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PRO-2BOX 3.0

User Guide

BY

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Acknowledgments

The framework and code for PRO-2BOX evolved largely as a product of the author's work with the Bluefin Tuna working group of the International Commission for the Conservation of Atlantic Tuna (ICCAT). Some of the concepts and algorithms used in the current software were inspired by two early versions of code written independently in the 1990s by Victor Restrepo and Andre Punt. Since then, the software has benefitted from over two decades of interactions with numerous other scientists from many different working groups, having been applied at one time or the other to most of the species managed under ICCAT, to Albacore by the International Scientific Committee for Tuna and Tuna-Like Species in the North Pacific Ocean (ISC), and to numerous species in the United States. The present version of this manual benefited from helpful reviews by Shannon Cass-Calay, Matthew Lauretta, Dan Goethel, Matthew Supernaw, Alex Chester and John Walter. Cover photo by Iñigo Onaindia (AZTI Tecnalia)

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1. GETTING STARTED

PRO-2BOX is a software tool developed to project the future abundance and mortality of exploited animal populations. It has been designed to accommodate all of the options available in program VPA-2BOX (Porch, 2017), including two intermixing stocks and sex-specific analyses. Other useful features include the ability to account for animals that are discarded dead and the ability to model individual fleets separately. The general theory behind the software is highlighted in Chapter 2. Specific details are reserved for Chapter 3, which covers all of the available options via a line by line discussion of the input files.

WHAT'S NEW IN VERSION 3.0?

This update of version 2.01 includes the following new features:

- 1) computes MSY with two-line model when the maximum yield per recruit is unsustainable
- 2) outputs selectivity for each year
- 3) includes option for steepness parameterizations of spawner-recruit curves
- 4) implements bias correction for spawner-recruit curves with lognormal error structure
- 5) writes ASC-ii files with bootstrap results
- 6) Generates uncertainty in N, F using input standard deviations (if bootstraps unavailable)
- 7) Generates uncertainty in future natural mortality rate as a uniform random variable
- 8) Adds capability to estimate autocorrelated recruitment
- 9) Allows user to specify target SPR values

DISCLAIMER AND CONDITIONS OF USE

The manual and executable versions of PRO-2BOX can be obtained free of charge either by contacting the author or by visiting <http://www.iccat.es/>. Source code is available at <https://github.com/ICCAT/software/>. Copies of the executable code and manual for PRO-2BOX may be distributed without restriction. The development of PRO-2BOX is ongoing, and the author appreciates comments regarding it, including any suspected bugs. However, no formal technical support is offered.

There is no warranty of any kind. While considerable effort has been made to ensure the program performs as described in the manual (see Appendix 3), the author and the U.S. government cannot be held responsible for any errors therein.

SYSTEM REQUIREMENTS

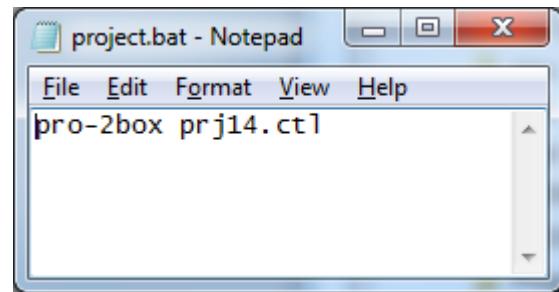
- Compatible with 80486, Pentium and above processors (standard PC's and clones)
- MS-DOS, IBM OS/2, or Microsoft Windows (9x and above) operating systems²
- 1 MB of available hard disk space (30 MB for some bootstrap applications)

INSTALLING AND RUNNING PRO-2BOX

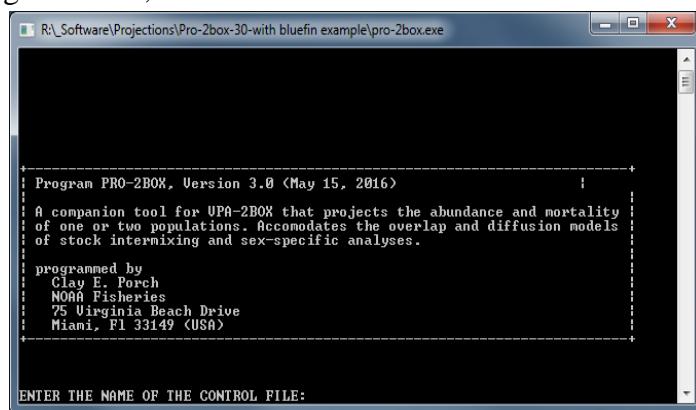
The only file needed for a complete installation is the executable PRO-2BOX.exe. To run the program you can either

- place the executable in a directory of your choosing and add that directory to your PATH statement as described in the documentation for your operating system and restart or
- place a copy of PRO-2BOX.exe in the directory where you plan to do the analyses.

The program may be run from the Windows Run dialog, entering the name PRO-2BOX at a DOS prompt, or double clicking on the PRO-2BOX.EXE icon in Windows Explorer. It may also be run in batch mode from the Windows command line, DOS or other shell environments. For example, a .bat file may be written such as the example project.bat to the right. The program may be started by double clicking or otherwise calling the batch file. In this example the name of the executable pro-2box is followed by the name of an ASCII text file that contains the specifications needed to make the run (in the example the name of the control file is prj14.ctl, but the user may specify the name and extension).



If the name of the control file is not entered in the command line, the program will prompt the user as shown in the screen capture below. There is no graphical user interface; PRO-2BOX runs only as a console-mode program that takes all input from binary or ASCII text files (described in chapter 3). The screen is used only to enter the name of the control file and to display certain error and advisory messages. Hence, the user must be able to create and edit ASCII text files.



²Reference to trade names does not imply endorsement by NOAA or the U.S. Government.

It is also possible to compile PRO-2BOX on linux and mac platforms. An example of code for a batch file, Makefile.bat, that builds the program and places the executable in a directory called “build” is included in the text box below (courtesy of Matthew Supernaw, Southeast Fisheries Science Center). Note that the compiler, in this case gfortran, is specified on the 12th line by FC = gfortran.

```
## -*- Makefile -*-

## User: matthewsupernaw
## Time: Jul 1, 2016 9:54:54 AM
## Makefile created by Oracle Developer Studio.

##
## This file is generated automatically.

##
# Remove the conflicting .mod extension. Make thinks .mod is a Modula2
# extension but the f90 compiler uses it for a module file.SUFFIXES
.SUFFIXES: .o .f90 .f90~

##### Compiler and tool definitions shared by all build targets #####
FC = gfortran
BASICOPTS = -O
FFLAGS = $(BASICOPTS)

# Define the target directories.
TARGETDIR_pro-2box=build
all: $(TARGETDIR_pro-2box)/pro-2box

## Target: pro-2box
OBJS_pro-2box = \
    $(TARGETDIR_pro-2box)/pro-2box.o
USERLIBS_pro-2box = $(SYSLIBS_pro-2box)
DEPLIBS_pro-2box =
LDLIBS_pro-2box = $(USERLIBS_pro-2box)

# Link or archive
$(TARGETDIR_pro-2box)/pro-2box: $(TARGETDIR_pro-2box) $(OBJS_pro-2box) $(DEPLIBS_pro-2box)
    $(LINK.f) $(FFLAGS_pro-2box) $(CPPFLAGS_pro-2box) -o $@ $(OBJS_pro-2box) $(LDLIBS_pro-2box)

# Compile source files into .o files
$(TARGETDIR_pro-2box)/pro-2box.o: $(TARGETDIR_pro-2box) pro-2box.f90
    $(COMPILE.f) $(FFLAGS_pro-2box) $(CPPFLAGS_pro-2box) -o $@ pro-2box.f90

##### Clean target deletes all generated files #####
clean:
    rm -f \
        $(TARGETDIR_pro-2box)/pro-2box \
        $(TARGETDIR_pro-2box)/pro-2box.o
    rm -f *.mod
    rm -f -r $(TARGETDIR_pro-2box)

# Create the target directory (if needed)
$(TARGETDIR_pro-2box):
    mkdir -p $(TARGETDIR_pro-2box)

# Enable dependency checking
.KEEP_STATE:
.KEEP_STATE_FILE:.make.state.GNU-x86_64-Linux
```

2. THEORY BEHIND PRO-2BOX

PRO-2BOX projects the future state of the resource from estimates of its present state by making certain assumptions about fishery selectivity and the reproductive capability of the stock. The calculation framework is based on developments described by Shepherd (1982), Restrepo et al. (1994), SCRS (1997), Powers (1999), Porch and Turner (1999), Butterworth and Geromont (1999) and Restrepo and Porch (2000). The most distinctive feature of PRO-2BOX is its ability to examine two distinct groups simultaneously, making it amenable to sex-specific or two-stock analyses.

Note that the following conventions apply in the remainder of this document:

- *Italics* indicate mathematical variables or text to be replaced by the user.
- `Courier` font indicates text in a file or keystrokes.

DETERMINISTIC POPULATION DYNAMICS

The program is set up to model two populations simultaneously, either two sexes or two areas. In the case of two areas, the model is structured to accommodate a unique stock associated with each area (or management zone). The user can choose between two types of box-transfer models to simulate intermixing between the two stocks: Diffusion and overlap (see Table 1 below). The diffusion model assumes a fraction T_{jk} of the population located in management zone j will migrate to management zone k at the beginning of the year and then, if it is mature, contribute to the spawning biomass of the population in zone k (i.e., movement and spawning tendencies are determined based on the area an individual is currently in). The overlap model, in contrast, assumes a fraction \tilde{T}_{sk} of stock s resides in management zone k at any given time, but all mature fish spawn only in their natal area. Both models reduce to the equivalent of two single-stock VPA's when the transfer fractions are set to zero, otherwise T and \tilde{T} are not directly comparable inasmuch as the diffusion model allows fish born in one zone to accumulate in the other (see Porch et al, 2001; Porch, 2002, 2018).

The number of fish in the youngest age class (α) is presumed to be a function R of the spawning stock fecundity α years earlier (see discussion of spawner-recruit relationship file for available choices). Spawning stock fecundity is computed as the number of mature adults multiplied by some measure of their per capita fecundity. Typically this measure is weight, read from a file or computed via a growth curve, but other measures such as number of eggs produced can be used (see discussion of line 57 in the control file).

Table 1. Diffusion and overlap equations for population dynamics.

Diffusion equations

$\hat{N}_{k,a+1,y+1}$	$\begin{cases} R(E_{k,y-\alpha}) & (a = \alpha - 1) \\ \sum_{j=1}^2 \hat{N}_{j,a,y} T_{j,k,a} e^{-Z_{kay}} & (a < A - 1) \\ \sum_{a=A-1}^A \sum_{j=1}^2 \hat{N}_{j,a,y} T_{j,k,a} e^{-Z_{kay}} & (a = A - 1) \end{cases}$	Number [of animals] in zone k that are age $a+1$ at the beginning of year y just <i>before</i> mixing (note accent over N), where A represents a ‘plus-group’ (age A and older) and $R(E)$ represents the spawner-recruit relationship (discussed later under Maximum Sustainable Yield).
$N_{k,a,y}$	$\sum_j T_{j,k,a} \hat{N}_{j,a,y}$	Number in zone k at beginning of the year just <i>after</i> mixing (both stocks combined)
$T_{j,k,a}$		Fraction of population in zone j that moves to zone k at the beginning of the year
$Z_{kay} = F_{kay} + M_{kay}$		Loss rate coefficients representing the effect of fishing (F) and natural mortality (M)
$E_{k,y} = \sum_a p_{k,a} f_{k,a,y} \sum_{j=1}^2 N_{j,a,y} T_{j,k,a} e^{-Z_{kay} t}$		Aggregate fecundity of spawners in zone k at time of spawning (t) during year y
$p_{k,a}$		Proportion of stock in zone k that spawns
$f_{k,a,y}$		Fecundity (proxy) of individuals in zone k

Overlap equations

$\tilde{N}_{s,a+1,y+1}$	$\begin{cases} R\{E_{k,y-\alpha}\} & (a = \alpha - 1) \\ \tilde{N}_{s,a,y} \sum_{k=1}^2 \tilde{T}_{s,k,a} e^{-Z_{kay}} & (a < A - 1) \\ \sum_{a=A-1}^A \tilde{N}_{s,a,y} \sum_{k=1}^2 \tilde{T}_{s,k,a} e^{-Z_{kay}} & (a = A - 1) \end{cases}$	Number of stock s that are age $a+1$ at the beginning of year y , where A represents a ‘plus-group’ (age A and older) and $R(E)$ represents the spawner-recruit relationship (described later under Maximum Sustainable Yield)
$N_{k,a,y}$	$\sum_s \tilde{T}_{s,k,a} \tilde{N}_{s,a,y}$	Number in zone k at the beginning of year y just after redistribution (both stocks combined)
$\tilde{T}_{s,k,a}$		Fraction of stock s residing in zone k at the beginning of the year
$Z_{k,a,y} = F_{k,a,y} + M_{k,a,y}$		Loss rate coefficients representing the effect of fishing (F) and natural mortality (M)
$E_{s,y} = \sum_a p_{s,a} f_{s,a,y} \tilde{N}_{s,a,y} \sum_k \tilde{T}_{s,k,a} e^{-Z_{kay} t}$		Aggregate fecundity of spawners in stock s at time of spawning (t) during year y
$p_{s,a}$		Proportion of stock that spawns
$f_{s,a,y}$		Fecundity (proxy) of individuals in stock

As its name suggests, PRO-2BOX considers only two zones, in which case $\tilde{T}_{s,2,a,y} = 1 - \tilde{T}_{s,1,a}$ and $T_{j,2,a} = 1 - T_{j,1,a}$. For convenience of notation the second subscript has henceforth been omitted. In the case of the overlap model, $\tilde{T}_{s,a}$ ($= \tilde{T}_{s,k,a}$) is the fraction of stock s that sojourns away from the natal area and $1 - \tilde{T}_{s,a}$ is the fraction that remains in the natal area. Similarly, for the diffusion model, $T_{j,a}$ ($= T_{j,k,a}$) is the fraction of the population residing in area j that moves to the opposite area and $1 - T_{j,a}$ is the fraction that remains in j .

