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Recommendations

When modelling multiple fleets in a GYM assessment, we recommend the use of the presented extension to the Grym package based on its shown capacity to model more complex fisheries and fishing practices with a high degree of consistency in results.

Abstract

Grym is an implementation of the Generalized Yield Model in R that provides greater transparency and extensibility (Maschette et al., 2020, Wotherspoon & Maschette, 2020). This paper describes an extension of the Grym to permit multiple fleets within a season, allowing the Grym to model more complex fishery behavior and evolving fisheries practices. Results from the expansion are compared with existing analyses from the Grym. The model can include vessels using different gear types (e.g. trawl and longline) or identical selectivity. An example is presented for Patagonian toothfish.

Introduction

Recently, the Generalized Yield Model (GYM) was re-implemented into the open source R software as the 'Grym' package to improve computer compatibility and model transparency (Wotherspoon and Maschette, 2020, Maschette et al., 2020). The basic purpose of the Grym is to provide a toolbox of functions that realize the core functionality of the GYM software (described by Constable and de la Mare (1996)) that could be used as a base package to support a range of population assessment and management strategy applications (Maschette *et al.*, 2020).

The GYM and the current version of the Grym assume a single fishing fleet in each season, represented though a single fishing selectivity. Here, we address a request from SC-CAMLR in 2003 to extend the GYM assessment to multiple fleets which has not been addressed previously (SC-CAMLR-XXII, Annex 5, para 9.6 (viii)). We present a series of functions, designed to extend the projection functions in Grym to allow multiple fleets.

This paper first presents the methods and mathematical formulas used in the GYM and Grym models to predict stock abundance, biomass and yield. Based on these formulas, we expand and add new formulas and methods generated to extend the prediction functions to allow multiple fleets. These methods are applied to write new multi-fleet functions in R. We also provide a series of tests to demonstrate the use of these functions, and compare to single fleet Grym fits for a Patagonian toothfish example. Finally, we give a detailed description and code of the multi fleet functions developed and the tests carried out (Appendix 1).

The basic population model for GYM

The GYM is an age-structured cohort model, it uses numerical integration to calculate the annual change of stock abundance, biomass and the yield for each cohort over a single year. Iterating this process allows the stock projections arbitrarily forward in time.

Within each year the abundance in an age class is assumed to satisfy the Baranov catch equation (Xiao, 2005)

$$\frac{dN_a}{dt} = -\big(M(a,t) + F(a,t)\big)N_a \tag{1}$$

Here $N_a(t)$ is the abundance in age class a at time t within the year, and $M(a,t)$ and $F(a,t)$ are the instantaneous natural and fishing moralities experienced by an individual in age class a at time t. The natural mortality is represented as the product

$$M(a,t) = M_y\, m(a,t) \tag{2}$$

where $m(a,t)$ describes the pattern of intra-annual variation in mortality for each age class, and M_y is an annual scaling that can be randomly varied to represent any year to year variability in natural mortality. Similarly, fishing mortality is represented as the product

$$F(a,t) = F_y E(t) S(a,t) \qquad (3)$$

where $E(t)$ represents the distribution of fishing effort over the year, $S(a,t)$ the age-dependent gear selectivity, and F_y is an overall annual scaling of fishing effort.

The GYM assumes a strict deterministic relationship between weight an age. The weight $W_a(t)$ of an individual in age class a at time t must be specified, and this factor is used to convert the abundance in each age class to the corresponding biomass

$$B_a(t) = w_a(t)N_a(t) \qquad (4)$$

and the total biomass $B(t)$ is determined by summing the contributions from each age class

$$B(t) = \sum_a B_a(t) \qquad (5)$$

Similarly, the yield in each age class is the number of harvested individuals re-expressed as biomass

$$\frac{dY_a}{dt} = w_a(t)F(a,t)N_a \qquad (6)$$

and the total yield $Y(t)$ is then determined by summing the contributions from each age class

$$Y(t) = \sum_a Y_a(t). \qquad (7)$$

At the end of each year, surviving individuals advance to the next highest age class, and the youngest age class is filled with new recruits generated randomly according to an assumed recruitment model.

