Dear Code Reviewer,

Please see below: I’ve annotated in red the draft ToR for the Code review with the appropriate R scripts / admb files highlighted in green.

All of the code is available in the iccat/abft-mse GitHub repository (I just pushed a streamlined file directory – still 6Gb). The repo is private so you may have to obtain permission to use it.

The code for components 1 and 2 (below) are cross referenced with sections, equations and tables of the TSD:

C:\GitHub\abft-mse\manuals\_and\_design\_documents\ BFTMSE\_TSD21-01\_2June2021.docx

Feel free to skype me at thomascar or call direct on +1 604 805-6627. Often a quick chat is faster than a lengthy to and fro by email.

Good luck!

Tom

**Proposed Terms of Reference and schedule for M3 & ABTMSE R package code review**

Tom Carruthers

*This is for initial discussion only during the developers’ informal meeting starting on Monday 8 March; any decisions about this must await the BFT WG meeting in early April.*

**Components of code review**

There are three principal components of the Atlantic bluefin tuna MSE framework:

1. The M3 ADMB model used to condition the operating model on data;

Simple enough, this template includes all the equations of the population dynamics. Best way to review this is to use TextPad with the admb tpl.syn syntax file (C:\GitHub\abft-mse\m3\tpl.syn). You load that in TextPad View > Document Properties > syntax

C:\GitHub\abft-mse\m3\m3.tpl

Note that these equations are recreated exactly in the ABTMSE R package from the same leading parameter estimates. To find out more about the checks already built into the package you can take a look at the CMP developers guide:

C:\GitHub\abft-mse\manuals\_and\_design\_documents\CMP-Developers-Guide-7-1-1.html

1. R Code to organize data and model inputs for use in the operating model conditioning (e.g. formatting of data, calculation of master indices, specification of selectivities for fleets and survey indices, likelihood weights for data types etc.);

The R coding starts by going step by step through the construction of an initial operating model input (OMI) object which can be modified to make the various OMs for conditioning.

C:\GitHub\abft-mse\RScripts\Operating\_models\Step 1 Build Base OMI.R

This ‘base’ OMI is then modified to make the reference grid of OMs.

C:\GitHub\abft-mse\RScripts\Operating\_models\Step 2 Build OMs.R

The procedure goes like this:

* loop over all the OMs that need conditioning (these do not include recruitment level 3 OMs that are just a future chance based on recruitment level 1) and alter the maturity, M, recruitment, scale and length composition weighting attributes accordingly.
* For all these OMs, fit the M3 model
* Then take the MLE estimates from these fitted M3 models and construct the full range of reference grid OMs (duplicating the fit for recruitment level 3 OMs). The code for OM construction is in C:\GitHub\abft-mse\R\_package\ABTMSE\R\OM\_object.R

Similarly, robustness set OMs are made from the reference grid OMs in script:

C:\GitHub\abft-mse\RScripts\Operating\_models\Step 3 Build robustness OMs.R

Once the reference grid and robustness set OMs are constructed, these can then be copied over to the R package directory, along with historical catches, allocations, OM weights etc. This happens in script:

C:\GitHub\abft-mse\RScripts\Packaging

Again, you can check historical matching of population quantities using

checkMSE <- new('MSE', OM=OM\_1d, check=T)

1. An R package that recreates the ADMB conditioning model equations and allows for closed loop simulation testing of CMPs in projection years.

This is the bit I’ve yet to fully comment (it is partially commented), but its all basically in a single script here:

C:\GitHub\abft-mse\R\_package\ABTMSE\R\MSE\_Object.R

This is the MSE object that includes all the MSE forward projection code. From there you should be able to find all the code you need in the ABTMSE/R folder.

You can check future projection of recruitment using the function:

plot\_Recruitment(MSE\_example)

**General terms of reference for code review**

For several years the bluefin tuna working group has recorded MSE technical specifications in a Trial Specifications document (TSD). This covers a wide range of issues including data processing, fleet structure, operating model structure, likelihood functions for model conditioning and statistical properties of data for projections. Where applicable the TS doc includes mathematical equations that can be directly compared to ADMB and R code. The primary purpose of the code review is to check that the description of the operating model detailed in the TSD is correctly implemented in the code of the M3 model and the ABTMSE R package. The review is not focused on the suitability of the specifications described in the TSD.

The review should highlight:

* Incorrect recreation of TSD equations in code of M3.tpl file and ABTMSE R package;
* Code that is used in modelling that is not documented in the TSD;
* Areas where code may be made more computationally efficient.

**Tentative schedule for code review**

A reconditioning of the model is scheduled for April to mid-May which would alter code for organising data (component 2), conditioning and also the R code of the forward projections (component 3), but will not affect component 1. In order to make initial progress with a code review is it therefore efficient to organize it in relation to these components.

**Component 1 (by end of April).** Provide fully commented M3.tpl to the external reviewer crossed referenced against the latest version of the TS doc.

**Component 2 (by end of June).** Provide a complete set of R scripts for processing data and fitting the M3 model, again commenting and cross referencing all code against the relevant sections of the TS doc.

**Component 3 (by end of July).** Provide a complete set of R scripts for converting fitted M3 models into operating models of the ABTMSE package and then doing closed loop projections.

**A note on ‘internal’ code checking completed so far.**

The historical reconstruction of the M3 model is recreated in the R framework and these have been checked for consistency (matching of all quantities to the sixth decimal place). It follows that any coding errors in the population and fishing dynamics of the M3 model would have to be recreated exactly in the R coding language which is relatively unlikely. The current version of the R package includes these checks as an argument to the function used to run MSEs.

Line-by-line checking of R package code for projecting indices and recruitment has gone through relatively detailed scrutiny during an informal code review in 2020.