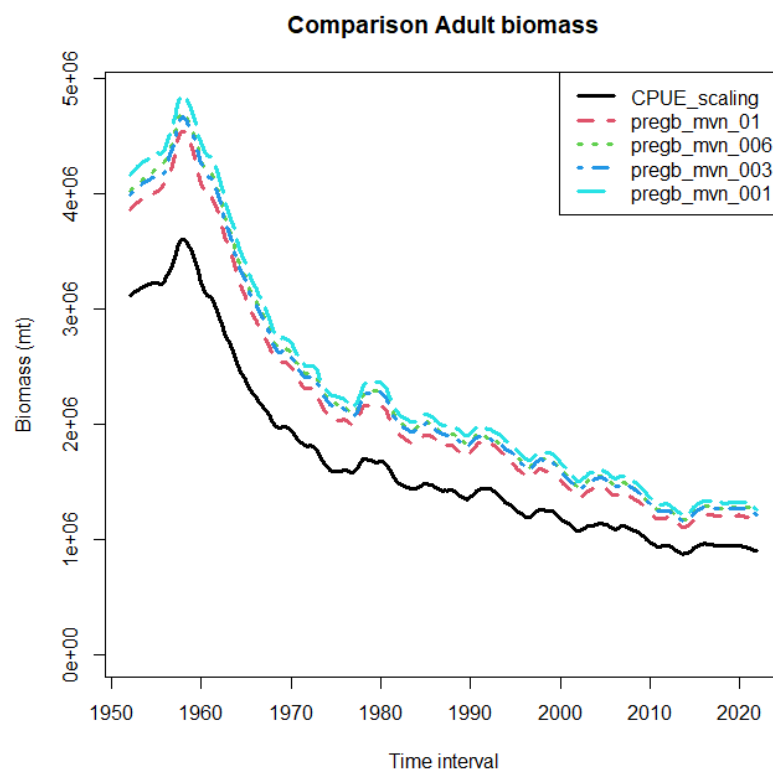
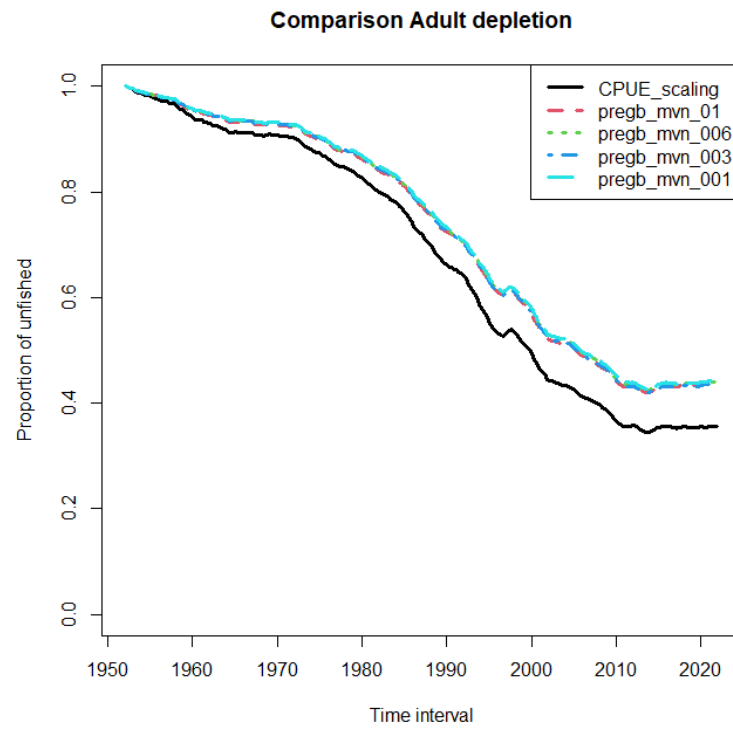