The original implementation of the GYM (Constable and De la Mare, 1996) integrated the governing equations (1)-(7) with a standard Runge Kutta method (Burden and Faires, 2005). Grym takes a more direct approach. The governing equations may be solved directly to yield (Maschette *et al.*, 2020)

$$N_a(t) = N_a(0)\exp\left(-M_y \int_0^t m(a,\tau)d\tau - F_y \int_0^t E(\tau) S(a,\tau)d\tau\right) \qquad (8)$$

$$B_a(t) = w_a(t)N_a(t) \tag{9}$$

$$Y_a(t) = F_y \int_0^t E(\tau)\, S(a,\tau)B_a(\tau)d\tau \tag{10}$$

and the integrals in (8) and (10) are evaluated with the composite trapezoidal rule (Burden and Faires, 2005). If the intra-annual mortalities $m(a,t)$ and $f(a,t)$ are assumed piecewise linear, this yields exact solutions for the abundance $N_a(t)$ and biomass $B_a(t)$.

Equations (8) – (10) provide the abundance, biomass and yield for given initial abundances $N_a(0)$. But as the governing equations are linear, any rescaling of a solution is also a valid solution. Rescaling $N_a(t)$, $B_a(t)$ and $Y_a(t)$ by the factor

$$r = \frac{B_{ref}(t_1 - t_0)}{\sum_a \int_{t_0}^{t_1} B_a(\tau)d\tau} \tag{11}$$

generates an annual projection that has initial relative abundances $N_a(0)$ and mean total biomass B_{ref} in the time interval $[t_0, t_1]$, allowing the projection to be scaled to a total biomass estimate from a survey.

Typically, the annual scaling F_y is not known *a priori* and is determined by matching the total annual yield $Y(1)$ to a known historic or target catch. When there is only a single fleet, F_y can be determined through an appropriate univariate root finding method. Both the GYM and the current implementation of Grym use Brent's method (Burden and Faires, 2005) for this purpose.

Multiple Fleets

The single fleet model described above generalizes naturally to a multiple fleet model in which each fleet makes a separate contribution to the total mortality. However, the task of determining the annual effort required reproduce known historic or target catches is much more complex in the multiple fleet case.

To generalize the GYM to multiple fleets, the total mortality is decomposed into contributions from each fleet

$$F(a, t) = \sum_k F_k(a, t) = \sum_k F_{k,y} \, E_k(t) \, S_k(a, t). \tag{12}$$

Here $F_k(a, t)$ is the contribution to the total fishing mortality from fleet k, and this is further decomposed into a distribution $E_k(t)$ of fishing effort over the year, an age-dependent gear selectivity $S_k(a, t)$ and the annual scaling $F_{k,y}$ of fishing effort for that fleet, as the fishing season, gear selectivity and overall investment of effort will vary from fleet to fleet.

With these definitions the governing equations become

$$\frac{dN_a}{dt} = -\left(M(a, t) + \sum_k F_k(a, t) \right) N_a. \tag{13}$$

$$B_a(t) = w_a(t) N_a(t) \tag{14}$$

$$\frac{dY_{k,a}}{dt} = w_a(t) F_k(a, t) N_a \tag{15}$$

where the yield is now calculated for each fleet and age class, and the total yield per fleet is determined by summing contributions from each age class

$$Y_k(t) = \sum_a Y_{k,a}(t). \tag{16}$$

In turn these governing equations have solution

$$N_a(t) = N_a(0) \exp\left(-M_y \int_0^t m(a, \tau) d\tau - \sum_k F_{k,y} \int_0^t E_k(\tau) \, S_k(a, \tau) d\tau \right) \tag{17}$$

$$B_a(t) = w_a(t) N_a(t) \tag{18}$$

$$Y_{k,a}(t) = F_{k,a} \int_0^t E_k(\tau) \, S_k(a, \tau) B_a(\tau) d\tau \tag{19}$$

where again the necessary integrals can be evaluated with the composite trapezoidal rule.

As in the case of a single fleet case, Equations (16) – (17) determine the abundance, biomass and yield for known initial abundances $N_a(0)$. If only relative initial abundances are known, then rescaling $N_a(t)$, $B_a(t)$ and $Y_a(t)$ by the factor

$$r = \frac{B_{ref}(t_1 - t_0)}{\sum_a \int_{t_0}^{t_1} B_a(\tau)d\tau} \tag{20}$$

again scales the projection to a mean total biomass estimate B_{ref} from a survey taken over the time interval $[t_0, t_1]$.