Once the relationship between recruitment and spawning biomass has been specified, the only other requirements are related to specifying the age-specific variables M and T (read from files) and the future values of F_{kay} for each age group. Program PRO-2BOX assumes that future F vectors are separable into an age-specific relative-vulnerability vector v (which implicitly includes gear selectivity, regulatory controls, and the fraction of the stock exposed to the fishery) and a year-specific apical fishing mortality rate ϕ (the F on the most vulnerable age class):

$$F_{kay} = \phi_{k,y} v_{k,a} \quad (2.1)$$

The vulnerability vector may be specified manually or computed from historical estimates (see discussion of line 29 in the `control` file). The apical fishing mortality rate may be specified manually, set to some average of the historical estimates, equated with one of several benchmarks (e.g., $F_{0.1}$, F_{MSY}), or computed so as to achieve a prescribed total allowable catch (see discussion of `quotas` file).

PRO-2BOX also allows for the possibility that some fraction of the catch may not be landed, but discarded dead. In that case the fishing mortality rate coefficients should reflect those losses, but the computations of future landings should not. Accordingly, PRO-2BOX allows the user to discriminate between the total removals C (catch that was killed, see `catch` file) and the fraction that was discarded dead δ (see `discard` file). Thus, the relevant equations for the total removals in number and net yield to the fishery (landed catch) in weight that was extracted from area k are

$$C_{k,a,y} = \frac{\phi_{k,y} v_{k,a}}{Z_{k,a,y}} N_{k,a,y} (1 - e^{-Z_{kay}}) \quad Y_{k,a,y} = (1 - \delta_{k,a,y}) C_{k,a,y} w_{kay} \quad , \quad (2.2)$$

where $w_{k,a,y}$ represents the average weight of individuals in the catch.

PER-RECRUIT STATISTICS

Program PRO-2BOX computes a number of the common benchmark statistics used in fisheries management, including maximum sustainable yield and spawning potential ratios. These benchmarks fundamentally depend on calculations of yield per recruit and spawning product per recruit, which are explained below. Note that per recruit statistics may be computed for the two stocks combined, or for one stock in particular (see discussion of line 16 in the `control` file). In the case of the diffusion model, where stock identity changes with the management zone of residence,

the per recruit statistics are calculated based on the point of origin (management zone where the recruit was born).

Yield per recruit for single stock/zone analyses

The yield in weight that can be expected from each recruit under constant fishing conditions (constant apical fishing mortality rate ϕ and vulnerability v) is given by

$$\left\{ \frac{Y}{R} \right\}_\phi = \phi \sum_{a=\alpha}^{\Omega} \left[\frac{v_a w_a (1-\delta_a) (1-S_a)}{z_a} \prod_{i=\alpha-1}^{a-1} S_i \right] \quad (2.3)$$

where

α is the age at recruitment

Ω is the maximum attainable age

$Z_a = \phi v_a + M_a$ is the instantaneous mortality rate coefficient at age a

$S_a (= e^{-Z_a})$ is the probability that the recruit will survive from age a to age $a+1$ (here $S_{\alpha-1} \equiv 1$).

v_a is the relative vulnerability of age class a

w_a is the expected weight at age in the retained catch

δ_a is the fraction of the kill that is discarded dead

In the case of a plus-group, where fish aged A and older are presumed to have the same relative vulnerability and natural mortality rate, the yield per recruit equation may be written

$$\begin{aligned} \left\{ \frac{Y}{R} \right\}_\phi &= \phi \sum_{a=\alpha}^{A-1} \left[\frac{v_a w_a (1-\delta_a) (1-S_a)}{z_a} \prod_{i=\alpha-1}^{a-1} S_i \right] + \\ &\quad \phi \left(\frac{v_A w_A (1-\delta_A) (1-S_A)}{z_A} \prod_{i=\alpha}^{A-1} S_i \right) \sum_{j=0}^{\Omega-A} S_A^j \end{aligned} \quad (2.4a)$$

where again it is understood that $S_{\alpha-1} \equiv 1$. Note that the summation over j on the far right of equation (2.4a) is a geometric series with solution $(1-S_A^{\Omega-A+1})/(1-S_A)$, which in the limit as Ω goes to infinity is simply $1/(1-S_A)$ and equation 2.4a reduces to

$$\left\{ \frac{Y}{R} \right\}_\phi = \phi \sum_{a=\alpha}^{A-1} \left[\frac{v_a w_a (1-\delta_a) (1-S_a)}{z_a} \prod_{i=\alpha-1}^{a-1} S_i \right] + \phi \left(\frac{v_A w_A (1-\delta_A)}{z_A} \prod_{i=\alpha}^{A-1} S_i \right) \quad (2.4b)$$

The limit form (2.4b) is consistent with the use of the plus-group calculations used in the temporal projections (Tables 1 and 2), which do not impose a finite lifespan.

The weight term representing the plus-group, w_A , is the average over all age groups represented in the plus group. To the extent growth is approximately linear for age classes older than the plus group, w_A can be computed accurately from the growth curve using the average age of the plus-group at equilibrium:

$$\bar{t}_A = \frac{\sum_{t=0}^{x-1} (A+t) S_A^t}{\sum_{t=0}^{x-1} S_A^t} + \tau$$

$$= A + \frac{\sum_{t=0}^{x-1} t S_A^t}{\sum_{t=0}^{x-1} S_A^t} + \tau \quad (2.5)$$

where τ is the time of the year during which the catch takes place and x is the number of ages in the plus group ($=\Omega - A + 1$). The two geometric series in (2.5) have solutions

$$\sum_{t=0}^{x-1} S_A^t = \frac{(1-S_A^x)}{(1-S_A)}$$

$$\sum_{t=0}^{x-1} t S_A^t = \left(\frac{(1-S_A^x)}{(1-S_A)} - (x-1)S_A^x - 1 \right) / (1 - S_A)$$

Substituting these expressions into (2.5) and simplifying we obtain

$$\bar{t}_A = A + \frac{S_A}{1-S_A} - \frac{x S_A^x}{1-S_A} + \tau \quad , \quad (2.6a)$$

which in the limit as x goes to infinity reduces to

$$\bar{t}_A = A + \frac{S_A}{1-S_A} + \tau \quad . \quad (2.6b)$$

PRO-2BOX uses the limit equations (2.4b and 2.6b) when a single stock or sex-specific analysis (below) is specified, thereby ensuring that the equilibrium calculations will be consistent with the results from the long-term projections for any given value of ϕ .

Yield per recruit for sex-specific analyses

In this case the expected yield per recruit depends on whether the recruit is male or female:

$$\left\{ \frac{Y}{R} \right\}_{\phi,s} = \phi \gamma_s \sum_{a=\alpha}^{A_s-1} \left[\frac{v_{s,a} w_{s,a} (1-\delta_{s,a}) (1-S_{s,a})}{Z_{s,a}} \prod_{i=\alpha-1}^{a-1} S_{s,i} \right] + \phi \left(\frac{v_{s,A_s} w_{s,A_s} (1-\delta_{s,A_s})}{Z_{s,A_s}} \prod_{i=\alpha}^{A_s-1} S_{s,i} \right) \quad (2.7)$$

where γ_s is the probability that a recruit is sex s and it is understood that $S_{\alpha-1} \equiv 1$. The average age of the plus-group (used for computation of w_A) is computed as in (2.6b), but with the sex-specific coefficients. Note that the age of the plus-group may vary between the sexes.

Yield per recruit for two-stock analyses with the overlap model

Limit equations analogous to (2.4b) and (2.6b) have not yet been derived for two-stock analyses, therefore PRO-2BOX uses variants of (2.3) with Ω set to the arbitrary large number of 100. For the overlap model, the yield per recruit is calculated by stock across both management zones combined using the following equations

$$\left\{ \frac{Y}{R} \right\}_{\phi,k} = \sum_{a=\alpha}^{\Omega} w_{k,a} \left((1 - \tilde{T}_{k,a}) H_{k,a} + \tilde{T}_{k,a} H_{j,a} \right) \prod_{l=a-1}^{a-1} \left((1 - \tilde{T}_{k,l}) S_{k,l} + \tilde{T}_{k,l} S_{j,l} \right) \quad (2.8)$$

$$H_{x,a} = \phi_x v_{x,a} (1 - \delta_{x,a}) \frac{1 - S_{x,a}}{Z_{x,a}}$$

where

k denotes the stock and its home range (management zone)

j denotes the management zone opposite to k

α is the age at recruitment

Ω is the maximum attainable age (100)

$Z_{ax} = \phi_x v_{ax} + M_{ax}$ is the instantaneous mortality rate coefficient for age a in zone x ($x=j,k$)

$S_{ax} = e^{-Z_{ax}}$ is the fraction surviving from age a to age $a+1$ in zone x (here $S_{\alpha-1,x} \equiv 1$).

$\tilde{T}_{k,a}$ is the fraction of the stock originating in zone k that sojourns in zone j .

v_{ax} is the relative vulnerability of age class a in zone x ($x=j,k$)

w_{ak} is the expected weight at age for stock k in the retained catch

δ_{ak} is the fraction of the kill that is discarded dead

H_{ax} is the fraction of the population in zone x that is retained in the catch

Yield per recruit for two-stock analyses with the diffusion model

Computing the yield per recruit under the diffusion model is somewhat problematic because migrating animals are assumed to be completely assimilated into the population they migrate into (i.e., a recruit born in one zone changes its affiliation after it moves to the other zone). Thus, the effective number of ‘recruits’ in one zone depends on the number of fish immigrating from the other zone, which changes with the level of fishing. In the special case where the recruitment to each zone/stock is identical, the yield per recruit associated with zone k may be expressed by the recursion:

$$\left\{ \frac{Y}{R} \right\}_{\phi,k} = \phi_k \sum_{a=\alpha}^{\Omega} w_{k,a} v_{k,a} (1 - \delta_{k,a}) \frac{1 - S_{k,a}}{Z_{k,a}} \left((1 - T_{k,a}) n_{k,a} + T_{j,a} n_{j,a} \right)$$

$$n_{k,a} = \begin{cases} 1 & (a = \alpha) \\ (n_{k,a-1} (1 - T_{k,a-1}) + n_{j,a-1} T_{j,a-1}) S_{k,a-1} & (a > \alpha) \end{cases}$$

where $n_{k,a}$ is the fraction of the recruits identified with zone k that survive to age a , $T_{k,a}$ is the fraction of the population residing in zone k that moves to zone j (j indexes the zone opposite k). This is the default calculation in previous versions of PRO-2BOX (version 2.1 and earlier) and may be interpreted as the expected yield per recruit of an individual that was equally likely to be born in either management zone. The utility of this calculation is limited and similar analytical solutions have not been derived for cases where the spawner-recruit relationship is density dependent.

Version 3.0 of PRO-2BOX employs an alternative approach that is more generally applicable—the expected yield per recruit for an individual spawned in a given management zone. In that case the relevant recursion is:

$$\left\{ \frac{Y}{R} \right\}_{\phi,k} = \sum_{a=\alpha}^{\Omega} w_{k,a} H_{k,a} n_{k,k,a} + w_{j,a} H_{j,a} n_{k,j,a} \quad (2.9)$$

$$H_{x,a} = \phi_x v_{x,a} (1 - \delta_{x,a}) \frac{1 - S_{x,a}}{Z_{x,a}}$$

$$n_{k,k,a} = \begin{cases} (1 - T_{k,\alpha}) & (a = \alpha) \\ n_{k,k,a-1} S_{k,a-1} (1 - T_{k,a}) + n_{k,j,a-1} S_{j,a-1} T_{j,a} & (a > \alpha) \end{cases}$$

$$n_{k,j,a} = \begin{cases} T_{k,\alpha} & (a = \alpha) \\ n_{k,k,a-1} S_{k,a-1} T_{k,a} + n_{k,j,a-1} S_{j,a-1} (1 - T_{j,a}) & (a > \alpha) \end{cases}$$

where $n_{k,x,a}$ is the fraction of the recruits born in zone k that have survived to age a and are currently occupying zone x ($x = k, j$). Note that the diffusion equations imply that the weight of the animal (w) changes with the zone.

Spawn per recruit for single stock/zone analyses

The equations describing the expected spawning product (or eggs or related measure) produced over the lifetime of a recruit are similar to those describing the expected yield per recruit. For a single stock the relevant equation is similar to equation (2.4b):

$$\left\{ \frac{E}{R} \right\}_{\phi} = \sum_{a=\alpha}^{A-1} p_a f_a S_a^{\tau} \prod_{i=\alpha-1}^{a-1} S_i + \frac{p_A f_A S_A^{\tau}}{1 - S_A} \prod_{i=\alpha}^{A-1} S_i \quad (2.10)$$

S_a fraction surviving from age a to age $a+1$ (where $S_{\alpha-1} \equiv 1$).

τ average time of year when spawning occurs

p_a proportion of age class a actively contributing to reproduction

f_a expected per capita egg production (or proxy such as weight)

The average egg production for the plus group, f_A , may be computed from the average age of the plus-group given by (2.6b).

Spawn per recruit for sex-specific analyses

The spawn per recruit equations for sex-specific analyses are similar to (2.10) except that they are multiplied by the fraction belonging to that sex (γ_s):

$$\left\{ \frac{E}{R} \right\}_{\phi,s} = \gamma_s \sum_{a=\alpha}^{A-1} p_{s,a} f_{s,a} S_{s,a}^{\tau} \prod_{i=\alpha-1}^{a-1} S_{s,i} + \gamma_s \frac{p_{s,A} f_{s,A} S_{s,A}^{\tau}}{1 - S_{s,A}} \prod_{i=\alpha}^{A-1} S_{s,i} \quad (2.11)$$

Spawn per recruit for two-stock analyses with the overlap model

The equations for the two-stock overlap model are a straightforward extension of (2.10) except the geometric series solution for the plus group is not used (consistent with the yield per recruit calculations discussed earlier):

$$\left\{ \frac{E}{R} \right\}_{\phi,k} = \sum_{a=\alpha}^{\Omega} p_{k,a} f_{k,a} \left((1 - \tilde{T}_{k,a}) S_{k,a}^{\tau} + \tilde{T}_{k,a} S_{j,a}^{\tau} \right) \prod_{i=\alpha-1}^{a-1} \left((1 - \tilde{T}_{k,i}) S_{k,i} + \tilde{T}_{k,i} S_{j,i} \right) \quad (2.12)$$

Spawn per recruit for two-stock analyses with the diffusion model

The recursion for the two-stock diffusion model computes expected spawning product per recruit for an individual born in a given management zone, consistent with the calculation of yield per recruit in equation (2.9):

$$\left\{ \frac{E}{R} \right\}_{\phi,k} = \sum_{a=\alpha}^{\Omega} p_{k,a} f_{k,a} S_{k,a}^{\tau} n_{k,k,a} + p_{j,a} f_{j,a} S_{j,a}^{\tau} n_{k,j,a} \quad (2.13)$$

$$n_{k,k,a} = \begin{cases} (1 - T_{k,a}) & (a = \alpha) \\ n_{k,k,a-1} S_{k,a-1} (1 - T_{k,a}) + n_{k,j,a-1} S_{j,a-1} T_{j,a} & (a > \alpha) \end{cases}$$

$$n_{k,j,a} = \begin{cases} T_{k,a} & (a = \alpha) \\ n_{k,k,a-1} S_{k,a-1} T_{k,a} + n_{k,j,a-1} S_{j,a-1} (1 - T_{j,a}) & (a > \alpha) \end{cases}$$

Note that the diffusion equations imply that the reproductive characteristics of the animal (p, f) change with the zone.