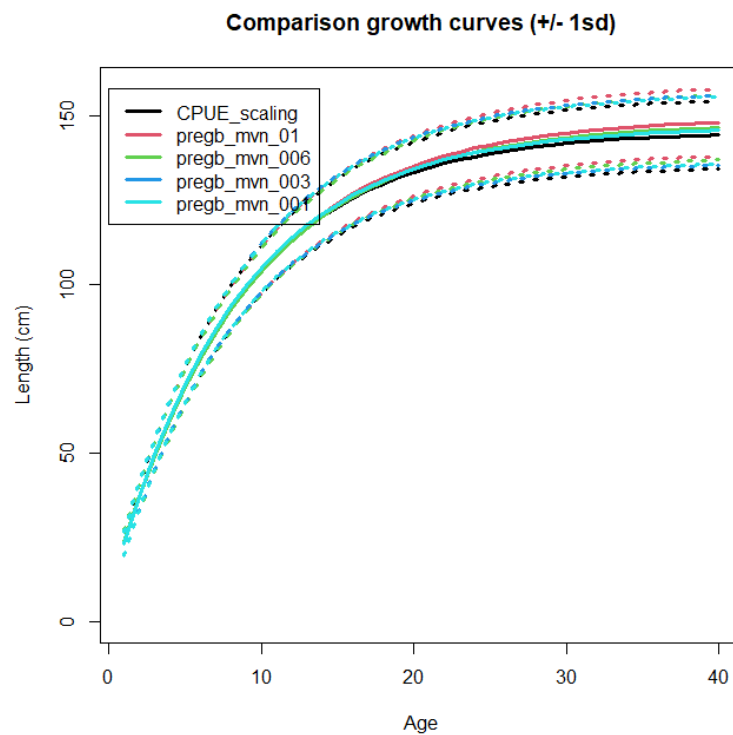


