

Draft

06/26/97

Draft

Review of Salmon Management Model Migration Algorithms

by

James G. Norris
Columbia Basin Research
School of Fisheries
University of Washington
Box 358218
Seattle, WA 98195

jnorris@olympus.net
(360) 385-4486

Prepared For:

NMFS Salmon Model Review Committee

June 19, 1997

Introduction

The National Marine Fisheries Service (NMFS) has responsibility for administering the US Endangered Species Act (ESA) for anadromous fish and shared responsibility for managing ocean salmon fisheries. Because of this dual responsibility, NMFS has a need to evaluate the constraints of ESA considerations on harvest management, and the impacts of harvest and habitat management on the recovery of depleted stocks. These evaluations need to be made on a coastwide basis and should be internally consistent and consistent with models used in other management arenas.

In 1997 NMFS contracted with the University of Washington School of fisheries to begin developing a single broad modeling framework that will assist NMFS in meeting its salmon management responsibilities. A Review Committee, composed of State, Tribal, and Federal salmon biologists and modelers, was formed to help develop model specification, identify research priorities, ensure consistency with existing models, and certify research models for management use.

The overall project has the following objectives:

1. Provide a common framework for both conservation risk assessment and harvest management analysis;
2. Expand the geographic scope of current harvest models;
3. Link coho and chinook models;
4. Incorporate life cycle (production) models for both species to evaluate long-term harvest and conservation strategies;
5. Allow flexibility to accommodate new methods and model designs;
6. Provide an interface with a large subset of ocean and freshwater databases maintained by the Pacific States Marine Fisheries Commission.

The two salmon management models currently used most extensively for fisheries that impact stocks listed under the ESA are the Pacific Salmon Commission (PSC) Chinook Model and the Fishery Regulation Analysis Model (FRAM). Neither of these models include specific migration algorithms to simulate the movement of fish through a gauntlet fishery. Three new models have been proposed to simulate salmon migration more accurately: a State Space Model (Newman, 1995), the PSC Selective Fishery Model (PSC 1995), and the Proportional Migration (PM) Model (Moore et al., 1996). The purpose of this report is to describe the migration algorithms used in these five salmon management models.

The State Space Model is the most general of the five models and has been proposed for use in a new salmon life cycle model. Thus, this report describes the existing algorithms in terms common with the State Space Model.

Notation

The notation used in this report follows that commonly used by the State Space Model. I describe the migration algorithms with reference to a single cohort of fish. A cohort may be a single age class from a single stock, or it may be a marked/tagged sub-component of that age class. No stock or age subscripts are used to make the notation easier to read. All of the models use discrete time steps and the notation is defined with respect to time interval $[t-1, t)$. Table 1 lists the notation and Fig. 1 illustrates the notation graphically.

Table 1. Common notation used in this report (also see Fig. 1).

Variable	Definition
<u>Index Variables</u>	
t	Time
r	Geographic region. For models in which there is a one-to-one correspondence between geographic region and fishery, r also indexes fishery.
R	The total number of geographic regions in the model.
<u>State Variables</u>	
$n_{r,t}$	Abundance of fish in region r at time t
$c_{r,t}$	Observed catch in region r during the time interval $[t-1, t)$.
$ns_{r,t-1}$	Abundance of fish in region r that do not suffer natural mortality and/or fishing mortality during the time interval $[t-1, t)$.
<u>Natural Mortality and Survival Parameters</u>	
$M_{r,t}$	Instantaneous natural mortality rate in region r during the time interval $[t-1, t)$.
$v_{r,t}$	Fraction of the cohort in region r killed by natural mortality during the time interval $[t-1, t)$.
$s_{r,t}$	Total survival rate in region r during the time interval $[t-1, t)$.
<u>Fishing Mortality Parameters</u>	
$E_{r,t}$	Amount of fishing effort in region r during the time interval $[t-1, t)$.
$h_{r,t}$	Regional harvest rate defined as the fraction of the cohort located in region r harvested as legal catch in region r during the time interval $[t-1, t)$.
$F_{r,t}$	Instantaneous total fishing mortality rate in region r during the time interval $[t-1, t)$.
$\mu_{r,t}$	Fraction of the available cohort in region r killed by all types of fishing mortality (including incidental mortalities) during the time interval $[t-1, t)$.
<u>Migration Parameters</u>	
$D_{r,t}$	A set of donor regions D that contribute fish to region r at the end of time period $t-1$ (e.g., used in the PM Model).
$m_{i,j}$	For a given cohort and time, the fraction of the abundance in region j moving to region i .