The formulation used in earlier versions of PRO-2BOX,

$$\left\{ \frac{E}{R} \right\}_{\phi,k} = \sum_{a=\alpha}^{\Omega} p_{k,a} f_{k,a} S_{k,a}^{\tau} \left((1 - T_{k,a}) n_{k,a} + T_{j,a} n_{j,a} \right)$$

$$n_{k,a} = \begin{cases} 1 & (a = \alpha) \\ (n_{k,a-1} (1 - T_{k,a-1}) + n_{j,a-1} T_{j,a-1}) S_{k,a-1} & (a > \alpha) \end{cases}$$

is no longer supported because it is less useful than (2.13) as it assumes relative recruitment levels in each zone are the same.

MANAGEMENT BENCHMARKS

PRO-2BOX computes several common biological reference points based on achieving measures of yield from the fishery or spawning capacity of the stock. In this regard, relative measures like yield per recruit and spawner per recruit (see previous section) are attractive because their computation does not require knowledge of the reproductive potential of the stock (i.e., the spawner recruit relationship). They are implicitly sustainable in the sense that their use as reference points conveys a belief that there exists a non-zero equilibrium population level, albeit unknown, associated with the measure of choice. The computation of explicitly sustainable reference points, such as the maximum sustainable yield or the equilibrium spawning capacity associated with a given level of fishing, requires the specification of the spawner-recruit relationship (in which case PRO-2BOX provides several options).

It is also important to realize that any reference points based on yield will vary with the assumed vulnerability patterns. The overall (or global) maximum sustainable yield (MSY) or maximum yield per recruit is typically attained by intensive fishing beginning at a certain optimal age (the point where population growth is offset by losses in natural mortality). In practice, however, this sort of knife-edge selection pattern is difficult to achieve either because the fishery cannot avoid under-aged fish or because managers do not wish to regulate the fishery in that way. One common practice is to compute the sustainable yield or yield per recruit under some combination of the existing mix of fisheries. PRO-2BOX allows such computations to be accomplished through a variety of means (for details see the section on vulnerability specifications in connection with line 29 in the control file). It should be understood, however, that the MSY and maximum yield per recruit calculations made using these suboptimal vulnerability patterns will be less than the true (global) MSY and maximum yield per recruit and that the corresponding biomass reference points may also be lower than the biomass that would support the global maxima.

Finally, there are no direct analogs to single stock reference points for two intermixing stocks inasmuch one cannot generally achieve the same reference point for each stock simultaneously. Moreover, for even moderate levels of mixing it is usually possible to achieve nearly the same reference points with many combinations of ϕ_1 and ϕ_2 values. PRO-2BOX gives a number of options in this regard, which are described in detail below. Other alternatives may be explored by running a series of long-term projections with different values of ϕ_i and identifying the values that achieve the desired objectives.

Implicitly Sustainable (Per-Recruit) Reference Points

As mentioned previously, important advantage of yield per recruit or spawner per recruit statistics is that they do not require any knowledge of the spawner recruit relationship $R(E)$. The primary metric of interest for management is the fishing mortality rate. PRO-2BOX numerically solves for the apical fishing mortality rate coefficient ϕ that produces the desired per recruit statistic. The program automatically computes the corresponding absolute measures such as long-term (equilibrium) yield and spawning capacity based on the input specifications for $R(E)$ as described below in the section on Explicitly Sustainable Reference Points. However, these equilibrium calculations are only meaningful to the extent that the input $R(E)$ is intended to reflect the dynamics of the stock and should otherwise be disregarded as placeholders.

Maximum yield per recruit (F_{max})

The maximum yield per recruit is computed by a numerical search for the apical fishing mortality rate coefficient ϕ that produces the highest yield per recruit (see equations 2.3 to 2.9):

$$\left\{ \frac{Y}{R} \right\}_{Max} = \max_{\phi} \left\{ \frac{Y}{R} \right\} \quad (2.14)$$

The corresponding apical fishing mortality rate (value of ϕ that produces the maximum) is termed F_{max} . Note that the maximum level of yield per recruit often cannot be sustained indefinitely unless recruitment is independent of spawning biomass.

In the case of the two-stock analyses, the default approach is a numerical search for the apical fishing mortality rates for each stock/zone (ϕ_1 and ϕ_2) that maximize either the total yield per recruit from the two stocks combined, or from one stock in particular (see discussion of line 16 in the control file). Alternatively, one can impose an assumption about the relative apical fishing mortality rates in management zone 2 relative to management zone 1 such that $\phi_2 = \beta\phi_1$ (see discussion of line 99 in the control file). In the case of the diffusion model, where stock identity changes with the management zone of residence, the per recruit statistics are calculated based on the point of origin (management zone where the recruit was born).

Related quantities output by PRO-2BOX that are sometimes used as reference points are 75% of F_{max} ($F_{0.75Fmax}$) and the value that produces 90% of the maximum yield per recruit ($F_{0.9Y/R}$). Note that there is no direct analog to $F_{0.9Y/R}$ for two stocks inasmuch as an infinite combination of ϕ_k values can achieve the same criteria. Accordingly, PRO-2BOX adopts the arbitrary procedure of setting ϕ_1 and ϕ_2 initially equal to $F_{max,1}$ and $F_{max,2}$ and reducing each by the same increment (0.001) until the corresponding yield per recruit value is less than or equal to 90% of $(Y/R)_{max}$.

10% Maximum slope of yield per recruit ($F_{0.1}$)

This benchmark is defined as the value of ϕ where the slope of the yield per recruit curve is ten percent of the slope at the origin. Inasmuch as $F_{0.1}$ is always less than F_{max} , it is located by stepping back from F_{max} in steps of 0.001 and computing the value of the slope at that point by a forward difference approximation (with step size = 0.001). This procedure locates $F_{0.1}$ to within an error of less than 0.0005. Note that there is no direct analog to $F_{0.1}$ for two stocks inasmuch as an infinite combination of ϕ_k values can achieve the same criteria. Accordingly, PRO-2BOX adopts the arbitrary procedure of setting ϕ_1 and ϕ_2 initially equal to $F_{max,1}$ and $F_{max,2}$ and then reducing each by the same increment (0.001) until the corresponding slope of the yield per recruit curve is less than or equal to 10% of the slope at the origin. Alternatively, one can impose an assumption about the relative apical fishing mortality rates in management zone 2 relative to management zone 1 such that $\phi_2 = \beta\phi_1$ (see discussion of line 99 in the control file). In that case only ϕ_1 is decremented by 0.001.

Spawning potential ratio ($F_{x\%}$)

One of the more popular management benchmarks is the equilibrium spawning potential ratio, defined as the ratio of the spawn per recruit expected at a given level of fishing ϕ to the spawn per

recruit under virgin conditions ($\phi=0$):

$$SPR_\phi = \left\{ \frac{E}{R} \right\}_\phi / \left\{ \frac{E}{R} \right\}_0 \quad (2.15)$$

where the spawn per recruit $\{E/R\}$ is calculated according to equations (2.10)-(2.13). It is located by incrementally reducing ϕ from a starting value of 3.0 yr^{-1} in steps of 0.001 until the calculated SPR reaches the target value. In case of two stocks, both ϕ_1 and ϕ_2 are initially set equal 3.0 and then reduced by the same increment (0.001). Alternatively, one can impose an assumption about the relative apical fishing mortality rates in management zone 2 relative to management zone 1 such that $\phi_2 = \beta\phi_1$ (see discussion of line 99 in the control file), in which case only ϕ_1 is decremented by 0.001. The target SPR can be computed for both stocks combined or based on one stock/zone in particular as described for line 16 in the control file). In the case of both stocks combined, one stock may be larger than another, so the SPR is calculated as

$$SPR_{\vec{\phi}} = \frac{\left\{ \frac{E}{R} \right\}_{1,\vec{\phi}} + \left\{ \frac{E}{R} \right\}_{2,\vec{\phi}}}{\left\{ \frac{E}{R} \right\}_{1,0} + \left\{ \frac{E}{R} \right\}_{2,0}} \quad (2.15a)$$

where $\vec{\phi}$ denotes the vector ϕ_1, ϕ_2 and the subscripts 1 and 2 denote stocks.

Explicitly Sustainable Reference Points

The general procedure for determine sustainable reference points involves solving for the apical fishing mortality rate coefficient ϕ that produces the desired target (F_{target}) at equilibrium and then computing the corresponding equilibrium values of yield (Y_{target}) and spawning stock (E_{target}). The sequence is illustrated for the maximum sustainable yield below.

Maximum Sustainable Yield (F_{MSY})

The concept of maximum sustainable yield remains one of the most pervasive tenets in fisheries management and is the stated goal of many management commissions. Estimates of this quantity were originally associated with production models (e.g., Pella and Tomlinson 1969), but can be derived from age-structured models provided one can express the expected equilibrium recruitment R as a function of the equilibrium fishing mortality rate ϕ (see Shepherd, 1982; Restrepo et al., 1994):

$$MSY = \max_\phi \left[R(E_\phi) * \left\{ \frac{Y}{R} \right\}_\phi \right] \quad (2.16)$$

PRO-2BOX accommodates four types of spawner-recruit relationships: constant, two-line, Beverton-Holt and Ricker.

In the simplest case where recruitment is assumed to be a constant value ω , then the value of ϕ that produces the maximum sustainable yield is F_{max} and

$$MSY = \omega \left\{ \frac{Y}{R} \right\}_{Max}$$

$$E_{MSY} = \omega \left\{ \frac{E}{R} \right\}_{Max} \quad (2.17)$$

In the case where recruitment is assumed to follow the two-line (hockey stick) relationship,

$$R = \begin{cases} \frac{\omega}{\beta} E & E < \beta \\ \omega & E \geq \beta \end{cases}, \quad (2.18)$$

the solution is the same as (2.17) provided $\left\{ \frac{E}{R} \right\}_{Max} \geq \beta/\omega$. Otherwise the spawning capacity produced per recruit would be insufficient for the population to replace itself, implying $F_{MSY} < F_{max}$. One way to handle this problem is to set F_{MSY} equal to the value of ϕ that keeps the equilibrium spawning capacity just above the hinge point of the two line curve (i.e., $E > \beta$), however the actual value of F_{MSY} can lie below the hinge point. In theory, the best estimate of F_{MSY} is the value of ϕ that keeps the equilibrium spawning capacity $\left\{ \frac{E}{R} \right\}_\phi$ just above β/ω . However, in the presence of stochastic variations in recruitment this strategy is often not sustainable because the population cannot recover from a series of poor recruitments. As a result, the central tendency of a series of stochastic projections tends to be less than expected when F_{MSY} is defined this way. PRO-2BOX handles this problem by setting F_{MSY} equal to the value of ϕ that keeps the equilibrium spawning capacity $\left\{ \frac{E}{R} \right\}_\phi$ ten percent above β/ω (a strategy that has performed well in practice, but which can result in point estimates of F_{MSY} that are a few percent below the true value).

The continuous Beverton and Holt (1957) or Ricker (1954) functions are

$$R = \begin{cases} \frac{\omega E}{\beta + E} & \text{Beverton and Holt} \\ \omega E e^{-\beta E} & \text{Ricker} \end{cases}$$

At equilibrium $E = R \left\{ \frac{E}{R} \right\}_\phi$, hence the equations for the sustainable recruitment may be recast as

$$R_\phi = \begin{cases} \omega - \beta / \left\{ \frac{E}{R} \right\}_\phi & \text{Beverton and Holt} \\ \frac{\log_e \left[\omega \left\{ \frac{E}{R} \right\}_\phi \right]}{\beta \left\{ \frac{E}{R} \right\}_\phi} & \text{Ricker} \end{cases} \quad (2.19)$$

Accordingly, the value of MSY may be found by maximizing the expressions below over ϕ

$$MSY = \begin{cases} \max_{\phi} \left[\left\{ \frac{Y}{R} \right\}_{\phi} \left(\omega - \beta / \left\{ \frac{E}{R} \right\}_{\phi} \right) \right] & \text{Beverton and Holt} \\ \max_{\phi} \left[\left\{ \frac{Y}{R} \right\}_{\phi} \frac{\log_e \left[\omega \left\{ \frac{E}{R} \right\}_{\phi} \right]}{\beta \left\{ \frac{E}{R} \right\}_{\phi}} \right] & \text{Ricker} \end{cases} \quad (2.20)$$

and the corresponding equilibrium spawning capacity is the product of R_{MSY} (eq. 2.19) and $\left\{ \frac{E}{R} \right\}_{MSY}$.

PRO-2BOX uses the Nelder-Mead simplex algorithm to accomplish the search (see discussion of numerical optimization in Porch 2002, 2018). Note that the ω terms in (2.20) will be biased low if they were fitted assuming a lognormal error structure and should be multiplied by the correction factor $\exp(\sigma^2/2)$. PRO-2BOX does this internally (see the section on Stochastic Dynamics below for details).

In the case of the two-stock analyses, the MSY may be computed for the two stocks combined or for one stock in particular (see discussion of line 16 in the control file). Alternatively, one can impose an assumption about the relative apical fishing mortality rates in management zone 2 relative to management zone 1 such that $\phi_2 = \beta \phi_1$ (see discussion of line 99 in the control file). In the case of the diffusion model, where stock identity changes with the management zone of residence, the MSY for each “stock” is calculated conditional on the point of origin (management zone where the recruits was born).

The sustainable yields for benchmarks other than MSY may be similarly computed, e.g., by application of equations 2.17 - 2.20 using the values of $\left\{ \frac{E}{R} \right\}_{\phi}$ and $\left\{ \frac{Y}{R} \right\}_{\phi}$ corresponding to the target value of ϕ (e.g., $F_{0.1}$ or $F_{30\%}$).