Figure 7. Comparison of the estimated spawning biomass for the BET2023 model options as described in the text.



**Figure 8.** Comparison of the estimated spawning biomass depletion for the BET2023 model options as described in the text.



**Figure 9.** Comparison of the estimated growth for the BET2023 model options as described in the text.

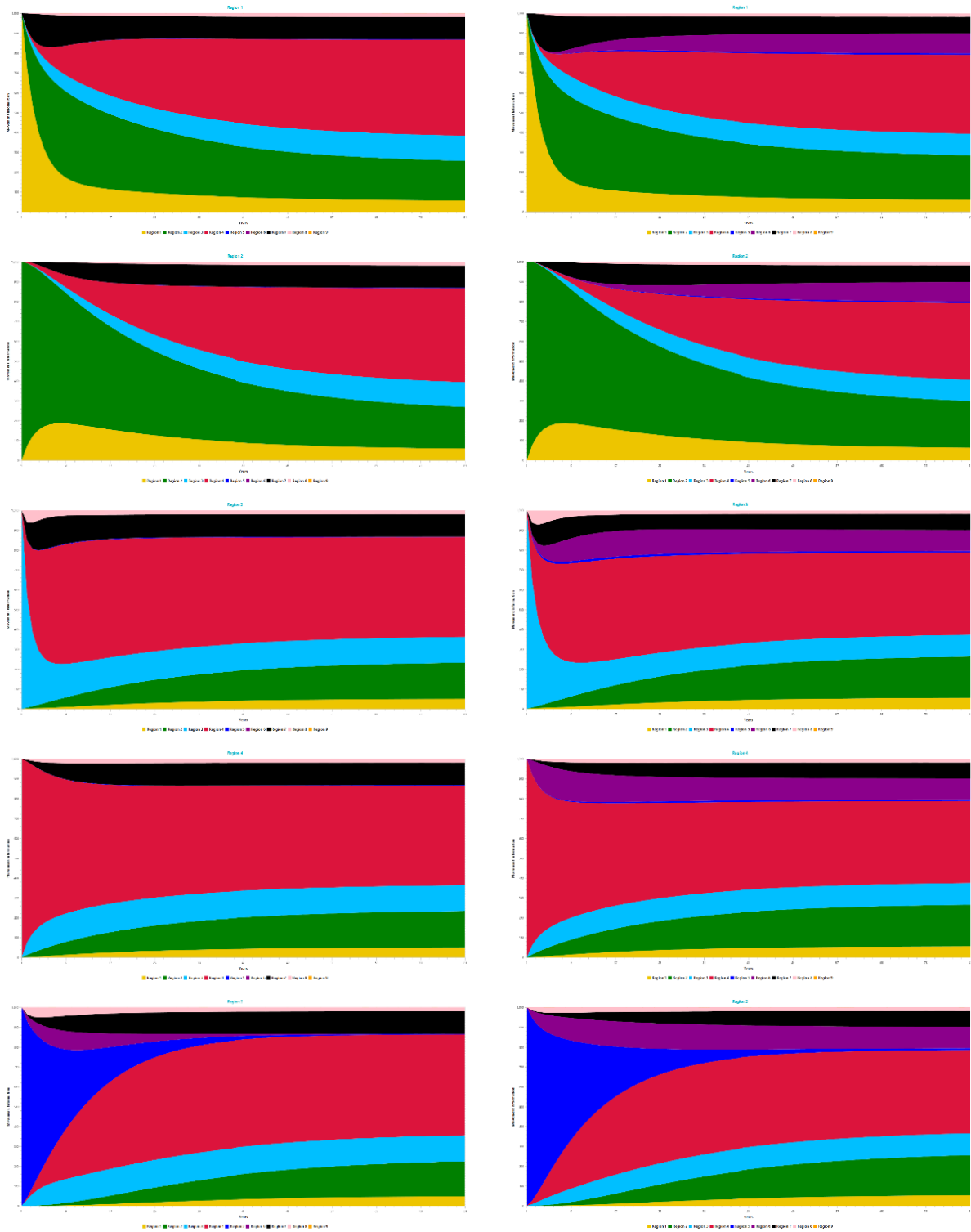


Figure 10. Comparison of estimated movement shown in terms of regional numbers of fish within a cohort's lifetime (rows for regions 1 to 9) for the BET2023 model using the total mortality-conditioned negative-binomial tagging likelihood (fmort\_cond, left-hand panels), and a model using the recaptures-conditioned modified Dirichlet likelihood (recaps\_cond, right-hand panels).