Note that the total fishing mortality rate includes both legal and incidental mortalities. Thus, the legal harvest rate is not necessarily equal to the total fishing mortality rate (i.e., $h_{r,t} \neq \mu_{r,t}$). Also note the following relationships:

$$\begin{aligned} s_{r,t} &= e^{-(M_{r,t}+F_{r,t})} \\ v_{r,t} &= 1 - e^{-M_{r,t}} \\ \mu_{r,t} &= 1 - e^{-F_{r,t}} \\ ns_{r,t-1} &= n_{r,t-1}s_{r,t} \end{aligned}$$

The variable $ns_{r,t-1}$ can be thought of as the number of fish in region r at the end of time interval $[t-1, t)$ just before they are redistributed among the geographic regions for the start of the next time interval $[t, t+1)$.

State Space Model

In matrix notation, the deterministic State Space Model consists of two equations:

$$\begin{aligned} \mathbf{n}_t &= \mathbf{M}_t \mathbf{S}_t \mathbf{n}_{t-1} \\ \mathbf{c}_t &= \mathbf{H}_t \mathbf{n}_t \end{aligned}$$

The abundance vectors \mathbf{n}_t and \mathbf{n}_{t-1} are composed of R elements (one abundance for each region). Each migration matrix \mathbf{M}_t is an $R \times R$ square matrix of $m_{i,j}$ elements, and the elements in each column must sum to one. Each survival matrix \mathbf{S}_t is a diagonal matrix with R elements (e.g., $s_{r,t}$). In expanded form equations (1) and (2) look like this:

$$\begin{aligned} \begin{bmatrix} n_{1,t} \\ \vdots \\ n_{R,t} \end{bmatrix} &= \begin{bmatrix} m_{1,1} & \cdots & m_{1,R} \\ \vdots & & \vdots \\ m_{R,1} & \cdots & m_{R,R} \end{bmatrix} \begin{bmatrix} s_{1,t} & & \\ & \ddots & \\ & & s_{R,t} \end{bmatrix} \begin{bmatrix} n_{1,t-1} \\ \vdots \\ n_{R,t-1} \end{bmatrix} \\ \begin{bmatrix} c_{1,t} \\ \vdots \\ c_{R,t} \end{bmatrix} &= \begin{bmatrix} h_{1,1} & \cdots & h_{1,R} \\ \vdots & & \vdots \\ h_{R,1} & \cdots & h_{R,R} \end{bmatrix} \begin{bmatrix} n_{1,t-1} \\ \vdots \\ n_{R,t-1} \end{bmatrix} \end{aligned}$$

Note that we can define a new vector $\mathbf{ns}_{r,t-1} = \mathbf{S}_t \mathbf{n}_{t-1}$ that represents the fish that do not suffer natural or fishing mortality during the interval $[t-1, t)$. Thus, the migration matrix can be thought of as being applied to the surviving cohort at the end of the time interval, and each element of the new abundance vector can be written

$$n_{r,t} = \sum_{j=1}^R m_{r,j} n s_{j,t-1} .$$

In Ken Newman's application of the State space Model, he sets $M_{r,t} = 0$ for all r and t . Thus, in his application we have

$$\begin{aligned} s_{r,t} &= e^{-F_{r,t}} \\ v_{r,t} &= 0 \\ \mu_{r,t} &= 1 - e^{-F_{r,t}} = 1 - s_{r,t} . \end{aligned}$$

PSC Chinook Model

The PSC Chinook Model defines no specific geographic regions, and therefore has no specific fish migration algorithm. However, by separating the 25 model fisheries into preterminal and terminal categories, the model assumes a de facto concept of fish migration from the preterminal area to the terminal area. The preterminal fisheries are generally offshore ocean fisheries (e.g., ocean troll fisheries), while terminal fisheries are generally nearshore and river fisheries (e.g., ocean net and sport fisheries).

Once the preterminal fishery harvests and incidental mortalities have been taken, the model separates each cohort into an ocean run (that stays in the ocean and is available for harvest the following year) and a terminal run (that is available for harvest by terminal fisheries). Thus, what are termed maturation rates in the PSC Chinook Model can be thought of as migration rates from the ocean (preterminal area) to the nearshore and river areas (collectively called the terminal area).

Some ocean net fisheries are considered to be terminal fisheries for older age classes, even though these fisheries are not physically located near the natal stream. The idea is that at some point during the year the older (mature) members of each cohort decide to start migrating down the coast. It is assumed that the older fish captured by the nearshore net fisheries are part of the mature migrating portion of the stock.