When the annual scaling $F_{k,y}$ of fishing effort are known, projecting stock abundance, biomass and yield forward over a year for multiple fleets model follows essentially the same process as for the single fleet case, except that yield is calculated on a per fleet basis, and total fishing mortality consists of a contribution from each fleet.

But when there are multiple fleets, determining annual scaling $F_{k,y}$ that match the annual yield for each fleet to known historic or target catches is more difficult. In the single fleet case, only a single F_y need be determined in each year, and any reliable univariate root finding methods can be employed. In the multiple fleet case, a scaling $F_{k,y}$ must be determined for each fleet, but these scalings are not independent. Although the individual fleets operate independently, increasing the effort of one fleet reduces the available biomass, making is more difficult for the other fleets to attain their targets.

When the simulated stock is highly depleted, the target catch for some or all fleets may be unattainable, as there is insufficient biomass in the population for some fleets to catch their target. With a single fleet, this event is easily detected and the entirety of the attainable yield can be attributed to the only fleet. But when there are multiple fleets the attainable yield must be correctly apportioned amongst the fleets.

When there are multiple fleets, annual scaling $F_{k,y}$ that match the annual yield to a given target can be determined through modified form of Newton's method (Burden and Faires, 2005). Let $F = (F_1, F_2, \dots, F_m)$ denote the vector of scalings for the m fleets fishing in the current year, $Y(F) = \big(Y_1(F), Y_2(F), \dots, Y_m(F)\big)$ the vector of yields for the m fleets, and $C = (C_1, C_2, \dots, C_m)$ the corresponding vector of target catches. Then the required scalings are the root of the equation

$$Y(F) - C = 0. \tag{21}$$

Newton's method generates a sequence of successively better approximations $F^{(1)}, F^{(2)}, \ldots$ to the root of this equation according the

$$F^{(n+1)} = F^{(n)} - J^{-1}(Y - C) \tag{22}$$

where J is the Jacobian matrix with elements

$$J_{ij} = \frac{\partial Y_i}{\partial F_j}. \tag{23}$$

When the projection is not rescaled to match a reference biomass, the elements of the Jacobian can be determined directly from Equations (16) - (18). Writing $f_k(a,t) = E_k(t) S_k(a,t)$ and suppressing subscripts in y for clarity, differentiating equations (16) - (18) with respect to F_j shows that

$$\frac{\partial N_a}{\partial F_j} = -N_a(0) \int_0^t f_j(a,\tau)d\tau \exp\left(-M_y \int_0^t m(a,\tau)d\tau - \sum_k F_k \int_0^t f_k(a,\tau)d\tau \right) \tag{24}$$

$$\frac{\partial B_a}{\partial F_j} = w_a(t)\frac{\partial N_a}{\partial F_j} \tag{25}$$

and hence

$$\frac{\partial Y_{i,a}}{\partial F_j} = \delta_{ij} \int_0^t f_i(a,\tau)B_a(\tau)d\tau - \int_0^t F_i f_i(a,\tau)B_a(\tau)\int_0^\tau f_i(a,\sigma)d\sigma \, d\tau \tag{26}$$

where δ_{ij} denotes the Kronecker delta and again the required integrals are evaluated with the composite trapezoidal rule.

When the projection is scaled to match a reference biomass, the yield $Y_{k,a}(t)$ is scaled by the additional factor r from Equation (20), and it can be shown that

$$\frac{\partial Y_{i,a}}{\partial F_j} = r\left(\delta_{ij} \int_0^t f_i(a,\tau)B_a(\tau)d\tau - \int_0^t F_i f_i(a,\tau)B_a(\tau)\int_0^\tau f_i(a,\sigma)d\sigma \, d\tau \right) +$$
$$\frac{\sum_a \int_{t_0}^{t_1}\int_0^\tau f_j(a,\sigma)d\sigma \, B_a(\tau)d\tau}{\sum_a \int_{t_0}^{t_1} B_a(\tau)d\tau} \int_0^t F_i f_i(a,\tau)B_a(\tau)d\tau. \tag{27}$$

In both cases the entries of the Jacobian are the sums of these derivatives over the age classes

$$J_{ij} = \frac{\partial Y_i}{\partial F_j} = \sum_a \frac{\partial Y_{i,a}}{\partial F_j}. \tag{28}$$

The Newton iteration (20) is initialized with $F^{(1)} = 0$, and the is terminated when the projected yield $Y(F^{(n+1)})$ reproduces the target C to within an appropriate tolerance.