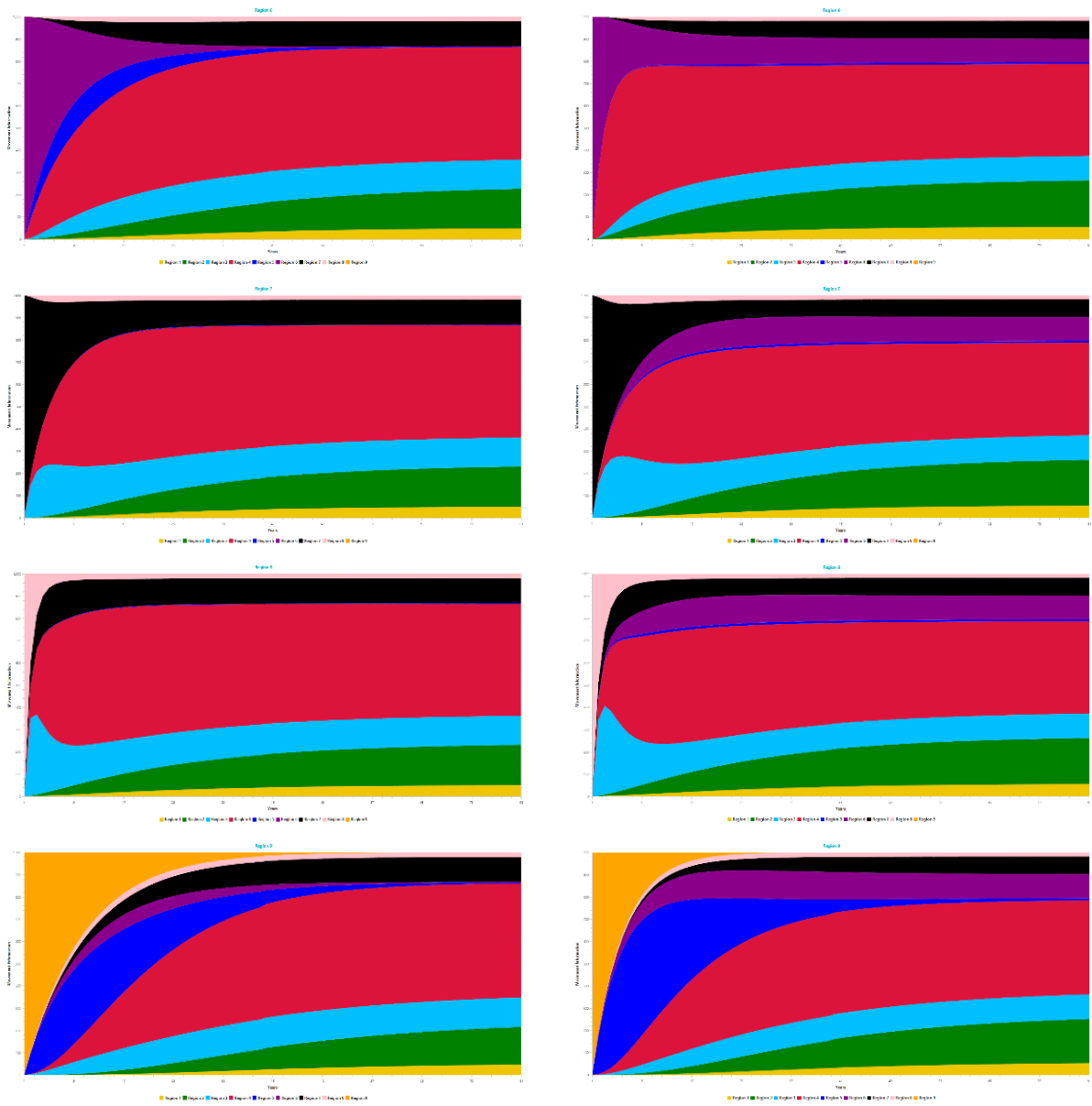


Figure 10 cont.

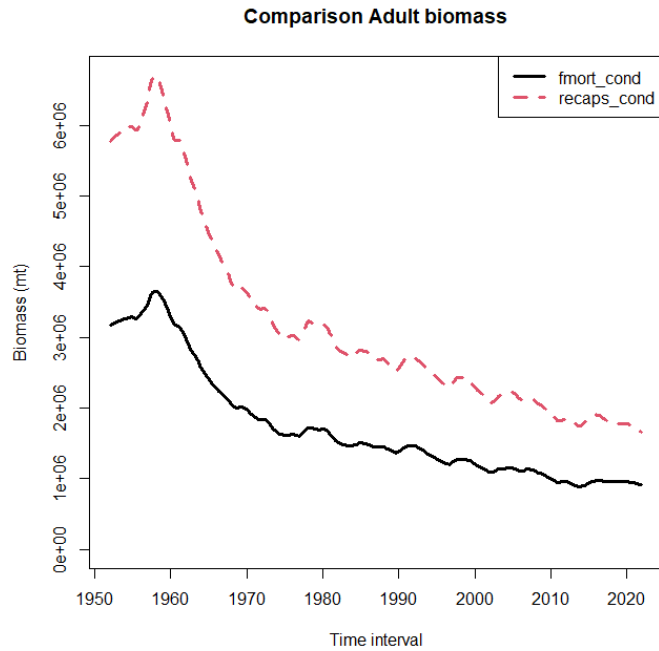


Figure 11. Comparison of the estimated spawning biomass for the BET2023 model using the total mortality-conditioned negative-binomial tagging likelihood (fmort\_cond), and a model using the recaptures-conditioned modified Dirichlet likelihood (recaps\_cond).