STOCHASTIC DYNAMICS

Stochastic variations in the population dynamics may be introduced by projecting bootstrapped runs of the original assessment model (read from a series of binary files discussed in chapter 3) and by incorporation of process error in recruitment and natural mortality. Process error in recruitment is accomplished in two ways: by fitting separate spawner-recruit relationships to each bootstrap run (when available) and by allowing recruitment to deviate from the prediction of the spawner-recruit curve. Process error in natural mortality is accomplished by allowing the magnitude of the natural mortality rate to vary annually as a uniformly distributed random variable (see the description of line 90 in the section entitled Control file). In cases where bootstrapped runs are not available, it is also possible to generate uncertainty in stock status by drawing the abundance or fishing mortality rate at age associated with the last year of data (beginning of the projections) from a normal distribution with specified variance (see the description of lines 81-82 in the section entitled Control file).

Fitting the spawner-recruit curve to data

The present version of PRO-2BOX can express future recruitment according to four basic models: constant, two-line (hockey stick), Ricker and Beverton/Holt. In the case of the first two types, the fitting procedure merely involves the computation of arithmetic or geometric mean levels of historical recruitment and spawning biomass (for more details see the discussion of the spawner-recruit relationship file in Chapter 3). When the Ricker or Beverton/Holt models are used, however, the parameters are estimated from the input historical values of recruitment (N_a) and spawning product (SSF) by nonlinear regression assuming either an additive (normal) or multiplicative (lognormal) autocorrelated AR(1) model as described in Porch (1998).

The additive AR(1) model has the form

$$\begin{aligned} R_y &= \hat{R}(E_{y-\alpha}) + \varepsilon_y \\ \varepsilon_y &= \rho \varepsilon_{y-1} + \eta_y \end{aligned} \quad (2.21)$$

$\hat{R}(E_{y-\alpha})$ is the expected recruitment predicted by the spawner recruit relationship

$E_{y-\alpha}$ is the observed level of spawning capacity in the year $y - \alpha$

α is the age of the first age class in the analysis

ρ is correlation coefficient

η is normal distributed random variable with mean 0 and variance σ^2

Maximum likelihood estimates for the parameters of $R(E)$ are obtained by minimizing the concentrated likelihood function.

$$-LL = \frac{n}{2} (1 + \log_e \hat{\sigma}^2) - \frac{1}{2} \log_e (1 - \rho^2) \quad (2.21b)$$

$$\hat{\sigma}^2 = \frac{(1 - \rho^2)(\hat{R}(E_{Y_0-\alpha}) - R_{Y_0})^2 + \sum_{y=Y_0+1}^Y (\hat{R}(E_{y-\alpha}) - R_y)^2 - \rho(\hat{R}(E_{y-\alpha-1}) - R_{y-1})^2}{Y - Y_0}$$

where Y_0 and Y are the first and last years of recruitment estimates used in the analysis, respectively. Note that this is equivalent to the least-squares solution when $\rho = 0$.

The multiplicative AR(1) model has the form

$$\begin{aligned} R_y &= \hat{R}(E_{y-\alpha})e^{-\varepsilon_y} \\ \varepsilon_y &= \rho\varepsilon_{y-1} + \eta_y \end{aligned} \quad (2.22)$$

In which case maximum likelihood estimates are obtained by minimizing the concentrated likelihood formulation

$$-LL = \frac{n}{2}(1 + \log_e \hat{\sigma}^2) - \frac{1}{2}\log_e(1 - \rho^2) \quad (2.22b)$$

$$\hat{\sigma}^2 = \frac{(1 - \rho^2)(\log_e(\hat{R}(E_{Y_0-\alpha})/R_{Y_0}))^2 + \sum_{y=Y_0+1}^Y (\log_e(\hat{R}(E_{y-\alpha})/R_y) - \rho \log_e(\hat{R}(E_{y-\alpha-1})/R_{y-1}))^2}{Y - Y_0}$$

where Y_0 and Y are the first and last years of recruitment estimates used in the analysis, respectively. Note that when $\rho = 0$, the maximum likelihood estimates of the parameters ω and β that minimize (2.22b) are equivalent to the least-squares solution with logarithmically transformed variates. The maximum likelihood estimates of ω and β are unbiased on the logarithmic scale such that the expectation of $\log_e(R)$ is $\log_e(\hat{R}(E))$, however the expectation of R is $\hat{R}(E)e^{0.5\sigma^2}$. This is important to remember for the next section.

In some instances there may be too little contrast or too much scatter in the data to reliably estimate the shape of the spawner-recruit curve, as when aberrant solutions arise during bootstrapping. In order to avoid situations where the maximum recruitment level ω is estimated to be unreasonably large, the following optional constraint may be added to the likelihood expressions above:

$$\text{penalty} = \begin{cases} \frac{1}{\text{var}(R)}(\omega - \tilde{\omega})^2 & \text{if } \omega > \tilde{\omega} \\ 0 & \text{otherwise} \end{cases} \quad (2.23)$$

$$\text{var}(R) = \frac{1}{Y - Y_0} \sum_{y=Y_0}^Y \left(R_y - \frac{\sum_{y=Y_0}^Y R_y}{Y - Y_0 + 1} \right)^2$$

$$\tilde{\omega} = \begin{cases} \max_y R_y & \text{option 1: maximum observed recruitment} \\ \frac{1}{Y_2 - Y_1} \sum_{y=Y_1}^{Y_2} R_y & \text{option 2: average recruitment during interval } [Y_1, Y_2] \end{cases}$$

where Y_1 and Y_2 are the first and last of a span of years specified by the user (see discussion of the spawner-recruit relationship file). In the case of a multiplicative error structure the observed recruitments in the calculations of (2.23) would be replaced by their log transformed values. The rationale for this constraint is that, if the variance in observed recruitment $\text{var}(R)$ is much larger than the variance about the fitted line (σ^2), then the data probably contain enough information to produce meaningful estimates of ω and the penalty for large values of ω should be relatively small. On the other hand, if the two variances are about the same then the fitted curve does nothing to

explain recruitment and the penalty for large ω should be stronger. Moreover, the penalty becomes relatively less important as the number of data points used in the fitting increases.

Projecting autocorrelated deviations in recruitment

Future (projected) recruitment is allowed to deviate from its expectation $\hat{R}(E)$ as a first-order autocorrelated process that is either additive (2.21) or multiplicative (2.22) according to the choice for the estimation procedure above. Generally the multiplicative structure is preferred because it does not admit negative recruitments and because it allows the variance in recruitment to increase with its expectation.

Additive errors are accommodated by drawing at random from the normal distribution centered on the expectation with variance equal to σ^2 (which may be prescribed by the user or estimated as in equation 2.21). In practice this is accomplished by multiplying a standard normal deviate η by the value of σ :

$$\begin{aligned} N_{\alpha,y} &= \hat{R}(E_{y-\alpha}) + \varepsilon_y \\ \varepsilon_y &= \rho \varepsilon_{y-1} + \sigma \eta_y \\ \eta_y &\sim \text{Normal}(0,1) \end{aligned} \quad (2.24)$$

Note that σ^2 refers to the variance of the random component only. The total variance of the autocorrelated recruitment deviations is $\xi^2 = \sigma^2 / (1 - \rho^2)$.

In the case of multiplicative errors, future recruitments are drawn from the lognormal distribution with parameters μ and σ^2 , where $\mu = \log_e \hat{R}(E_{y-\alpha})$ and σ^2 is the variance of the random component of the logged deviations. In practice this is accomplished by noting that if a variate x is lognormal distributed with parameters μ and σ^2 , then $\log_e x$ is normal distributed with parameters μ and σ^2 . Hence,

$$\begin{aligned} N_{\alpha,y} &= e^{\mu + \varepsilon_y} \\ \varepsilon_y &= \rho \varepsilon_{y-1} + \sigma \eta_y \\ \eta_y &\sim \text{Normal}(0,1) \end{aligned} \quad (2.25)$$

It is important to note that the expectation of the random variates generated in (2.25) is not $e^\mu \cdot 1$ (the median of the lognormal distribution), but rather $e^{\mu + \sigma^2/2}$ (the true mean). Accordingly, the average of a set of recruitment projections should give an unbiased picture of the expected trend in recruitment (all other things being equal). The MLE itself, however, must be adjusted by the factor $e^{\sigma^2/2}$. Previous versions of PRO-2BOX did not apply this correction to the MLE in deference to the prescription adopted by the ICCAT SCRS during the 1990s (Anon. 2003, 2015), and as a result, the deterministic projections of the base run tended to fall below the average of the corresponding stochastic projections. An option to exclude the bias correction has been retained to enable version 3.0 to duplicate previous versions of PRO-2BOX.

MULTIPLE FLEETS

Many stocks are fished by several fleets employing different gears or operating in different management zones. In some cases there may be a desire to regulate these fleets differently, either by reducing their total allowable catch or by altering their selection practices. This requires modeling each fleet separately. PRO-2BOX calculates the historical fishing mortality rate attributable to the i 'th fleet from the overall fishing mortality rate (F_{ay}) and the fleet-specific catches (C_{iay}) as follows:

$$F_{iay} = \frac{C_{iay}}{\sum_i C_{iay}} F_{ay} \quad (2.26)$$

As in the case of a single fleet, PRO-2BOX assumes that future F_{iay} matrices are separable into age-specific relative-vulnerability vectors v_{ia} and a year-specific apical fishing mortality rate ϕ_i (the maximum F over all age classes). The vulnerability vector may be specified manually or computed from historical partial fishing mortalities F_{iay} . The apical fishing mortality rates for each fleet may be specified manually, set to some average of the corresponding historical estimates, or computed so as to achieve prescribed total allowable catch.

The software only computes benchmark statistics based on an overall vulnerability vector calculated from the overall fishing mortality and discard rates (all fleets combined). It does not directly compute benchmark statistics for alternative fleet arrangements and produces an error message when the user attempts to run multi-fleet projections with the values of ϕ_i fixed to one of the benchmark values (see discussion in regards to the Quotas file). Benchmarks for alternative fleet arrangements can only be obtained by running a series of long-term projections with different values of ϕ_i and identifying the values that achieve the desired objectives.

3. INPUT FILES

Program PRO-2BOX always requires two ASCII text files: a control file containing most of the technical specifications for the projections and a quota file specifying the total allowable catch or fishing mortality rate for each year in the projection. A template for each of these files appears in an appendix. The explanation for each line item in the appropriate appendix is then given under the corresponding heading below.

Note that each of the files is read in free-format fashion, that is, the input data need not be in any particular column. However, if there are multiple entries on one line, they must be entered in the proper sequence. Comment lines may be inserted anywhere in the file provided they are preceded by a # symbol in the first column. Text placed after a # symbol will not be read. Comments may also appear at the end of the line after all required inputs. For example, the following comments are acceptable:

```
# First & last years in data file
# |           | Last year in projections
 1975     1999     2040
```

or

```
1975     1999     2040     First & last years in data, last year of projections
```

In contrast, the comment forms below are unacceptable:

```
# First & last years in data file
# |           | Last year in projections
 1975     1999     2040
```

or

```
1975 (first year in data) 1999 (last year in data) 2040 (projection year)
```

PRO-2BOX also reads a number of other files containing the historical data and other information (abundance, fishing mortality rate, natural mortality rate, catches, weights etc). Some of these must be ASCII text files while others must be binary direct access files (for inputs from multiple runs such as a series of bootstraps from VPA-2BOX). Some of these files are not required. If these optional files are not included the program will send a warning and invoke default settings. The list of input files is provided in Table 2 and each file is discussed individually after the sections on the control and quotas files below.

Finally, if you specify a negative integer for the number of bootstrap replicates on line 12 of the control file (discussed below), then the program will look for an ASCII text file named **BAD.OUT** that contains a list of the bootstrap runs you wish to exclude from the projections. The integer indexing the bad loop must be the first entry on each line with any comments appearing after this integer or at the end of the file.

Table 2. Input files read by PRO-2BOX. All names can be specified by the user except BAD.OUT.

Type	Content	Required?
Control	General specifications for projections	Yes
Quotas	Specifies future catch or fishing mortality rate limits	Yes
Abundance	Historical stock size in numbers (can be ASCII or binary)	Yes
Fishing Mortality	Historical fishing mortality rate (can be ASCII or binary)	Yes
Weight	Fecundity and weight information by age and year	Yes
Catch	Total removals (landings and dead discards) by age and year	Yes
Natural Mortality	Natural mortality rate by age (can be ASCII or binary)	Yes
Vulnerability	Vulnerability (selection) modifiers by age	No
Recruitment	Spawner-recruit relationship specifications	No
Movement	Transfer coefficients by age	No
Discards	Fraction of removals that are discarded by age and year	No
Rec-Mod	Modifiers to allow future recruitments to vary from expectations based on the Recruitment file above	No
F-sigma	Standard error of fishing mortality rate in last year	No
N-sigma	Standard error of abundance in last year	No
Bad.out	Identifies error-prone bootstrap replicates to be ignored	No

CONTROL FILE: See appendix 1

This is the only file PRO-2BOX will prompt the user for. It contains the file names of all the other input files and most of the model specifications. What follows is a line by line explanation of the entries in Appendix 1.