When the target is unattainable for one or more fleets, the scaling for that fleet will increase with each Newton iteration as the method tries to drive the yield toward the target. But for very large F the trapezoidal rule provides a poor approximation to the yield and the projection can become unreliable. To avoid this, each F_k is capped at some maximum F_{max} that corresponds to a fishing effort that would be impossible to deliver. In each Newton iteration, for those fleet for which the scaling F_k exceeds F_{max} and yet the annual yield $Y_k(1)$ remains below the target C_k, the scaling F_k is fixed at F_{max} and the Newton iteration recalculated for the remaining fleets. The iteration is terminated when for each fleet, either $F_k = F_{max}$ or the projected yield $Y_k(F^{(n+1)})$ reproduces the target C_k to within an appropriate tolerance This process is summarized in Figure 1.

Examples and Tests

A number of simple tests were conducted to test the basic functionality of the package.

The first test compared the multiple fleet implementation to the original single fleet implementation. Two identical fleets, with identical fishing seasons, selectivities and target catches. As the two fleets are identical, the two fleets should have identical yields and annual scaling of fishing effort. If the catch is unattainable, the attainable catch will be equally apportioned between the two fleets and the annuals scaling should be capped at its maximum.
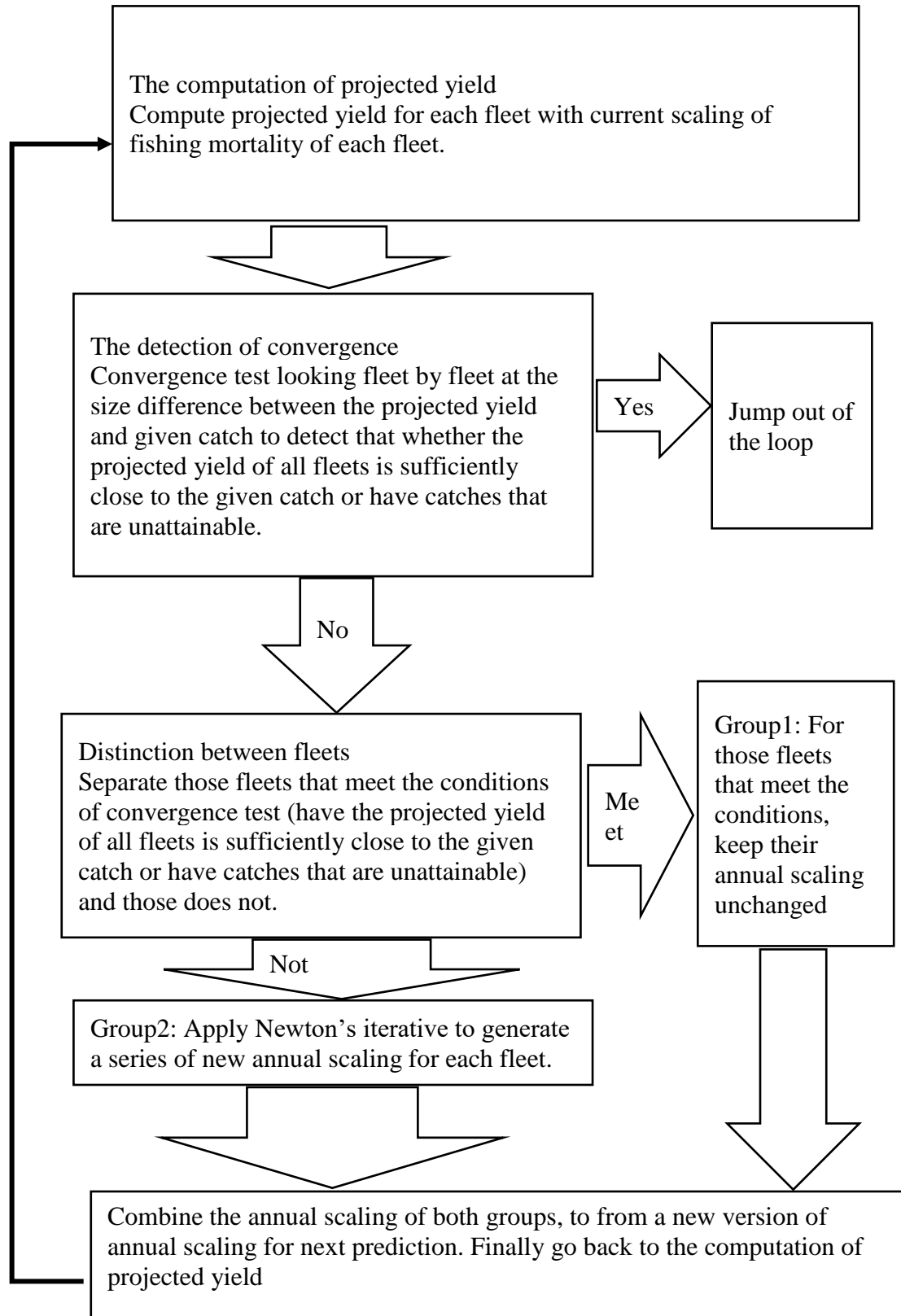
The computation of projected yield
Compute projected yield for each fleet with current scaling of fishing mortality of each fleet.