Using the mathematical notation of the PSC Chinook Model, the maturation rates are applied to each cohort as follows:

$$TermRun = (OcnRun - PreTermMort) \cdot MatRt$$

where

TermRun = the abundance of fish in the terminal area at the start of the terminal time period;

OcnRun = the abundance of fish in the preterminal area during the preterminal time period after natural mortalities have been removed;

PreTermMort = total fishing mortalities (i.e., legal catches plus incidental mortalities) in the preterminal area during the preterminal time period.

The term “*OcnRun - PreTermMort*” is the abundance of fish not suffering natural mortality and surviving the fishing process during the preterminal time period. In the notation of the State Space Model, this term is equivalent to the first element of the \mathbf{ns}_{t-1} vector. The second element of the \mathbf{ns}_{t-1} vector is zero because it is assumed that no fish are located in the terminal area during the preterminal time period.

The term “*TermRun*” is equivalent to the second element of the \mathbf{n}_t vector (i.e., abundance in region 2 at the start of time period 2). The first element of the \mathbf{n}_t vector is the number of fish from the cohort that remain in the preterminal (or ocean) area.

In matrix notation the annual migration pattern for each cohort is expressed as follows (where 1 = preterminal area and time step; 2 = terminal area and time step):

$$\begin{bmatrix} n_{1,2} \\ n_{2,2} \end{bmatrix} = \begin{bmatrix} m_{1,1} & m_{1,2} \\ m_{2,1} & m_{2,2} \end{bmatrix} \cdot \begin{bmatrix} ns_{1,1} \\ ns_{2,1} \end{bmatrix} = \begin{bmatrix} m_{1,1}ns_{1,1} + m_{1,2}ns_{2,1} \\ m_{2,1}ns_{1,1} + m_{2,2}ns_{2,1} \end{bmatrix}$$

where

$n_{1,2}$ = preterminal area (i.e., ocean) abundance at the start of the terminal time step

$n_{2,2}$ = terminal area abundance at the start of the terminal time step

$m_{1,1}$ = $1 - MatRt$

$m_{1,2}$ = 0 (i.e., no fish move from the terminal area to the preterminal area)

$m_{2,1}$ = $MatRt$

$m_{2,2}$ = 0 (i.e., there are no fish in the terminal area to keep in the terminal area)

$ns_{1,1}$ = preterminal area (i.e., ocean) abundance at the end of the preterminal time step

$ns_{2,1}$ = 0 (i.e., no fish in the terminal area at the end of the preterminal time step)

These equations are now in the same form as Equation (3) for the State Space Model. In terms of the maturation rate we have

$$n_{1,2} = (1 - MatRt) \cdot ns_{1,1}$$

$$n_{2,2} = MatRt \cdot ns_{1,1} .$$

PSC Selective Fisheries Model

This model can have any number of marine geographic areas, but in its initial application contains just five:

- West Coast Vancouver Island (OCNN);
- Washington/Oregon Ocean (OCNS);
- Strait of Georgia (GEOS);
- Strait of Juan de Fuca and San Juan Islands (SJDF);
- South Puget Sound (SSND).

Some stocks also have terminal areas (e.g., CRTM = Columbia River terminal area) and all stocks have a generic escapement, or spawning, area (ESCP).

This model was designed primarily as a coho model in which all members of a cohort (or brood) mature and return to the natal stream in the same year. The model is generally used to examine the potential effects of selective fishery management on a limited number of stocks during a single year. Thus, this model is not designed to simulate the effects of coastwide management regulations on all stock and fisheries.

This model can be run in either deterministic or stochastic mode. The model flow is as follows:

1. Compute initial abundance of each stock;
2. Distribute initial abundance to the five fishing areas;
3. Time loop with:
 - a. Natural mortality;
 - b. Fishing mortality;
 - c. Redistribute the fish (including escapement).

Several simplifying assumptions were made to estimate the proportion of each stock in each area migrating in each time step:

1. No migration occurred between geographic regions during statistical weeks 1 through 32;
2. All migration was directed toward the river of origin;
3. Hatchery and wild fish had the same migration timing and pathway;
4. 33% of InStk1 in the OCNN region migrated around the north end of Vancouver Island to the GEOS region; and
5. Catch per unit effort in a fishery provided an unbiased measure of stock abundance.