Specifications common to stocks/sexes

<u>Line</u>	<u>Explanation</u>
1 – 9	Comments preceded by the # symbol in the first column.
10	The class of model being used (1=diffusion, 2=overlap; 3=sex-specific). If only 1 stock (one or two sexes) is considered, then the overlap and diffusion models are the same.
11	Number of population groups to be considered (1=single stock with both sexes lumped together, 2=two stocks/zones or two sexes).
12	Number of bootstrap replicates to be projected. Enter 0 if only a single deterministic run is desired. The first record in the binary input files should contain the estimates produced by the stock assessment algorithm (see below). Enter a negative integer if you want to cull the bootstrap runs listed in the file BAD.OUT.
13	Width of confidence interval in percent (CI). The program generates confidence limits using the percentile method, whereby each bootstrap replicate is ranked in ascending order. For example, entering 80 for the <i>CI</i> when there are 100 bootstrap replicates will cause the lower confidence limit to be set equal to the bootstrap replicate with the tenth lowest value and the upper confidence interval to be set equal to the replicate with the tenth highest value.
14	Seed used to initiate the random number generator for stochastic projections (must be a negative integer). This feature was originally designed to allow distinct bootstrap replicates to be generated on several different machines simultaneously, which could later be combined into a single larger bootstrap analysis. Such is seldom necessary with today's faster PC's, however the feature is still useful as a variance reduction technique to facilitate comparisons between sets of projections (e.g., with different selection or natural mortality specifications).
15	Replace the historical estimates of recruitment for the last n years ($N_{\alpha,y}$) with values estimated from the spawner-recruit relationship $R(E)$ specified in the spawner-recruit relationship file (discussed below). This procedure provides an objective means of replacing the recruitment estimates for the most recent years in the time series, which are often poorly estimated in stock assessment models. The program uses Newton-Raphson iteration to solve for the fishing mortality rate vector necessary to reproduce the observed removals (landings plus dead discards) over the life of the cohort (up to the last year in the data), i.e., the values of F that satisfy:

$$F_{k,a,y} - \frac{c_{k,a,y} Z_{k,a,y}}{N_{k,a,y} (1 - e^{-Z_{k,a,y}})} = 0 \quad (3.1)$$

where the input value for the youngest age of the affected cohort ($N_{\alpha,y}$) is replaced by $R(E_{y-\alpha})$ and the abundance at subsequent ages is ($N_{\alpha+1,y+1}, N_{\alpha+2,y+2} \dots$) is calculated as described for the overlap and diffusion models in Table 1. Occasionally it may happen

that the new recruitment value is too small to support the observed catches, particularly when stochastic variations are introduced. In such cases the program sets the new recruitment equal to the value that allows the observed catches to be achieved with an apical fishing mortality rate of 3.0 yr^{-1} .

16 **Stock/sex to use when computing reference points.** The search algorithms will find the apical fishing mortality rates that achieve the prescribed spawning potential ratio, maximum yield per recruit or maximum sustainable yield of the selected stock/sex:

- 1 Base reference points on stock/sex 1 (ignore stock/sex 2)
- 2 Base reference points on stock/sex 2 (ignore stock/sex 1)
- 3 Base reference points on both stocks/sexes combined.

17 **Sex that is most limiting for recruitment:**

- 1 Recruitment depends on fecundity of sex 1 (sex 2 is not limiting)
- 2 Recruitment depends on fecundity of sex 2 (sex 1 is not limiting)
- 3 Recruitment depends on combined spawning products of both sexes

18 **Fraction of new recruits (age α) belonging to sex 1.** Enter a value > 0 and < 1 .

19 **Method of computing the weight and fecundity of each age class:**

- 0 Weights (w) and fecundity parameters (f) are computed from the growth curve for all ages in all years (see line 62)
- 1 Weights (w) and fecundity parameters (f) are computed from the growth curve for the plus-group in projection years, but otherwise read from the WEIGHT file (see below). For ages other than the plusgroup, the values for w and f used in the projections are set equal to the last year of inputs.
- 2 Weights (w) and fecundity parameters (f) for all ages are read from the WEIGHT file. Weights in projection years are set equal to the values corresponding to the last year of inputs.

21 **The first and last years in the data file followed by the last year in the projections.**

22 **The youngest (α) and oldest (A) age classes in the data file.** The oldest age class is assumed to be a plus-group (i.e., it represents ages A and older). In the case of two-stock or two-sex projections, a total of three entries are required: one entry for α (because it must be the same for both groups) and two entries for A (which may differ between sexes, but not between stocks).

29 **Vulnerability specifications.** A negative entry tells the program to use the vulnerability vector listed in the vulnerability input file (see below). Alternatively, two positive integers are interpreted as the endpoints of the range of years to be used in computing the vulnerability vector v_a from a weighted geometric mean of historical estimates of fishing mortality rate:

$$v_a = \frac{\lambda_a e^{\frac{1}{n} \sum y \log_e F_{a,y}}}{\max_a \left[\lambda_a e^{\frac{1}{n} \sum y \log_e F_{a,y}} \right]} \quad . \quad (3.2)$$

where n is the number of years in the specified range and the weighting factors λ_a are set equal to the values in the vulnerability input file (for the purpose of modifying the future vulnerability vector to account for such things as proposed minimum size limits, see discussion of vulnerability file below). Note that the age-specific vector of geometric means is normalized by dividing the through by its maximum value over all ages, creating a relative vulnerability vector with a maximum value of one. This method essentially

assumes that the future vulnerability of the stock to the fishery will be equivalent to the average vulnerability over the range of years selected.

In the case of two sexes, there is only one apical fishing mortality rate and therefore the vulnerability vectors for each sex s are relative to one another and obtained as:

$$v_{s,a} = \frac{\lambda_{s,a} e^{\frac{1}{n} \sum y \log_e F_{s,a,y}}}{\max_{s,a} \left[\lambda_{s,a} e^{\frac{1}{n} \sum y \log_e F_{s,a,y}} \right]} \quad (3.3)$$

In the case of two stocks, there are two distinct apical fishing mortality rates (ϕ_k , $k=1,2$) and the vulnerability vectors for each stock k are independent:

$$v_{k,a} = \frac{\lambda_{k,a} e^{\frac{1}{n} \sum y \log_e F_{k,a,y}}}{\max_a \left[\lambda_{k,a} e^{\frac{1}{n} \sum y \log_e F_{k,a,y}} \right]} \quad (3.4)$$

When multiple fleets are considered equations (3.2) - (3.4) remain the same except for an additional subscript i indexing the fleet. Inasmuch as there are fleet-specific apical fishing mortality rates, the vulnerability vector for each fleet is normalized by its own maximum value, e.g., for one stock,

$$v_{i,a} = \frac{\lambda_{i,a} e^{\frac{1}{n} \sum y \log_e F_{i,a,y}}}{\max_a \left[\lambda_{i,a} e^{\frac{1}{n} \sum y \log_e F_{i,a,y}} \right]} \quad (3.5)$$

The overall vulnerability vector for the multifleet situation, which is used to compute the reference points, is computed by reweighting the fleet-specific input vulnerability vectors:

$$v_a = \begin{cases} \frac{\sum_i \lambda_{i,a} \max_a F_{i,a,Y}}{\max_a [\sum_i \lambda_{i,a} \max_a F_{i,a,Y}]} & \text{input vulnerability vectors} \\ \frac{\sum_i \lambda_{i,a} e^{\frac{1}{n} \sum y \log_e F_{i,a,y}}}{\max_a [\sum_i \lambda_{i,a} e^{\frac{1}{n} \sum y \log_e F_{i,a,y}}]} & \text{geometric mean option} \end{cases} \quad (3.6)$$

Note that in the case where input vulnerability vectors are used, the fleet-specific input vulnerabilities are weighted by the corresponding fleet-specific apical fishing mortality rates from the last year of input Y (that is, it assumes the relative effort of each fleet will be the same as for the last year of inputs). In the case of the geometric mean option, the fleet-specific input vulnerabilities are weighted by the geometric mean fishing mortality rates for each age (analogous to equation 3.2).

This option also specifies how the apical fishing mortality rate representing the recent condition of the stock ($F_{current}$) is calculated. If the two inputs represent years, then $F_{current}$ is set to the geometric mean of the historical estimates for those years (maximized

over age, essentially the denominator of equations 3.2-3.6). If the first input is negative, then $F_{current}$ is set equal to the apical F in the last year of the data file.

38 Range of years (first and last) defining the recruitment and spawning stock data to be used in calculations pertaining to spawner-recruit relationship (see discussion of spawner-recruit input file).

40 Error structure of projected recruitment and spawner-recruit regression:

- 1 Multiplicative (lognormal)
- 2 Additive (normal)

The choice of error structure applies to both the stochastic projections and the fitting procedure (see section on Stochastic dynamics above for more details).

Specifications unique to each stock/sex

Line Explanation

44 Number of fleets represented in the data file that fish for stock/sex 1 (note: this number should be the same for both sexes in a sex-specific analysis, but may differ between stocks in a two-stock analysis).

45 Average age of the plus-group at the beginning of the last year in the data. Entering a positive value tells the program to use the value of the input. Entering a negative value will cause the program to determine the average age from the average weight of the plus group observed in the catch of fleet 1 by inverting the growth equation. For example, if the Von Bertalanffy growth curve is specified on line **58**,

$$\bar{t}_A = t_0 - \frac{1}{K} \log_e \left[1 - \frac{(w_A/c)^{\frac{1}{b}}}{L_\infty} \right]$$

46 Contribution of each age class to the collective spawning capacity of the stock (p). This vector, along with the matrix f , is used to compute the annual spawning capacity of the stock E . For a single stock

$$E_y = \sum_a p_a f_{a,y} N_{a,y} e^{-Z_{ay} t_{spawn}}$$

(see Table 1 for the equivalent equations for the diffusion and overlap models). The vector p can be thought of as representing the relative frequency with which each age class spawns and the matrix f can be thought of as the number of eggs produced during each spawning event. However, p and f may also serve as containers for various proxies. For example, spawning biomass is often used as a proxy for spawning capacity, where p represents the fraction of each age class that spawns and f represents that average weight of the animal at the time of spawning (t_{spawn}). Values for f may be read in from the weight file described later or computed from a growth curve (line 62)

57 Growth curve parameters for determining fecundity (biomass) of spawners. This set of entries allow the user to specify the values for the fecundity parameters (f , see line 46) as a function of age. The first entry specifies one of two possible **curve types**:

- 1** Chapman-Richards equation,

$$f_a = c \left[L_\infty \left(1 - m e^{-K(a + \frac{t}{12} - \frac{offset}{12} - t_0)} \right)^{1/m} \right]^b \quad (3.7)$$

- 2** Gompertz equation,

$$f_a = W_\infty e^{-e^{-K(a+\frac{t}{12}-\frac{\text{offset}}{12})-t_0}} \quad (3.8)$$

The second through fourth entries correspond to the growth parameters L_∞ (or W_∞), K , and t_0 . The fifth entry is the skew parameter m (note that the Chapman-Richards option reduces to the von Bertalanffy curve when $m = 1$). The sixth and seventh entries correspond to parameters c and b of the weight-length power-function used for option 1 (equation 3.7). The entries for m , c and b are superfluous when the Gompertz curve is selected, but dummy values must still be inserted. The eighth entry is the time of the year t corresponding to the date of the spawning event in terms of elapsed months (e.g., if peak spawning occurs on April 15, enter 3.5).

The ninth and final entry is an offset parameter meant to convert the integer age class (a) used in the accounting of the assessment projection model to the age currency used for the growth curve (usually the actual age of the animal). The conversion is necessary because the definition of the year used in an assessment model is often chosen to coincide with the way the data are collected (e.g., a calendar year, January through December) rather than the birth date of the animal. In such cases, the usual way to keep track of individual year-classes (fish born in a particular year) is to assign them to an integer age class based on the real age of the animal at the beginning and end of the accounting year. For example, consider the case where the animals are born (peak spawning occurs) on May 1st, which is 4 months into the calendar year. On January 1st of its first year of life the year-class is 8 months old and on the 31st of the following December it is 20 months old. Accordingly, any fish caught during the calendar year that were deemed by the age determination process to be between the ages of 8 months to 20 months would be classified as belonging to age class 1, fish aged between 20 months to 32 months would be classified as belonging to age class 2 and so on (as shown in Figure 1 below). More generally, for a given cohort born x months into the year, the age range corresponding to age class a is $a-x/12$ to $a+1-x/12$. If the growth curve is calculated based on the true age of the fish, then x is the offset required in line 57.

In some cases the offset x will be equal to the spawning date (eighth entry above), in which case the two adjustments t and offset cancel each other out. However, the offset is still needed to compute growth in weight (line 58 below). Moreover, for a variety of reasons it is possible that the age class was determined using a different birth date than the *spawnmonth* used in the projections (e.g., to compensate for protracted spawning or the timing of the formation of the first ring in a hard part). Care should be taken to understand how that animals are being assigned to age classes to make sure the correct offset is used (it is the amount that must be subtracted from the integer age class used in the model in order to arrive at the actual age at the beginning of the accounting year). In the above example the offset to be subtracted is +4 month. However, suppose the convention had been to assign animals between the ages 8 months to 20 months to age class 0. In that case the true age of an animal belonging to age class a at the beginning of the calendar year is $a-4/12+1 = a+8/12$. Accordingly, the offset is -8, because 8 months must be added to (-8 months must be subtracted from) the model age.

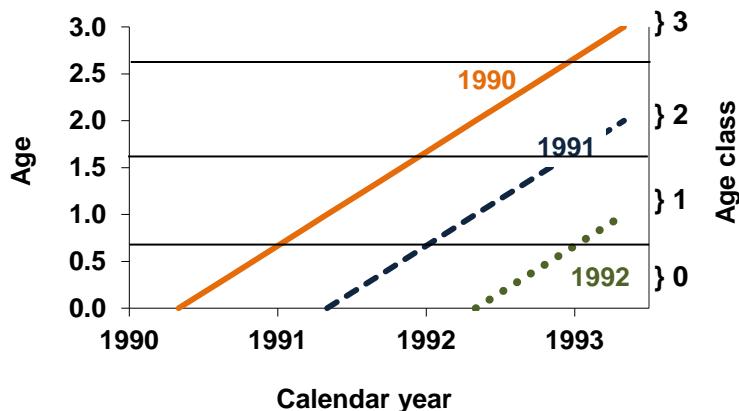


Figure 1. Relationship between the true age of a year-class born on May 1st and the age class it is assigned to. The solid, dashed and dotted lines track 1990, 1991 and 1992 yearclasses, respectively.

58 **Growth curve parameters for determining weight of catch.** The format is exactly the same as for line 57, the only difference being that these parameters apply to the catch of fleet 1 (for example, the timing parameter t refers to the month of the calendar year at the peak of the catch). A distinct set of specifications should be included for each fleet. If there are five fleets there should be five corresponding lines with growth parameters. Note that the parameters for fleet 1 are used to compute the overall benchmark statistics; therefore the fleet designated first should be the one with growth parameters most reflective of the catch of the overall fishery. Alternatively, one could create a dummy fleet 1 with zero catch.

64-66 **Here the sequence from lines 48-63 would be repeated for stock/sex 2**, with corresponding parameters (in this example there is in view only a single stock with both sexes combined, therefore no information on the ‘second’ stock/sex is required).

Specifications for required files

Line Explanation

69-74 The two entries on each line give the **format type** where 0=ASCII or 1=direct access (some files) and **name** (up to 50 characters long) for each of seven additional required files:

- Quota file with catch/effort limit scenarios
- Number in each population by age and year
- Fishing mortality rate at age by area and year
- Weight at age by stock and year
- Catch at age by area and year (number)
- Natural mortality rate at age by area

The contents required for each of these files are discussed below under each specific file type heading.