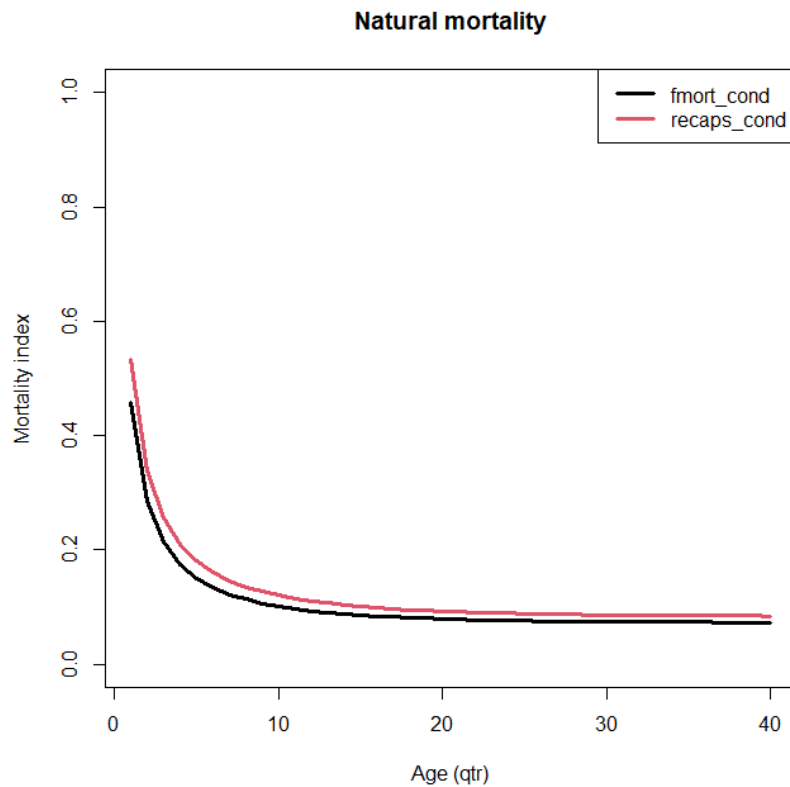


Figure 12. Comparison of the estimated age-specific natural mortality for the BET2023 model using the total mortality-conditioned negative-binomial tagging likelihood (fmort\_cond), and a model using the recaptures-conditioned modified Dirichlet likelihood (recaps\_cond).