The detection of convergence
Convergence test looking fleet by fleet at the size difference between the projected yield and given catch to detect that whether the projected yield of all fleets is sufficiently close to the given catch or have catches that are unattainable.

Yes → Jump out of the loop

No

Distinction between fleets
Separate those fleets that meet the conditions of convergence test (have the projected yield of all fleets is sufficiently close to the given catch or have catches that are unattainable) and those does not.

Meet → Group1: For those fleets that meet the conditions, keep their annual scaling unchanged

Not

Group2: Apply Newton's iterative to generate a series of new annual scaling for each fleet.

Combine the annual scaling of both groups, to from a new version of annual scaling for next prediction. Finally go back to the computation of projected yield

Figure1: Flow chart of a single determinization of the scaling of fishing mortality,

The second test simulated two identical fleets that fish sequentially. The selectivities and target catches are again identical but the fishing season is split in half, with the first fleet fishing only in the first half of the season, and the second fleet fishing only in the second half. In this case, the fleet that fishes first should be able to attain its target catch with less effort. As the target catches increase, the catch for the second fleet should be become unattainable before the first, as the available biomass is depleted by the fishing of the first fleet.

When comparing fleets with the same fishing season to sequential season fleets the models behave largely as expected (Table 3). When two fleets fish at the same time each obtains the same catch with the same effort. In contrast when one fleet fishes after the other, the second fleet requires more effort to obtain the same catch, or if there is not enough biomass in the population hits the fmax of the model and receives less catch.

Table 1: Newly added Grym package functions with brief descriptions.

Functions	Description
projectMF	Projection function that projects the abundance, biomass and yield in each age class forward over one year, allow multiple fleets.
projectCMF	Projection function to project the abundance, biomass and yield in each age class forward over one year, given a known target catch for each fleet
Scale3	The function that scales a 3D array along its third dimension or optionally summing along the third dimension
Trapz, ctrapz,	Numerical quadrature by the composite trapezoidal rule that can deal with 3D arrays.

Comparisons

These comparisons are made using the parameters listed in Table 2 with the Grym code in Appendix 1.

A comparison was made using the Constable and De la Mare (1996) toothfish assessment fitted as a single fleet model, simulated for 1000 runs. This model was compared to 1) the same parameters fitted as a multifleet model where both fleets have the same selectivity as the single

fleet model, and 2) a multifleet model where the two fleets used a differing double normal selectivity, simulating a trawl and longline fleet.

When comparing models between the models (Table 4), the multifleet model with the same selectivities returns identical results as the single fleet model. The model using two double normal selectivities, as expected, generally leads to a higher probability of depletion and lower mean spawning stock escapement as a result of the differing selectivity.

Conclusion

This paper presents an extension of the Grym stock projection model to allow for multiple fishing fleets. The basic Grym model is extended to perform stock projections when the fishing mortality due to each fleet is known, and a modified form of Newton's method is developed for determining the annual scaling of fishing effort required to reproduce a known target catches for each fleet.

If the target catches are unattainable, the attainable component of the catch is correctly apportioned amongst the fleets.