Specifications for optional inputs

The contents for lines 82 to 96 reflect features that are new to version 3.0 and are optional in the sense that they may collectively be omitted. This allows version 3.0 of PRO-2BOX to read the shorter files used for earlier versions, in which case default settings will be invoked that will cause version 3.0 to perform identically to earlier versions. Please note that you must either enter all of the optional values below or none of them. You cannot, for example, enter only one of the six files mentioned below.

Line Explanation

78-84 The two entries on each line give the **format type** (0=ASCII and any other number indicates to ignore) and **file name** (up to 50 characters long) for each of seven additional optional files:

- Vulnerability modifiers at age by area
- Spawner-recruit parameters by stock
- Transfer coefficients at age by area
- Discarded fraction at age by area and year (number)
- Recruitment modifiers
- Standard error of abundance estimates in the last year
- Standard error of fishing mortality rate estimates in the last year

The contents required for each of these files and the calculations they specify are discussed below under each specific file type heading.

90 **Stochastic variation in natural mortality** (input a single fraction x). The magnitude of the natural mortality rate can be varied stochastically for each year of the projections as a random variable ξ that is uniformly distributed on the interval $(1-x)M_a$ to $(1+x)M_a$. The average of the stochastic realizations of M will be equal to the values input in the natural mortality file specified in line 74. The values of M_a for each age class are multiplied by the same annual deviation ξ , so the proportional change is the same for all age classes in any given year.

94 **Bias-correction and autocorrelation in recruitment** (input 2 integers). The first entry tells the program whether to (0) ignore bias-correction or (1) bias-correct when a lognormal error is assumed (option 1 in line 40). When selected, the recruitments are adjusted for the point estimate projections and benchmarks (run 0) and for the benchmark calculations for the bootstrap replicates using the correction factor $\exp(\sigma^2/2)$.

The second entry tells the program to (0) ignore autocorrelation when fitting the spawner-recruit curve or (1) estimate the autocorrelation parameter (see the discussions on fitting spawner-recruit relationships and the spawner-recruit file).

96 **Spawning potential ratio targets** can now be set by the user (rather than the default values of 0.2, 0.3 and 0.4 used in previous versions). Enter a fraction between 0 and 1.

99 **Ratio of apical fishing mortality rate on stock 2 to that on stock 1** can now be imposed by the user for computing reference points: $\phi_2 = \beta\phi_1$. Enter a number:

- -999 no ratio imposed;
- -value ratio is fixed to input value, $\beta=|value|$;
- +value ratio is proportional to recent estimates, $\beta = value * F_{current}(2) / F_{current}(1)$.

QUOTA FILE: See appendix 2

An example of the quota file is presented in Appendix 2. This file contains the specifications for future limits on the landings in weight (TAC) and fishing mortality rates. It is important to realize that PRO-2BOX employs both types of limits as if both were the expected result of management actions. Therefore, if the only effect of interest in a particular year is the TAC, then the fishing mortality rate coefficient should be set to a very large value (and vice-versa).

<u>Line</u>	<u>Explanation</u>
4	Number of management projection scenarios. Multiple scenarios with different combinations of fishing mortality rate limits and TAC's may be applied.
5-12	Comments. Descriptive headers identifying the first scenario (not required).
13-15	Specifications for TAC's for first scenario. The first entry is an integer indexing the stock or zone; if the projections are for a single stock/zone you would only enter 1's in this column as the quotas are <i>not</i> sex-specific. The second entry is an integer indexing the fleet (enter 1 if there is only one fleet). The remaining entries give the TAC's for each projection year. The TAC's are specified in thousand units. Thus, if the weights specified by the growth curve or in the weight file are measured in kilograms [pounds], then the TAC's should be specified in metric tons [thousands of pounds]. In this example the TAC's are set to an arbitrarily large value with the expectation that the fishing mortality limits specified next will be the primary control mechanism. Note that there must be at least as many TAC values entered as projection years (although for constant TAC one can use the shorthand $n*x$, where n is the number of times to repeat the value x).
16	A negative value tells the program to stop reading TAC values and go on to read fishing mortality rate limits. Any stocks/zones or fleets that were not represented in the preceding lines are assumed to have TAC's of zero.
17-21	Comments. Descriptive headers (not required).
22-24	Specifications for apical fishing mortality rate (ϕ) limits for first scenario. The first entry is an integer indexing the stock/zone; if the projections are for a single stock you would only enter 1's in this column as the limits are <i>not</i> sex-specific. The second entry is an integer indexing the fleet (enter 1 if there is only one fleet). The remaining entries give the ϕ limits (in units of yr^{-1}) for each projection year. In the example file, the first value is -999, which tells the program that the apical fishing mortality rate in the first projection year should be set to the geometric mean of the historical estimates for the years specified in the control file (line 29) or the estimate from the last year of the data file (if line 29 has a negative entry). The remaining values are 0.1, which tells the program to fix ϕ to 0.1 for the balance of the projection years. There are several options for controlling ϕ :

<u>Entry</u>	<u>Result</u>
-0.1	$\phi = F_{0.1}$ 10% of slope in y/r at origin
-0.75	$\phi = F_{75}F_{max}$ 75% of F_{max}
-0.9	$\phi = F_{90}Y_{max}$ 90% maximum yield per recruit
-1	$\phi = F_{max}$ maximum yield per recruit
-2	$\phi = F_{MSY}$ maximum sustainable yield

-11 (or -20)	$\phi = F_{SPR1}$	SPR (1 st entry in line 95 of the control file)
-12 (or -30)	$\phi = F_{SPR2}$	SPR (2 nd entry in line 95 of the control file)
-13 (or -40)	$\phi = F_{SPR3}$	SPR (3 rd entry in line 95 of the control file)
+x	$\phi = x$	positive entry interpreted as fixed value of ϕ
-999	$\phi = F_{current}$	ϕ set to historical values

Note that the alternative designations for SPR (-20, -30, -40) are retained to make version 3.0 backwards compatible with the quota files read by earlier versions of PRO-2BOX, however they will still correspond, respectively, to the first, second and third entries in line 95 of the control file.

25 **A negative value** tells the program to stop reading ϕ limits for that scenario and go on to read the TAC's for the next scenario. Any stocks/zones or fleets that were not represented in the preceding lines are assumed to have ϕ limits of zero.

26-46 This section repeats the sequence of lines 5-25 above to define a second scenario where the TAC is set to 1000 for every projection year and the ϕ limit is set to 2.0 yr^{-1} . In this case the TAC is expected to be the limiting factor, but if the future abundance declines sufficiently it may not always be possible to achieve the TAC except with unrealistically high ϕ values. Accordingly, the maximum value ϕ can attain is capped for this run at 2.0 yr^{-1} .

ABUNDANCE FILE

This required file contains the estimates of historical abundance produced by the assessment model. There are two file type options: an ASCII text file or a binary direct access file (such as produced by VPA-2BOX). The data entries in the ASCII file must be ordered by stock and by year as follows:

```

1 1994      39192.27355 31123.30448 15882.59242 7941.113854 43214.92703
1 1995      35308.48328 29034.35036 17080.83165 6457.380194 32196.44784
1 1996      32059.34889 26157.16776 17610.22368 9374.159166 25125.80978
2 1994      16796.68866 14726.65355 11211.34074 7566.689768 62609.83132
2 1995      15132.20712 13738.22047 10909.77328 7515.186444 42564.21163
2 1996      13739.72095 12376.82032 10177.52404 7313.039725 30374.69035
| |
| |
| |      abundance by age (starting from first age to last age)
| year
integer specifying stock or sex

```

The lines for stock (sex) 1 must always precede those for stock (sex) 2 and the lines for year y must always precede year y+1. Comments may only be inserted at the end of a line or the end of the file, after all data (as illustrated above). Every stock/year/age combination must have an entry associated with it (i.e., dummy values should be substituted for missing data).

The binary direct access file must have a record length of $[4*(Y-y_0+1)*(A-\alpha+1)*K]$, where y_0 and Y are the first and last years of historical estimates, α and A are the first and last age classes, and K is the number of stocks/sexes. Each abundance estimate N should be stored as a 4-bit single precision variable written in the following order: $((N(k,a,y),y=y_0,Y),a=\alpha,A),k=1,K$.

FISHING MORTALITY RATE FILE

This required file contains the estimates of historical fishing mortality rate produced by the assessment model. There are two file type options: an ASCII text file or a binary direct access file (the formats of both are the same as for the abundance file discussed file above).

WEIGHT FILE

This required ASCII text file contains the estimates for the spawning capacity (fecundity) of each age class at the time of spawning and the weight at the time when most of the catch is made by each fleet. The data entries must be ordered by stock/sex, fleet and year as follows:

The lines for stock (sex) 1 must always precede those for stock (sex) 2; the lines for fleet i must always precede fleet $i+1$; and year y must always precede year $y+1$. Comments may only be inserted at the end of a line or the end of the file, after all data (as illustrated above). Every stock/fleet/year/age combination must have an entry associated with it (i.e., dummy values should be substituted for missing data). Note that in the present example there are two stocks (or sexes) with two fleets covering three years (1994-1996). The zero entry in the fleet column tells the program that the entries to the right refer to spawning capacity.

CATCH FILE

This required ASCII text file contains the estimates for the total catch of each age class made by each fleet (including animals discarded dead) in each management zone. The data entries must be ordered by management zone/sex, fleet and year as follows:

The lines for zone (sex) 1 must always precede those for zone (sex) 2, the lines for fleet i must always precede fleet $i+1$, and year y must always precede year $y+1$. Comments may only be inserted at the end of a line or the end of the file, after all data (as illustrated above). Every stock/fleet/year/age combination must have an entry associated with it (i.e., dummy values should be substituted for missing data). Note that in the present example there is one stock with two fleets covering three years (1994-1996).

In projections for which there is only one fleet, the catch at age may also be read from a binary direct access file with the same format as the abundance file discussed above, i.e, a record length of $[4*(Y-y_0+1)*(A-\alpha+1)*K]$, where y_0 and Y are the first and last years of historical estimates, α and A are the first and last age classes, and K is the number of stocks/sexes. Each catch estimate C should be stored as a 4-bit single precision variable written in the following order: $((C(k,a,y),y=y_0,Y),a=\alpha,A),k=1,K$.

NATURAL MORTALITY RATE FILE

This required file contains the estimates of natural mortality rate produced by the assessment model (assumed constant for all years). There are two file type options: an ASCII text file or a binary direct access file (such as produced by VPA-2BOX). The required format of the ASCII file is

```

1 0.2 0.2 0.3 0.3 0.3 0.3 0.3 0.3 0.2 0.2 0.1 0.1
2 11*0.2
|
| natural mortality rate at age (from youngest to oldest)
integer specifying stock or sex

```

Note that, in the example, the entries for zone (sex) 2 are written in the shorthand notation 11*0.2, which is equivalent to typing 0.2 eleven times.

The binary direct access file must have a record length of $[4*(A-\alpha+1)*K]$, where α and A are the first and last age classes and K is the number of stocks/sexes. Each natural mortality value M should be stored as a 4-bit single precision variable written in the order $((M(k,a),a=\alpha,A),k=1,K)$.

DISCARD FILE

This optional ASCII text file contains the estimates for the fraction of the total catch of each age class made by each fleet that is discarded dead (see discussion pertaining to equation 2.2). The data entries must be ordered by zone/sex, fleet and year as for the catch file discussed above. There is no provision for reading discards from direct access files. If this file is not provided, it is assumed that dead discards are negligible (0).

TRANSFER COEFFICIENT FILE

This optional file contains the estimates of the overlap or diffusion transfer coefficients. There are two file type options: an ASCII text file or a binary direct access file (such as produced by VPA-2BOX). The required formats are the same as for the natural mortality rate files discussed above. If the file is not provided the default values are set to 0.0.

VULNERABILITY FILE

The entries in this optional ASCII file are interpreted as vulnerability coefficients if line 29 of the control file is negative. Otherwise, they are interpreted as the modifiers λ in the geometric mean calculations of equations (3.3) - (3.6). The required format is as follows:

```

1 1      0.0 0.1 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0
1 2      0.0 0.1 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0
1 3      1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0
2 1      11*1.0
2 2      11*1.0
| |
| |      vulnerability modifiers from youngest age to oldest
| |      integer specifying fleet
integer specifying stock or sex

```

In this example there are two stocks (and two management zones), the first with three fleets and the second with two fleets. If the value of line 29 in the control file were positive, the coefficients would be interpreted as modifiers intending to represent regulations that eliminate the catch of the youngest animals and drastically reduce the fishing mortality rate on the next youngest age by fleets 1 and 2 in zone 1, but have no effect on fleet 3 in zone 1 or either of the two fleets in zone 2. If the file is not provided the default multipliers are set to 1.0.

SPAWNER-RECRUIT FILE

This optional file contains the estimates of the parameters dictating the nature of the relationship between the number of recruits and the collective spawning capacity of the stock. If the file is not provided the default setting is constant recruitment (see type 6 below). There are two file type options: an ASCII text file or a binary direct access file. The ASCII file has the following format:

```

1 1      220000      16000 0.4   0   0
2 1      220000      16000 0.4   0   0
|       |           |       |       |       |
|       |           |       |       |       epsilon for autocorrelated recruitment
|       |           |       |       |       ρ the autocorrelation coefficient
|       |           |       |       |       ξ standard error of recruitment deviations
|       |           |       |       |       (interpreted as the absolute minimum for
|       |           |       |       |       stochastic projections)
|       |           |       |       |       β ssb parameter
|       |           |       |       |       ω recruitment parameter
|       |           |       |       |       type of spawner-recruit curve (negative entry tells program not to estimate)
|       |           |       |       |       integer specifying the stock

```

Only one set of parameters is needed if the projections are sex-specific rather than stock-specific.