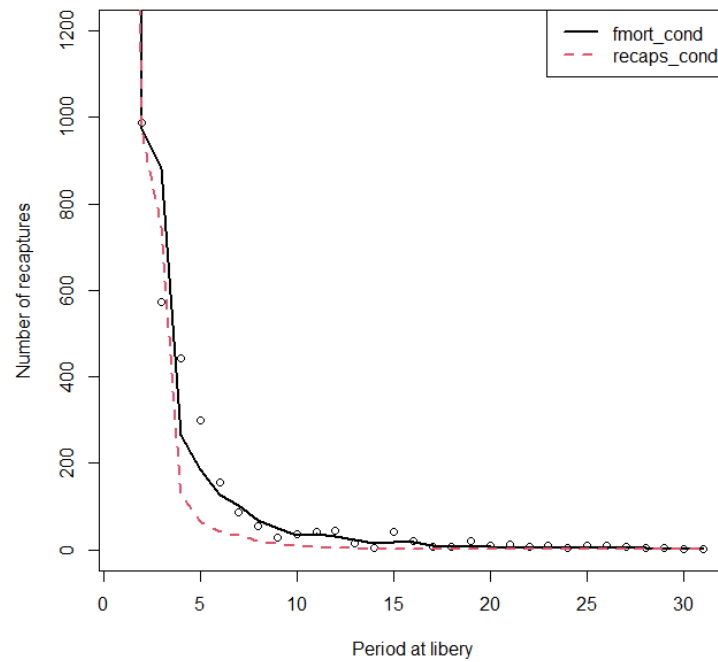


Figure 13. Comparison of the observed (circles) and predicted recaptures (lines) with respect to period at liberty for the BET2023 model using the total mortality-conditioned negative-binomial tagging likelihood (*fmort\_cond*), and a model using the recaptures-conditioned modified Dirichlet likelihood (*recaps\_cond*).

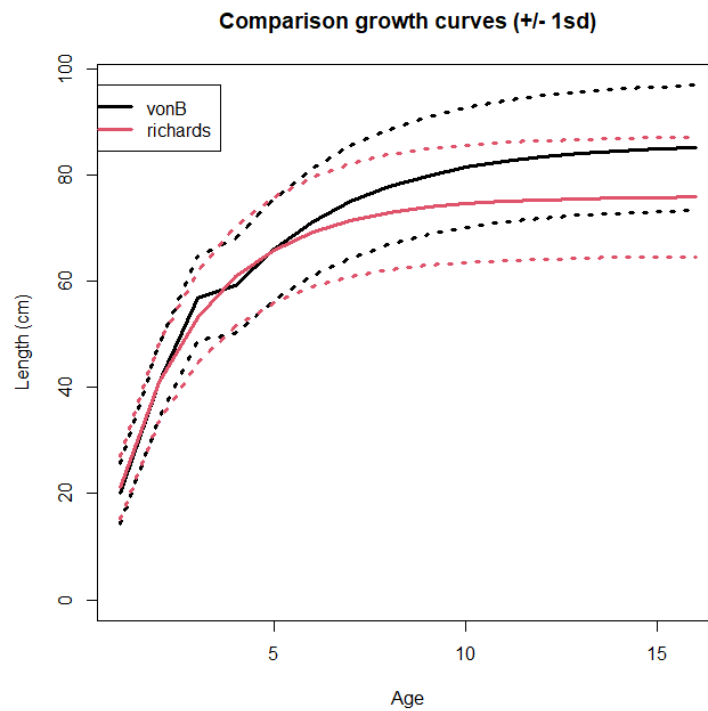


Figure 14. Comparison of the growth curves: von Bertalanffy (vonB) and Richards (Richards), estimated for the SKJ2025 model example.