We have demonstrated that the extension of Grym project functions to multiple fleets produces outputs that are very consistent with the results from Constable and de la Mare (1996) for the Patagonian toothfish fishery assessment when selectivity is the same. When selectivity is different the results are consistent with what may be expected.

Given the capacity to model more complex fisheries, fishing practices, and the demonstrated high degree of consistency in the outputs, we recommend that the extension of current Grym package to be used in future stock assessments to represent multiple fleets in the model.

Table 2: Input parameters for Grym and GYM software assessment comparisons conducted for *D. eleginoides*.

Category	Parameter	Toothfish
Ages	First Age class	4
	Last Age Class	35
von Bertalanffy growth	t0	0
	Linf	170.8 cm
	k	0.088
	Date - start growth period (dd/mm)	30-Nov
	Date - end growth period (dd/mm)	30-Nov
Weight at Length (kg, mm)	Weight-length parameter – A (kg)	2.50E-05
	Weight-length parameter - B	2.8
Maturity	Min length, 50% are mature	-
	Max length, 50% are mature	-
	Range over which maturity occurs	-
	Years over which maturity occurs	Jan-17
Spawning Season	First Day of Spawning Season (dd/mm)	1-Jul
	Last Day of Spawning Season (dd/mm)	1-Jul
Mortality	Min Mean Annual M	0.16
	Max Mean Annual M	0.16
Recruitment	Function	Log-Normal
	Mean recruitment	See Appendix 3
	Min Coefficient of Variation	1.162
	Max Coefficient of Variation	1.162
	Cohorts to project	-
Fishery parameters	Age fully selected	See Appendix 3
	Age first selected	See Appendix 3
	Min length, 50% Selected	-
	Max length, 50% Selected	-
	Range over which recruitment occurs	-
	Season	
	Catch between survey and season	0
	Initial Biomass	-

Category	Parameter	Toothfish
Simulation specifications	Number of runs in simulation	10001
	Evaluation Type	Constant Catch
Individual trial specifications	Years to remove initial age structure	1
	Year prior to projection	
	Reference Start Date in year	1-Dec
	Increments in year	365
	Years to project stock in simulation	35
	Reasonable upper bound for Annual F	4.5
	Tolerance for finding F in each year	0.000001
	Target Escapement	50%

Table 3: Comparison of single runs of Patagonian toothfish models for identical and sequential fleets on the multiple fleet implementation.

Target	Catch		Effort	
Identical fleets	Fleet 1	Fleet 2	Fleet 1	Fleet 2
2.0E8	100,000,000	100,000,000	0.2809625	0.2809625
3.0E8	150,000,000	150,000,000	0.5140667	0.5140667
4.0E8	200,000,000	200,000,000	0.9536835	0.9536835
5.0E8	237,273,831	237,273,831	4.5	4.5
Sequential fleets	Fleet 1	Fleet 2	Fleet 1	Fleet 2
2.0E8	100,000,000	100,000,000	1.129263	2.440313
3.0E8	150,000,000	82,284,240	2.059255	4.5
4.0E8	200,000,000	37,423,276	3.776633	4.5
5.0E8	211,519,365	27,058,807	4.5	4.5

Table 4: Comparison of the 1996 paper and multiple fleet implementation of Grym of the results of 1000 projection runs of six long-term annual yields for *D. eleginoides*. Single denotes the single fleet fit of the Grym, Multiple 1 is two fleets fishing with the same selectivity, and Multiple 2 is two fleets fishing with differing selectivity.

Long-term Annual Yield (tonnes)	Probability of Depletion Below Bound $S_{min}<0.2\widehat{S_0}$			Mean Spawning Stock Escapement $\hat{E}$		
Fleet	Single	Multiple 1	Multiple 2	Single	Multiple 1	Multiple 2
3500	0.015	0.015	0.045	0.807	0.807	0.758
4000	0.026	0.026	0.071	0.779	0.779	0.722
4500	0.046	0.046	0.091	0.751	0.751	0.689
5000	0.065	0.065	0.119	0.726	0.726	0.648
5500	0.082	0.082	0.147	0.695	0.695	0.681
6000	0.107	0.107	0.189	0.664	0.664	0.579

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Appendix 1: Grym assessment code for multi fleets version of project function.