The information in the binary direct access file is similar, but must contain unique specifications for each bootstrap run (such as produced by VPA-2BOX) and must have a record length of $[4*(5+Y)*K]$, where K is the number of stocks/sexes and Y is the number of years of historical estimates. Each value should be stored as a 4-bit single precision variable written in the following order:

$$\{ [type_k, \omega_k, \beta_k, \sigma_k, \rho_k, (\eta_{k,y}, y=1, n_Y)], k=1, K \}.$$

The absolute value of the entry for *type* (second entry in the ASCII file) defines the nature of the spawner recruit curve:

$$1 (11) \text{ Beverton and Holt curve:} \quad R = \frac{\omega E}{\beta + E}$$

$$2 (12) \text{ Ricker curve:} \quad R = \omega E e^{\beta E}$$

$$3-5 \quad \text{Hockey stick (two-line) curve:} \quad R = \begin{cases} \frac{\omega E}{\beta} & \forall E < \beta \\ \omega & \text{otherwise} \end{cases}$$

$$6 \quad \text{Constant recruitment:} \quad R = \omega$$

The sign of the second entry tells the program whether or not to estimate the parameters from input data. A positive value turns on the estimation, in which case the third and fourth entries are treated as starting guesses for parameters ω and β . A negative value turns off the estimation and the third and fourth entries on the line will be interpreted as known values. Note that there are three options for the hockey stick curve (3-5). These all have exactly the same formula, but allow the user different ways of estimating the parameters (see below). Options (11) and (12) are identical to

options 1 and 2 (specifying the Beverton/Holt and Ricker curves, respectively), except that they impose a penalty described below during the fitting process. If a lognormal error structure is assumed, the parameters are assumed to be median-unbiased rather than mean-unbiased (in which case a bias-correction can be applied as described for line 93 of the control file).

The fifth entry is σ , the standard error of the random component of recruitment (see discussion of equations 2.24 and 2.25 in Chapter 2). If the error structure defined in the control file is multiplicative (lognormal), then σ is interpreted as the standard error of the deviations in the logarithm of recruitment. As discussed in connection with equations (2.21) and (2.22), σ is estimated by its MLE. However, if a negative value is entered in the file, then the program will use the larger of the two (absolute value of the input versus the value estimated by the program) for the stochastic projections.

The sixth and seventh entries are the autocorrelation coefficient ρ and the value of the residual ε used to initiate the autocorrelated error structure in the projections. The value of ε can have an important effect during the first few years of the projections, especially if the value of ρ is close to 1.0. Typically, ε is set to the value estimated for the last year of the assessment model. However, if the historical recruitments during the most recent years are to be replaced via the algorithm discussed in connection with line 16 of the control file, then the value of ε should be set to that for the most recent year where the recruitment is not being replaced (the program will update the annual values of ε , in addition to the recruitments). The default setting for PRO-2BOX treats these as fixed quantities and does not estimate the values of ρ and ε . However, there is a switch (see line 93 of the control file) that allows them to be estimated.

Spawner-Recruit Curve estimation

PRO-2BOX can be configured to compute maximum likelihood estimates for the parameters ρ , σ , ω and β . In the case of the Beverton-Holt and Ricker relationships, the maximum likelihood estimates for ρ , ω and β are determined by numerically searching for the values of ρ , ω and β that minimize the relevant likelihood expression (equations 2.21b or 2.22b). In the case of the two-line relationships, the values for ω and β are determined first (see below), and then the value of ρ is determined by numerically searching for the value that minimizes the relevant likelihood expression (equations 2.21b or 2.22b).

The following options are available:

- 1 Beverton and Holt curve parameters ρ , σ , ω and β estimated by minimizing equations (2.21b) or (2.22b).
- 11 Beverton and Holt curve estimated as for option 1, but with an additional penalty restraining the predicted maximum recruitment from becoming too much larger than some reference point $\tilde{\omega}$ as described for equation (2.23). The program will prompt the user to specify the range of years (y_1 and y_2) over which to compute the reference point from the observed recruitments. A negative value for y_1 will set the reference point equal to the largest value observed over the time period specified for the fitting. Positive inputs are interpreted as the years y_1 and y_2 for computing the reference point as an average of the corresponding observed recruitments.

- 2 Ricker curve parameters ρ , σ , ω and β estimated by minimizing equations (2.21b) or (2.22b).
- 12 Ricker curve estimated as for option 2, but with the additional penalty described above for option 11.
- 3 Two-line, ω parameter estimated by linear regression with inflection at the maximum observed E (ρ , σ estimated by minimizing equations 2.21b or 2.22b given values of ω and β):

$$\hat{\omega} = \begin{cases} \beta \sum_{y=Y_1}^{Y_2} N_{\alpha,y} E_{y-\alpha} \sqrt{\sum_{y=Y_1}^{Y_2} E_{y-\alpha}^2} & \text{additive error} \\ \frac{\beta}{Y_2 - Y_1 + 1} \sum_{y=Y_1}^{Y_2} N_{\alpha,y} / E_{y-\alpha} & \text{multiplicative error} \end{cases}$$

$$\beta = \max_{\psi} E_{\psi}$$

where Y_1 and Y_2 are the first and last years defining the range of historical recruitments to use and ψ_1 and ψ_2 are the first and last years defining the range of historical E 's (see control file line 38).

- 4 Two-line, ω parameter estimated as mean recruitment with inflection at the minimum observed E (ρ , σ estimated by minimizing equations 2.21b or 2.22b given values of ω and β):

$$\hat{\omega} = \begin{cases} \frac{1}{Y_2 - Y_1 + 1} \sum_{y=Y_1}^{Y_2} N_{\alpha,y} & \text{additive error} \\ e^{\frac{\sum_{y=Y_1}^{Y_2} \log_e N_{\alpha,y}}{Y_2 - Y_1 + 1}} & \text{multiplicative error} \end{cases}$$

$$\beta = \min_{\psi} E_{\psi}$$

- 5 Two-line, ω parameter estimated as mean recruitment with inflection at the average observed E (ρ , σ estimated by minimizing equations 2.21b or 2.22b given values of ω and β)

$$\hat{\omega} = \begin{cases} \frac{1}{Y_2 - Y_1 + 1} \sum_{y=Y_1}^{Y_2} N_{\alpha,y} & \text{additive error} \\ e^{\frac{\sum_{y=Y_1}^{Y_2} \log_e N_{\alpha,y}}{Y_2 - Y_1 + 1}} & \text{multiplicative error} \end{cases}$$

$$\beta = \frac{1}{\psi_2 - \psi_1 + 1} \sum_{y=\psi_1}^{\psi_2} E_{\psi}$$

6 Constant recruitment at the arithmetic mean:

$$\hat{\omega} = \frac{1}{Y_2 - Y_1 + 1} \sum_{y=Y_1}^{Y_2} N_{\alpha,y}$$

- 7 Like 1, but Beverton and Holt curve parameters reparameterized in terms of steepness
- 8 Like 2, but Ricker curve parameters reparameterized in terms of steepness

RECRUITMENT MODIFIER FILE

The entries in this ASCII file are used as multipliers m to used to modify future recruitments ($N_{\alpha} = mR$). If the file is not provided the default multipliers are set to 1.0.

The required format is as follows:

```
1 0.0 0.1 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0
| |
| multiplier (from first to last years of projections)
integer specifying stock or sex
```

STANDARD ERRORS FILE

This option is enabled by entering 0 for the first entry (*filetype*). PRO-2BOX then expects a file with the following format:

```
1 0.1
1 0.1
1 0.1
1 0.3
1 0.2
2 0.0
2 0.0
2 0.0
2 0.0
|
| value of standard error of the point estimate for the last year
| of assessment (one value for each age, in this example there are
| 5 age classes)
integer specifying stock or sex
```

PRO-2BOX generates normally-distributed stochastic realizations for the abundance and fishing mortality rates in the last year of the inputs:

$$N_{a,Y,i} = N_{a,Y} + \sigma_{N_a} \varepsilon_{a,i} \quad (3.9)$$

$$F_{a,Y,i} = F_{a,Y} + \sigma_{F_a} \epsilon_{a,i} \quad (3.10)$$

where $N_{a,Y}$ and $F_{a,Y}$ are the point estimate of abundance and fishing mortality (read from the files in lines 70 and 71), $N_{a,Y,i}$ and $F_{a,Y,i}$ are the values of the i th replicates, σ_{N_a} and σ_{F_a} are the standard errors contained in the files specified here (see description of Abundance standard error files below), and the values of $\epsilon_{a,i}$ are iid random variables drawn from the standard normal distribution.

This feature useful for cases where only the point estimates of N and F are available from the assessment (rather than bootstrap or MCMC replicates). Note, however, that this procedure produces replicates of N and F that are statistically independent, whereas in practice they tend to be correlated because they are estimated from the catch. Employing (3.9) and (3.10) simultaneously can result in infeasible combinations and it is generally preferable to select one and turn off the other. When these files are not provided the default is not to invoke this procedure.

4. OUTPUT FILES

Program PRO-2BOX writes a pair ASC-II files for each of a large number of output statistics (see Table 3). The file with the `.out` extension contains results from each individual bootstrap run. The file with the `.sta` extension provides a summary of the bootstrap results with the central tendencies and confidence limits.

Table 3. Output files produced by PRO-2BOX. Where indicated by $[-k]$, separate files are written for each stock and the label -1 or -2 is appended to the file name. The file name is not so appended for single stock analyses. Note that a few files have headers with labels imbedded in the first row (SR_PARMS.OUT, SELECTIVITY.OUT, SSbyage.OUT, and BENCH-*.OUT), but most do not.

File name	Content	File types
BENCH $[-k]$	Benchmark statistics for stock/sex k	<code>*.sta, *.out</code>
BIO_f $[-k]$	Fishable biomass of stock/sex k $\sum_a v_a w_a N_a$	<code>*.sta, *.out</code>
BIO_t $[-k]$	Total biomass of stock/sex k $\sum_a w_a N_a$	<code>*.sta, *.out</code>
Fapex $[-k]$	Apical fishing mortality rate	<code>*.sta, *.out</code>
Fcurr $[-k]$	Current (recent historical) fishing mortality rate	<code>*.sta, *.out</code>
M-values	Projected natural mortality rates	<code>*.out</code>
RECRT $[-k]$	Number of age α recruits to stock/sex k	<code>*.sta, *.out</code>
SELECTIVITY	Vulnerability (selectivity) by area (all fleets combined)	<code>*.out</code>
SR-PARMS	Review of spawner-recruit parameters for both stocks	<code>*.out</code>
SSbyage	Spawning stock (E) by age for each stock/sex k	<code>*.out</code>
SSTot $[-k]$	Total spawning stock (E) for stock/sex k	<code>*.sta, *.out</code>
SSf01 $[-k]$	E divided by equilibrium E associated with $F_{0.1}$	<code>*.sta, *.out</code>
SSfmax $[-k]$	E divided by equilibrium E associated with $F_{0.1}$	<code>*.sta, *.out</code>
SSmsy $[-k]$	E divided by equilibrium E associated with $F_{0.1}$	<code>*.sta, *.out</code>
SSnum $[-k]$	Spawning stock in numbers	<code>*.sta, *.out</code>
SSspr1 $[-k]$	E divided by equilibrium E associated with first SPR ref. level	<code>*.sta, *.out</code>
SSspr2 $[-k]$	E divided by equilibrium E associated with second SPR ref. level	<code>*.sta, *.out</code>
SSspr3 $[-k]$	E divided by equilibrium E associated with third SPR ref. level	<code>*.sta, *.out</code>
YIELD $[-k]$	Total landings in weight of zone/sex k (all fleets combined)	<code>*.sta, *.out</code>

*.OUT FILES

The formats of the .out files generally follow the pattern below and do not have any explanatory headers. Separate files are written for each stock.

```

1 1 0.6042E+04 0.4958E+04 0.4051E+04 0.3268E+04 0.2628E+04 ...
| |
| | values for first historical year through last year of projection
| | Bootstrap run identifier (0=deterministic value if input from VPA-2BOX)
Scenario identifier

```

There are six exceptions to this: SR-PARMS.OUT, Fcurr-*.OUT, SELECTIVITY.OUT, M-values.OUT, SSbyage.OUT, and BENCH-*.OUT (the * referring to sex/stock 1 or 2).

SR_PARMS.OUT

Contains the spawner-recruit curve parameters:

RUN#	SR_TYPE	PARM 1	PARM 2	STD. DEV.	RHO	Last	Residual
0	1	344723.9202	42494.9883	0.3241	0.0000	0.0000	
1	1	338825.2036	39290.0469	0.3365	0.0000	0.4300	
2	1	412126.1279	57535.5085	0.3882	0.0000	-0.2427	
3	1	343796.9211	40461.2658	0.3164	0.0000	-0.1629	
4	1	325584.2043	36128.0223	0.3063	0.0000	0.0650	
		ω	β	σ	ρ	ξ	
Curve type stock for stock 1							
Bootstrap run identifier							

In the case of two stocks the parameters for the second stock follow those of the first on the same line (i.e., the sequence is run#, curve type for stock 1, ω_1 , β_1 , σ_1 , ρ_1 , ξ_1 , curve type for stock 2, ω_2 , β_2 , σ_2 , ρ_2 , ξ_2).

Fcurr[-k].OUT

Contains the calculated values of $F_{current}$ for each fleet, e.g., the geometric mean of the historical fishing mortality rates discussed in connection with lines 22-24 of the quota file (option -999):

```

1 0 0.3107E+00 0.2015E+00 0.7111E+00
1 1 0.3205E+00 0.2215E+00 0.6991E+00
| |
| | values of  $F_{current}$  for each fleet
| | Bootstrap run identifier (0=deterministic value if input from VPA-2BOX)
Scenario identifier

```

Separate files are output for each stock k .

SELECTIVITY.OUT

Contains the calculated values for the vulnerability coefficients (v) associated with each fleet. The values associated with fleet 0 represent overall vulnerability vector calculated for all fleets combined (see section on multiple fleets in Chapter 2).

RUN#	Stock	Fleet	Selectivity by age				
0	1	0	0.0038	0.1276	0.3864	0.4833	0.2876
0	1	1	0.0038	0.1276	0.3864	0.4833	0.2876
1	1	0	0.0025	0.0949	0.3229	0.4671	0.2833
1	1	1	0.0025	0.0949	0.3229	0.4671	0.2833
2	1	0	0.0041	0.1545	0.5212	0.6453	0.3544

M_values.OUT

Contains the values of time-varying M used in the projections for the oldest age class (see discussion of line 90 in the control file). Inasmuch as the same uniform random multiplier is applied to each age class for each run (but different multipliers for different runs), the age-specific M vector can be calculated from the M on the oldest age by multiplying the point estimates of M_a (run 0) by $M_{\text{oldest,run}\#} / M_{\text{oldest,run}0}$.

```

0 1 0.5 0.1400 0.1400 0.1400 0.1400 0.1400
0 1 0.5 0.1621 0.1621 0.1621 0.1621 0.1621
| | |
| | M on oldest age class for first thru last year of projections
| | bound of uniform distribution, i.e. x of (1-x)M_a to (1+x)M_a
| Stock
Run#, the bootstrap run identifier (0=point estimate)

```

SSbyage.OUT

Contains the projections of spawning stock by age (E) from the point estimates (run 0) for each scenario (in thousand units):

Stock	Scenario	year	Spawning stock by age				
1	1	1	0.0000E+00	0.0000E+00	0.7140E+04	0.6256E+04	
1	1	2	0.0000E+00	0.0000E+00	0.7140E+04	0.6256E+04	

BENCH[-k].OUT

Contains the management benchmarks with labels:

RUN #	F_MSY	MSY	Y/R_MSY	S/R_MSY	SPR_MSY	...
0	0.5496E-01	0.7975E+06	0.3628E+04	0.9842E+05	0.3284E+00	...
1	0.5222E-01	0.7899E+06	0.3141E+04	0.9123E+05	0.3784E+00	...

