CASAL²: a replacement for CASAL as a stock assessment productivity tool

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Summary

The National Institute of Water and Atmosphere, New Zealand (NIWA) has a major stock assessment program, CASAL (C++ Algorithmic Stock Assessment Laboratory); a flagship NIWA product that is well recognised within New Zealand and by international fisheries forums (e.g., CCAMLR). CASAL is a generalised age- or size-structured fish stock assessment model that can fit to a variety of survey and fishery data, and allows flexibility in specifying population dynamics, parameter estimation and model outputs. Similar analyses can be done with Stock Synthesis III. CASAL has been developed to enable the completion of stock assessments by non-mathematical scientists, benefiting NIWA by widening the staff pool for assessment work.

First available in 2002, early design decisions preclude further development of CASAL to incorporate advancements in assessment science. With financial help from MPI, NIWA has developed CASAL², a more flexible and powerful replacement to address the next generation of scientific assessment problems. We describe the design features and considerations for a CASAL² project, including examples to show how it works.

Introduction

NIWA's stock assessment tool, CASAL, was developed in 2000-01 to cope with the avalanche of stock assessments that built up over a decade after the transition in New Zealand to a quota management system. Designed as a productivity tool to allow faster application of stock assessments and incorporating Bayesian technology (not done at that time), CASAL enabled knowledgeable biologists to concentrate on assessments without the need to know specific mathematical details, while confident of using a validated code base. Whilst CASAL satisfied initial demand, the code base is now out of date and cumbersome to update. NIWA wants to retain a CASAL approach, but we also need to develop a tool to incorporate new fisheries developments and allow for easy adaption into MSE and simulation work so that a replacement for CASAL is needed, i.e., CASAL². A similar application is SS3 (Methot and Wetzel, 2013).

Materials and Methods

CASAL² development is focused around modern code design and maintainability to ensure the tool is still extendable in 10 years' time. Professional C++ development is used for all structural coding with scientist coding of equations where applicable. CASAL² design employs loose coupling and high cohesion modularity. It will be open source and interoperable with programs such as R, Julia, and python (for MSE and simulations).

CASAL² has been designed to read user supplied input files that are free flow and offer a standardised interface. Commands within the input files that drive the assessment are human readable and self-documenting. This standardised approach assists stakeholders as terminology is standard, mathematical descriptions are contained in one place, and outputs are more consistent - allowing easy comparison between models, over time, and across stocks.

To maintain flexibility and to future-proof the code, CASAL² does not "know" about the usual fisheries constructs like sex and maturity. Instead, these are defined by categories, operated on by processes, with movements defined into, out-of, and within the partition. Categories and processes are generic, and their interpretation is user-defined (*see* example below). In CASAL² most structures can be accommodated and we are not locked-in to today's decisions. CASAL² implements unit tests and automagically extracts contracts in the code base to populate documentation of command and subcommand syntax; the user manual reflecting the code as long as the coding system is followed. Companion R functions, using keywords from the generic code, extract CASAL² outputs into R list structures. CASAL² will also feature a simple interface into completed models for managers, time-varying parameters, and random effects.

Results and Discussion

CASAL² can reproduce existing CASAL assessments, and will be used for a new stock assessments in April 2016.

Input files are made up of command blocks that have a syntax "@command <label>", where "@" signals a block, with a list of sub-commands following. Commands and data are free flow, human readable, and self-documenting. The side box example is for a hake stock that has smaller fish in the west and larger spawning fish in the east. A fishery operates in each area with varying effort between the two and over the year. These are separated using double normal selectivities. Each selectivity is named (it could be applied to more than one fishery or survey) and the example has a peak at 10 years with a left standard deviation of 3 years and a more gradual slope on the right. The selectivity at the peak is 1.0 (alpha). One or more of these parameters can be estimated. The values given here are the starting ones.

The two fisheries are defined as a process of type mortality_instantaneous which specifies both natural mortality (sub-command m) and fishing via the catches from both in the table catches sub-command. Alternatively, catch input could be provided via a file specified by "%include Hake_catches.txt". The fisheries are defined in the table fisheries sub-command which links them to a selectivity, time step, and category in the population that the fishery operates on (in this example, "stock" is the only category as this is a uni-sex model with no maturity in the partition).

Example input

@selectivity westFSel

type double_normal mu 6 sigma_1 3 sigma_r 10 alpha 1.0

Fishing Mortality

@process fisheries

type mortality_instantaneous

m 0.19

table catches

year	FishingWest	FishingEast
1975	80	111
1976	152	336
2012	80	152
end t	able	

table fisheries

fishery category selectivity step FishingWest stock westFSel s_1 FishingEest stock eastFSel s_1 end table

We have deliberately separated the interpretation of partition types from their specification so that CASAL² (unlike CASAL) does not know about fishing, maturity, migration, or sex. The user explicitly defines the specification and this allows us to extend partitions into more complicated arrangements (at the expense of slightly more work by the user for simple cases). For example, CASAL had "sexes T" for 2 sexes, while CASAL² uses: *@categories sex* male.female

On the other hand, CASAL² can have male, female & unsexed by using "sex male female unsexed".

References

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