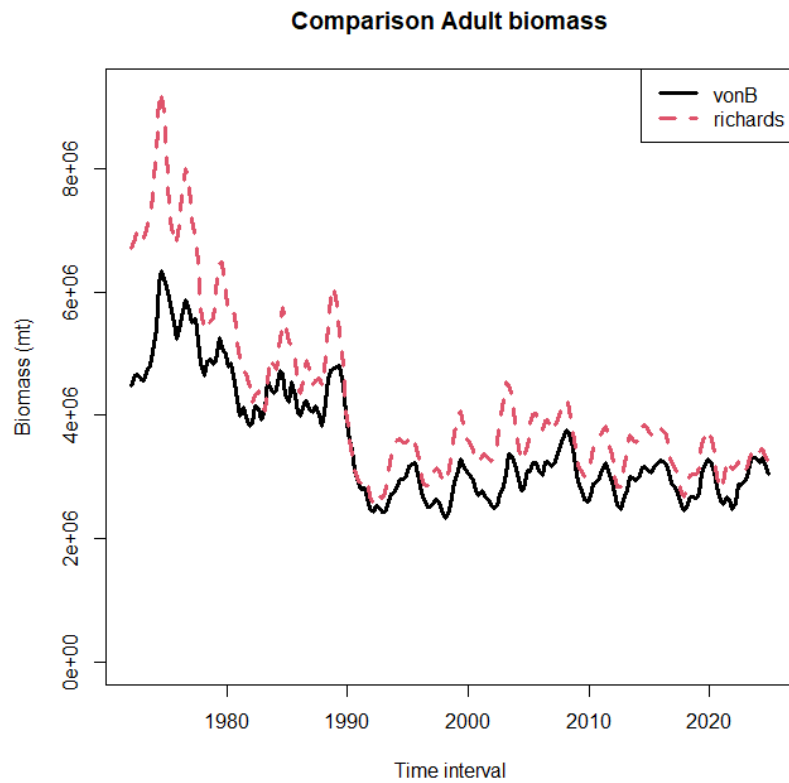


Figure 15. Comparison of adult spawning biomass estimated for the SKJ2025 model example with either: von Bertalanffy (vonB), or Richards (Richards) growth curves being implemented.

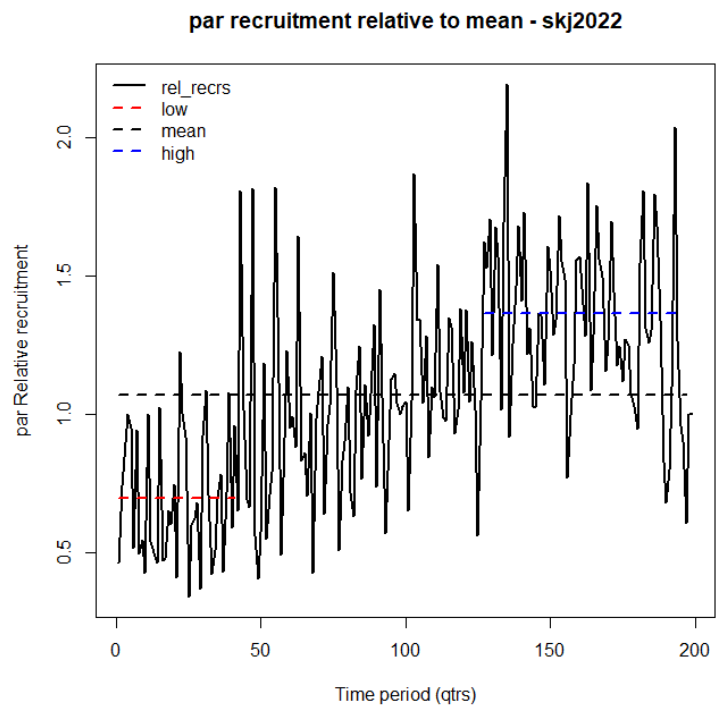


Figure 16. Relative recruitments (rel\_recrs) for the SKJ2022 model over the 200 model time periods, with those periods shown for the three models: mean, low and high, used for deriving the mean values assumed for the terminal recruitments.