The units for the yield (Y, MSY) and spawning stock biomass/fecundity (SS) statistics are in thousand units. The per recruit statistics, Y/R and S/R, are in the units of the entries in the weight file and growth curves (see description under BENCH[-k].STA).

*.STA FILES (Summaries)

The formats of the .sta files generally follow the pattern

SCENARIO	YEAR	LOWER_CL	MEDIAN	UPPER_CL	AVERAGE	RUN 0	STD_DEV.
1	1990	0.5578E+04	0.7325E+04	0.1051E+05	0.7221E+04	0.7508E+04	0.175EE+04
1	1991	0.4999E+04	0.7252E+04	0.1003E+05	0.7157E+04	0.7278E+04	0.2111E+04

Recall that run 0 is intended to refer to the original point estimates and the associated projections are deterministic; it is not used in the calculations of the central tendencies or confidence limits. One line will be present for each scenario in the quotas file and for each year (from the first year in the data to the last year in the projections).

There are two exceptions to the above format, Fcurr[-k].STA and BENCH[-k].STA (the [-k] referring to sex/stock $k=1$ or 2):

Fcurr[-k].STA

Contains the summary statistics for $F_{current}$ for each fleet

SCENARIO	YEAR	LOWER_CL	MEDIAN	UPPER_CL	AVERAGE	RUN 0	STD_DEV.
1	1	0.5578E+00	0.7325E+00	0.1051E+01	0.7221E+00	0.7508E+00	0.1754E+00
1	2	0.4999E+00	0.7252E+00	0.1003E+01	0.7157E+00	0.7278E+00	0.2111E+00

BENCH[-k].STA

Contains the management benchmarks with labels:

MEASURE	LOWER_CL	MEDIAN	UPPER_CL	AVERAGE	RUN_0	STD_DEV.
F at MSY	0.693442E-01	0.813030E-01	0.942305E-01	0.812152E-01	0.777773E-01	0.958843E-02
MSY	0.543481E+04	0.678537E+04	0.784920E+04	0.681265E+04	0.660894E+04	.149330E+04
Y/R at MSY	0.239792E+02	0.256828E+02	0.269936E+02	0.255384E+02	0.253901E+02	0.120879E+01
S/R at MSY	0.294099E+03	0.313702E+03	0.332703E+03	0.313841E+03	0.316389E+03	0.155677E+02
SPR AT MSY	0.437552E+00	0.466717E+00	0.494986E+00	0.466923E+00	0.470714E+00	0.231612E-01
SS AT MSY	0.619145E+05	0.809608E+05	0.106014E+06	0.852154E+05	0.823546E+05	0.288777E+05
F at max. Y/R	0.198157E+00	0.227456E+00	0.258736E+00	0.227906E+00	0.228382E+00	0.235342E-01
Y at max. Y/R	0.000000E+00	0.000000E+00	0.100078E+04	0.221780E+03	0.000000E+00	0.470986E+03
Y/R maximum	0.305291E+02	0.317891E+02	0.328528E+02	0.317269E+02	0.321928E+02	0.951368E+00
S/R at Fmax	0.112766E+03	0.120698E+03	0.128492E+03	0.120783E+03	0.112777E+03	0.613493E+01
SPR at Fmax	0.167770E+00	0.179571E+00	0.191167E+00	0.179697E+00	0.167786E+00	0.912736E-02
SS at Fmax	0.000000E+00	0.000000E+00	0.380749E+04	0.862069E+03	0.000000E+00	0.184561E+04
F 0.1	0.107557E+00	0.117561E+00	0.126836E+00	0.117442E+00	0.119382E+00	0.727688E-02
Y at F 0.1	0.461630E+04	0.572820E+04	0.650849E+04	0.568270E+04	0.537667E+04	0.801729E+03
Y/R at F 0.1	0.281721E+02	0.291198E+02	0.298334E+02	0.290453E+02	0.295360E+02	0.693062E+00
S/R at F 0.1	0.225660E+03	0.238738E+03	0.249600E+03	0.238637E+03	0.229016E+03	0.987732E+01
SPR at F 0.1	0.335731E+00	0.355187E+00	0.371348E+00	0.355037E+00	0.340723E+00	0.146952E-01
SS at F 0.1	0.367446E+05	0.468233E+05	0.558178E+05	0.468563E+05	0.416895E+05	0.789587E+04
F 20% SPR	0.178000E+00	0.204500E+00	0.241000E+00	0.208002E+00	0.198000E+00	0.244356E-01
Y at F 20%SPR	0.000000E+00	0.598875E+03	0.197898E+04	0.775246E+03	0.186233E+03	0.786280E+03
Y/R at F 20%SPR	0.290996E+02	0.303736E+02	0.314113E+02	0.303087E+02	0.304749E+02	0.921972E+00
S/R at F 20%SPR	0.202443E+03	0.202955E+03	0.203524E+03	0.202971E+03	0.203314E+03	0.404946E+00
SS at F 20%SPR	0.275088E+05	0.311101E+05	0.332064E+05	0.306561E+05	0.304643E+05	0.262137E+04
F 30% SPR	0.123000E+00	0.140000E+00	0.161000E+00	0.141818E+00	0.136000E+00	0.145270E-01
Y at F 30%SPR	0.393160E+04	0.464899E+04	0.514123E+04	0.458759E+04	0.456632E+04	0.501465E+03
Y/R at F 30%SPR	0.290996E+02	0.303736E+02	0.314113E+02	0.303087E+02	0.304749E+02	0.921972E+00
S/R at F 30%SPR	0.202443E+03	0.202955E+03	0.203524E+03	0.202971E+03	0.203314E+03	0.404946E+00
SS at F 30%SPR	0.275088E+05	0.311101E+05	0.332064E+05	0.306561E+05	0.304643E+05	0.262137E+04
F 40% SPR	0.889999E-01	0.999999E-01	0.112000E+00	0.100476E+00	0.969999E-01	0.917069E-02
Y at F 40%SPR	0.513431E+04	0.631185E+04	0.700913E+04	0.624649E+04	0.613871E+04	0.985417E+03
Y/R at F 40%SPR	0.290996E+02	0.303736E+02	0.314113E+02	0.303087E+02	0.304749E+02	0.921972E+00
S/R at F 40%SPR	0.202443E+03	0.202955E+03	0.203524E+03	0.202971E+03	0.203314E+03	0.404946E+00
SS at F 40%SPR	0.275088E+05	0.311101E+05	0.332064E+05	0.306561E+05	0.304643E+05	0.262137E+04
F 90% max Y/R	0.981098E-01	0.110236E+00	0.121954E+00	0.110158E+00	0.111382E+00	0.909922E-02
Y 90% max Y/R	0.492814E+04	0.601467E+04	0.671992E+04	0.597170E+04	0.569665E+04	0.887584E+03
Y/R 90% max Y/R	0.274571E+02	0.285573E+02	0.295096E+02	0.285171E+02	0.289655E+02	0.858353E+00
S/R 90% max Y/R	0.243447E+03	0.251864E+03	0.259429E+03	0.251811E+03	0.242975E+03	0.619577E+01
SS 90% max Y/R	0.437385E+05	0.526538E+05	0.604735E+05	0.528268E+05	0.477859E+05	0.876085E+04
F 75% of Fmax	0.148618E+00	0.170592E+00	0.194052E+00	0.170929E+00	0.171287E+00	0.176506E-01
Y 75% of Fmax	0.192460E+04	0.300746E+04	0.385417E+04	0.290493E+04	0.230417E+04	0.848353E+03
Y/R at 75% Fmax	0.300014E+02	0.312544E+02	0.323294E+02	0.312034E+02	0.316583E+02	0.969396E+00
S/R at 75% Fmax	0.160625E+03	0.168351E+03	0.176521E+03	0.168577E+03	0.160269E+03	0.607595E+01
SS at 75% Fmax	0.105007E+05	0.161991E+05	0.209812E+05	0.156909E+05	0.116648E+05	0.466881E+04

Here F *benchmark type* refers to the apical fishing mortality rate corresponding to the various benchmark statistics discussed in chapter 2. The labels Y and MSY refer to the equilibrium yield in thousand units of weight (if the growth curve and input weights were expressed in kilograms, then the entries here would be read as metric tons). The label SS is spawning stock (E), also in thousand units (a zero entry indicates that the corresponding level of F is not sustainable under the prescribed spawner-recruit relationship). The labels Y/R and S/R refer to yield per recruit and spawning product per recruit (E/R), respectively, in the actual units of the growth/fecundity inputs (e.g., kilograms rather than metric tons), and SPR refers to the unit-less spawning potential ratio.

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6. APPENDICES

APPENDIX 1. Sample control file

```

48 # | Linfinity
49 # | k
50 # | to
51 # | Chapman-Richards skew parameter (m=1 for von Bert)
52 # | weight parameter a of w=al^b
53 # | weight parameter b of w=al^b
54 # | months elapsed to compute growth
55 # | offset (months)
56 #
57 1 315.0 0.089 -1.13 1 0 .0000152 3.05305 6 4 growth in fecundity
58 1 315.0 0.089 -1.13 1 0 .0000152 3.05305 6 4 growth in weight (fishery 1)
59 #
60 # Sex/stock 2 specific information (do not enter values if number of sexes/stocks = 1)
61 #
62 #
63 #
64 # Enter names of required input files (you can input whatever names you prefer)
65 #
66 # file type (0=user supplied asc-ii, 1=VPA-2box binary format, -1=VPA-2box asc-ii format)
67 # | file name
68 # |
69 0 quotas.txt file with catch/effort limit scenarios (only file type is 0)
70 1 naa.out stock size in numbers (all 3 file types accommodated)
71 1 faa.out fishing mortality rate (all 3 file types accommodated)
72 0 waa.txt average weight at age (only file type is 0)
73 0 caa.txt catch at age (numbers) (all 3 file types accommodated)
74 0 m.txt natural mortality rate(all 3 file types accommodated)
75 #
76 # Enter names of optional input files (0=asc-ii,-9 = ignore)
77 #
78 0 S.txt selectivity modifiers (only file type is 0)
79 0 r.txt stock-recruitment parameters (only file type is 0)
80 0 t.txt transfer coefficients (only file type is 0)
81 0 daa.txt proportion from each fishery that is discarded (only file type is 0)
82 0 recmod.txt proportion from each fishery that is discarded (only file type is 0)
83 -9 FSIG.txt variance in fishing mortality rate estimates for last year
84 -9 NSIG.txt variance in abundance estimates for last year (only file type is 0)
85 #
86 # Other optional inputs
87 #
88 # fractional change in M to define interval for random uniform deviate: lower limit M =
89 # (1-input)*Mbase, upper limit of M = (1+input)*Mbase, value <= 0 means do not do it
90 0.5
91 # bias-correct recruitment with lognormal error structure (value <= 0 means do not do it)
92 # | estimate recruitment autocorrelation parameter (value <= 0 means do not do it)
93 # | |
94 1 1
95 # spawning potential ratio targets (enter three fractional values, e.g., 0.25 for 25% SPR)
96 0.4 0.3 0.2
97 # Ratio of F on stock 2 to F on stock 1 (-999 = no ratio, -value = fixed ratio, +value =
98 # ratio = value*observed ratio of Fcurrent(stock 2)/ Fcurrent(stock 2)
99 -999
100 # END OF FILE

```

APPENDIX 2. Sample Quota file

First column of file

```
1  #-----
2  # Enter the total number of projection scenarios
3  #-----
4  2
5  #-----
6  # SCENARIO 1 Current F in first year, followed by F fixed at 0.1 yr-1
7  #-----
8  # ***** CATCH LIMITS *****
9  # Stock
10 # | fleet
11 # | | TAC for each projection year in thousand units
12 # | |
13 1 1 100*100000000. #n*TAC is a convenient shorthand equivalent to entering the TAC n times
14 1 2 100*100000000.
15 1 3 100*100000000.
16 -1
17 # ***** F LIMITS *****
18 # Stock
19 # | fleet
20 # | | F limit for each projection year in thousand units
21 # | |
22 1 1 -9 100*0.1
23 1 2 -9 100*0.1
24 1 3 -9 100*0.1
25 -1
26 #-----
27 # SCENARIO 2 TAC of 1000 mt
28 #-----
29 # ***** CATCH LIMITS *****
30 # Stock
31 # | fleet
32 # | | TAC for each projection year in thousand units
33 # | |
34 1 1 100*1000. {n*TAC is a convenient shorthand equivalent to writing the TAC n times}
35 1 2 100*1000.
36 1 3 100*1000.
37 -1
38 # ***** F LIMITS *****
39 # Stock
40 # | fleet
41 # | | F limit for each projection year in thousand units
42 # | |
43 1 1 100*2
44 1 2 100*2
45 1 3 100*2
46 -1
```

APPENDIX 3. Code Verification

The author has written several spreadsheet programs to generate deterministic projections that were then analyzed by PRO-2BOX to verify that the routine performs as expected. This testing procedure has been applied to most of the options available in the program. In addition, a number of tests have been conducted in concert with others. The specifications used for stochastic projections of Bluefin tuna were validated by comparing outputs from software independently coded by A. E. Punt (ICCAT 1995) and H. Geromont (e.g., SCRS 1997, 1999, 2001a). The author also successfully duplicated the stochastic projections used as the basis for the 2000 SCRS assessment of North Atlantic albacore (SCRS 2001b).

M. Prager has developed a program in the R language, p2b.r, that is intended to replicate core functions of Fortran program Pro-2Box (Prager 2013). Output from this program was compared to output from Pro-2box for a number of options and no discrepancies were reported.

Two recent studies have explored the performance of the projection software in a simulation context (Kell et al. 2007, 2016).

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