A version of Grym that implements the multiple fleet functionality is available in the 'Multifleet' branch of the Github repository

https://github.com/AustralianAntarcticDivision/Grym

The new functions are briefly described in this appendix.

In the single fleet version of Grym, an *annual matrix* is a matrix with one row for the initial time and each subsequent time step through the year, and one column for each modelled age class. In the multiple fleet version, where appropriate these matrices are generalized to three dimensional arrays where again the first and second dimensions corresponds to time steps through the year and modelled age classes, and the third dimension corresponds to the separate fleets. The single fleet implementations of the functions trapz and ctrapz for computing the composite trapezoidal rule mut be generalized to these 3 dimensional inputs. The single fleet functions project and project must also be extended to compute projections for multiple fleets.

scale3

The function scale3 scales a 3D array along its third dimension, optionally summing over the third dimension.

```
scale3 <- function(A,b,sum=FALSE) {
  dm <- dim(A)
  if(sum)
    `dim<-`(`dim<-`(A,c(dm[1]*dm[2],dm[3]))%*%b,dm[1:2])
  else
    `dim<-`(`dim<-`(A,c(dm[1]*dm[2],dm[3]))%*%diag(b),dm)
}
```

trapz

The trapz function from the Grym has been generalized to allow 3D arrays as input.

Given a set of function values $f(x_k)$ sampled at even increments $x_k = x_1 + (k-1)h$, the integral $\int_{x_1}^{x_n} f(l)dl$ can be approximated by the composite trapezoidal rule:

$$\int_{x_1}^{x_n} f(l)dl = \frac{h}{2}f(x_1) + h\sum_{k=2}^{n-1} f(x_k) + \frac{h}{2}f(x_n)$$

The trapz function implements the composite trapezoidal rule. Given a vector fs of function values $f(x_k)$, trapz returns the trapezoidal approximation to $\int_{x_1}^{x_n} f(l)dl$. If fs is a 2D or 3D array, then each column is assumed to represent a different integrand f(x), and trapz acts on the columns to return a vector or matrix of approximate integrals.

```
trapz <- function(fs,h=1) {
  if(is.array(fs)) {
    dm <- dim(fs)
    if(length(dm)==2) {
      h*(colSums(fs)-(fs[1,]+fs[nrow(fs),])/2)
    } else {
      fs <- matrix(fs,dm[1],length(fs)/dm[1])
      array(h*(colSums(fs)-(fs[1,]+fs[nrow(fs),])/2),dm[-1])
    }
  } else {
    h*(sum(fs)-(fs[1]+fs[length(fs)])/2)
  }
}
```

ctrapz

The ctrapz function from the Grym has been generalized to allow 3D arrays as input. The ctrapz function is similar to trapz except that it returns the sequence of approximations:

$$\left(\int_{x_1}^{x_1} f(l)dl, \int_{x_1}^{x_2} f(l)dl, \ldots \ldots, \int_{x_1}^{x_n} f(l)dl \right).$$

In this case fs may be a vector or 2D or 3D array, and it returns a sequence of approximations of the same dimension as the input fs.

```
ctrapz <- function(fs,h=1) {
  if(is.array(fs)) {
    dm <- dim(fs)
    Fs <- matrix(fs,dm[1],length(fs)/dm[1])
    for(j in seq_len(ncol(Fs)))
      Fs[-1,j] <- cumsum((h/2)*(Fs[-1,j]+Fs[-nrow(Fs),j]))
    Fs[1,] <- 0
    array(Fs,dm)
  } else {
    c(0,cumsum((h/2)*(fs[-1]+fs[-length(fs)])))
  }
}
```

ProjectMF

The projectMF function generalizes the project function to compute the abundance, biomass and the yields when there are multiple fleets. This function differs from the project function in that the inputs relating to the fishing mortalities are specified on a per fleet basis, and a separate yield is be computed for each fleet. By assuming the matrix of scaled integrated fishing mortalities FFs has been summed over fleets, the implementation remains largely unchanged from the single fleet case.