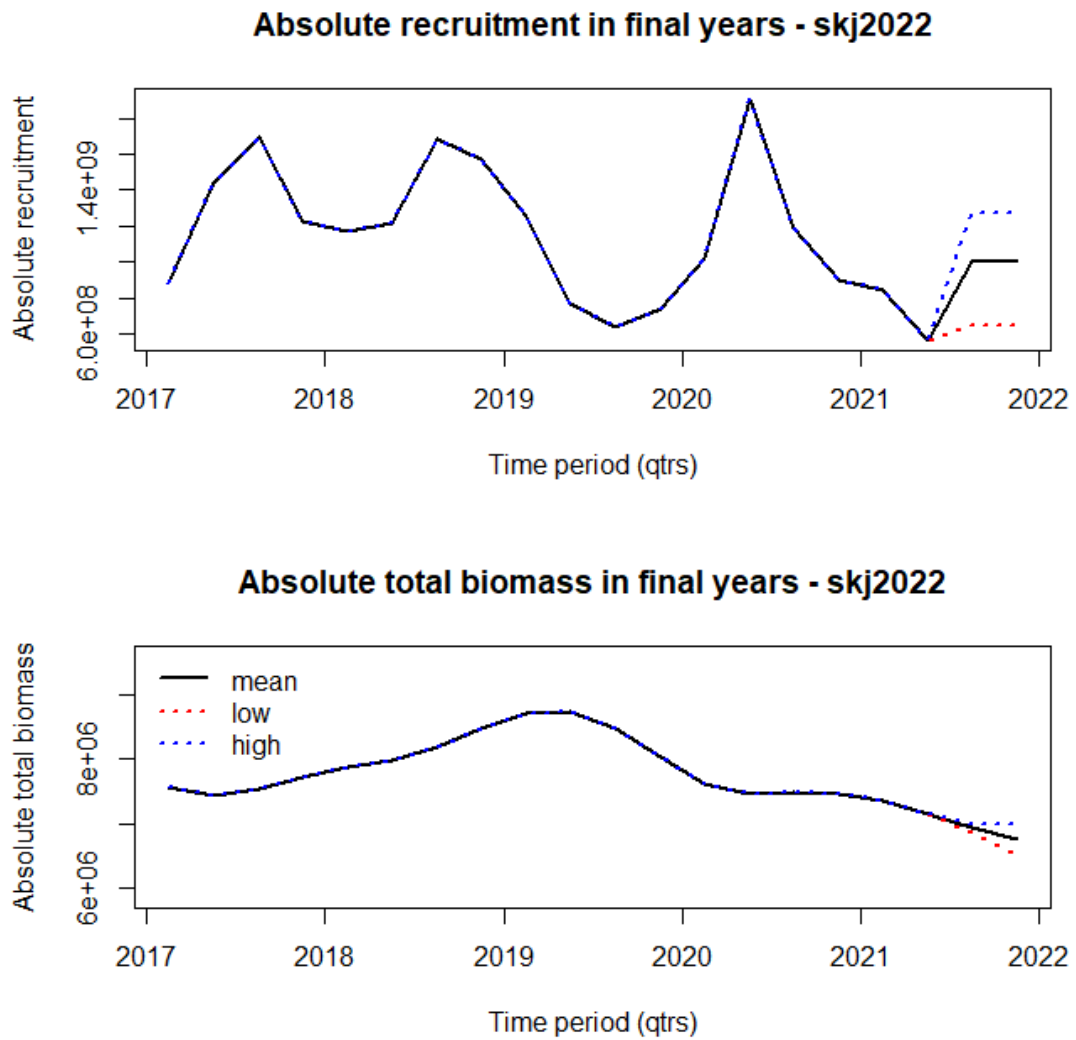


Figure 17. Absolute recruitments (normal space) and total biomass (top and bottom panels, respectively) for the SKJ2022 model over the 200 model time periods, with those shown for the three models: mean, low and high, used for deriving the mean recruitment values assumed for the terminal recruitments.

## 15 ANNEX 1

Modified source code files (29) during 2025-26:

|                                                                                                                                                                                                                                                                  |                                                                                                                                                                                                                              |
|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| callpen.cpp<br>catagfit.cpp<br>ests.cpp<br>indepvars.cpp<br>lmult_io.cpp<br>mfcl_thrd_linux64_debug.mak<br>mfcl_thrd_linux64_opt.mak<br>newgradc.cpp<br>newgradc_noeff.cpp<br>newl2.cpp<br>newl5.cpp<br>newmau5a.cpp<br>newmult.cpp<br>newmult.hpp<br>nmsort.cpp | nnewlan.cpp<br>plot.cpp<br>plotstuff.cpp<br>printfrq.cpp<br>recinpop_standard.cpp<br>recrpen.cpp<br>tagfit.cpp<br>tagfit_ss3.cpp<br>testnewl3.cpp<br>testsvdinv_noeff.cpp<br>variable.hpp<br>VERSION<br>version.h<br>xml.cpp |
|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|

One new source code file was added during 2025-26:

|                |
|----------------|
| regscalpen.cpp |
|----------------|