Given inputs
ws - matrix of weights at age
MMs - matrix of scaled integrated natural mortalities
FFs - matrix of summed scaled integrated fishing mortalities, which is the sum of each fleets' matrix of scaled integrated fishing mortalities
Ffs - array of scaled fishing mortalities
Nref - vector of reference abundances for each age class
nref - vector of time steps for which the reference abundance is known
Bref - reference biomass
bref - vector of time steps for which the reference biomass is known
yield - if yield=1 only calculate yield for the final time step, if yield=2 calculate yield for all time steps, otherwise yield is not calculated at all

the projectMF function computes the projections of abundance N, biomass B and the yield Y for each fleet Y.

```
projectMF <- function(ws,MMs,FFs=0,Ffs=0,Nref=1,nref=1,Bref=NA,bref=nref,yield=2) {

  if(length(Nref==1)) Nref <- rep.int(Nref,ncol(MMs))

  ## Integrate N and scale to reference abundance
  N <- exp(-MMs-FFs)
  for(j in seq_len(ncol(N))) N[,j] <- Nref[j]/mean(N[nref,j])*N[,j]

  ## Scale by weight at age
  B <- ws*N

  ## Rescale to match reference biomass
  if(!is.na(Bref)) {
    r <- Bref/sum(trapzMeans(B[bref,,drop=FALSE]))
    N <- r*N
    B <- r*B
  }

  ## Integrate yield
  Y <- switch(yield,
              trapz(Ffs*as.vector(B),1/(nrow(B)-1)),
              ctrapz(Ffs*as.vector(B),1/(nrow(B)-1)))

  list(N=N,B=B,Y=Y)
}
```

projectCMF

The projectCMF generalizes the projectC function to determine annual scalings of fishing effort for each fleet that reproduce known target yields for each fleet, using the modified version of Newton's method described in the text.

Given inputs
ws - matrix of weights at age
MMs - matrix of scaled integrated natural mortalities
Fs - array of unscaled integrated fishing mortalities
fs - array of unscaled fishing mortalities
Catch - target total annual catch
Nref - vector of reference abundances for each age class
nref - vector of time steps for which the reference abundance is known
Bref - reference biomass
bref - vector of time steps for which the reference biomass is known
yield - if yield=1 only calculate yield for the final time step, if yield=2 calculate yield for all time steps, otherwise yield is not calculated at all
Fmax - the maximum F to allow in the search
tol - the precision to which to reproduce the observed catch

the projectCMF function computes matrices of projected abundance N, biomass B, and also projected array of yield Y and annual scaling of fishing mortalities F that reproduces the target catch for each fleet.

```r
projectCMF <- function(ws,MMs,Fs,fs,Catch,Nref,nref=1,Bref=NA,bref=nref,yield=2,
                       Fmax=4.5,tol=1.0E-6) {
  nfleets <- dim(Fs)[3]
  F <- rep(0,nfleets)
  ## Apply Newton's method

  repeat {
    ## Compute projected yield
    FFs <- scale3(Fs,F,TRUE)
    Ffs <- scale3(fs,F,FALSE)
    pr <- projectMF(ws,MMs,FFs,Ffs,Nref,nref,Bref,bref,yield=1)
    Y <- colSums(pr$Y)

    ## Test for convergence
    if(all(abs(Y - Catch) < tol | (F==Fmax & Y < Catch))) break

    ## Jacobian of the yield
    J <- matrix(0,nfleets,nfleets)
    for(k in 1:nfleets) {
      J[k,k] <- sum(trapz(fs[,,k]*as.vector(pr$B),h))
      J[,k] <- J[,k]-colSums(trapz(Ffs*as.vector(pr$B*Fs[,,k]),h))
      if(!is.na(Bref))
        J[,k] <- J[,k]+colSums(pr$Y*sum(trapzMeans(Fs[bref,,k,drop=FALSE]*as.vector
(pr$B[bref,])))/sum(trapzMeans(pr$B[bref,,drop=FALSE])))
    }

    ## Protected Newton step
    F1 <- F - solve(J,Y-Catch)
    ok <- (Y >= Catch) | (F1 < Fmax) # | (F < Fmax)
```

```r
    if(all(ok)) {
      F <- pmin(pmax(F1,0),Fmax)
    } else {
      if(any(ok)) F[ok] <- F[ok] - solve(J[ok,ok,drop=F],(Y-Catch)[ok])
      F[!ok] <- Fmax
    }
  }

  ## Recalculate
  pr <- projectMF(ws,MMs,FFs,Ffs,Nref,nref,Bref,bref,yield)
  pr$F <- F
  pr
}
```