Mathematically, the migration component of this model is virtually identical in structure to the State Space Model. During each time step, natural and fishing mortalities (including incidental mortalities) are removed from the cohort first. The remaining fish in a given area are then redistributed among the areas by assigning “dispersion” rates to each area. In the notation of the PSC Selective Fishery Model, the new abundances are computed by the following equation:

$$N_{s,a',t} = \sum_{a=1}^A I_{s,a,a',t}^*$$

where

$N_{s,a,t}$ = the abundance of stock s in area a at time t ;

$I_{s,a,b,t}$ = the number of fish from stock s that move from area a to area b at time t .

In stochastic mode, the elements of the migration matrix are selected randomly from a multinomial distribution with parameters:

$\gamma_{s,a,b,t}$ = probability that a fish from stock s moves from area a to area b at time t

These probabilities are estimated from catch and effort data using a “solver” routine in Microsoft Excel. Table 2 lists the dispersion parameters. In deterministic mode, the probabilities are replaced by the fractions moving from one region to another. Thus, in the PSC Selective Fishery Model the $\gamma_{s,a,b,t}$ are equivalent to the $m_{i,j}$ elements of the migration matrix of the state space model.

Table 2. Dispersion parameters by week for the PSC Selective Fishery Model.

Stock	Donor	Receiver	32	33	34	35	36	37	38	39	40	41	42
WCVI	OCNN	ESCP	0.00	0.01	0.03	0.06	0.07	0.17	0.14	0.38	0.26	0.40	0.47
WCVI	SJDF	OCNN	0.17	0.19	0.16	0.17	0.13	0.13	0.10	0.12	0.16	0.24	0.35
LFGS	OCNN	SJDF	0.00	0.00	0.01	0.09	0.15	0.23	0.15	0.39	0.59	0.86	0.89
LFGS	OCNS	SJDF	0.00	0.12	0.12	0.28	0.30	0.56	0.40	0.26	0.00	0.00	0.00
LFGS	SJDF	GEOS	0.00	0.00	0.00	0.00	0.00	0.00	0.15	0.22	0.31	0.24	0.31
LFGS	GEOS	ESCP	0.00	0.00	0.00	0.05	0.05	0.11	0.11	0.16	0.16	0.29	0.29
NPSD	OCNN	SJDF	0.01	0.00	0.02	0.13	0.22	0.33	0.22	0.47	0.34	0.36	0.03
NPSD	OCNS	SJDF	0.00	0.07	0.07	0.23	0.30	0.62	0.52	0.43	0.11	0.38	0.67
NPSD	GEOS	SJDF	0.00	0.00	0.00	0.00	0.00	0.01	0.05	0.05	0.06	0.07	0.18
NPSD	SJDF	NSND	0.00	0.01	0.01	0.02	0.01	0.05	0.09	0.20	0.28	0.35	0.34
NPSD	NSND	ESCP	0.00	0.00	0.00	0.00	0.00	0.00	0.33	0.67	1.00	1.00	1.00
SPSD	OCNN	SJDF	0.00	0.00	0.00	0.12	0.20	0.31	0.19	0.44	0.67	0.98	0.98
SPSD	OCNS	SJDF	0.00	0.07	0.07	0.23	0.30	0.63	0.71	0.79	0.79	0.89	1.00
SPSD	GEOS	SJDF	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.03	0.07	0.15
SPSD	SJDF	SSND	0.00	0.00	0.00	0.02	0.03	0.03	0.10	0.12	0.21	0.16	0.29
SPSD	SSND	ESCP	0.00	0.00	0.00	0.00	0.00	0.33	0.33	0.67	0.54	0.87	0.87
NWAC	OCNN	OCNS	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.24	0.40	0.40	0.50
NWAC	OCNS	WCTM	0.00	0.00	0.00	0.09	0.22	0.43	0.68	0.88	1.00	1.00	1.00
NWAC	SJDF	OCNS	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.06	0.14	0.27
NWAC	WCTM	ESCP	0.01	0.00	0.34	0.33	0.33	0.00	0.00	0.00	0.00	0.14	0.14
CRIV	OCNS	CRTM	0.00	0.06	0.10	0.21	0.42	0.38	0.60	0.65	0.99	0.99	1.00
CRIV	SJDF	OCNS	0.00	0.00	0.00	0.00	0.00	0.00	0.12	0.12	0.22	0.11	0.31
CRIV	CRTM	ESCP	0.10	0.10	0.19	0.17	0.17	0.07	0.00	0.00	0.29	0.40	0.40

Table 2. Concluded.

Stock	Donor	Receiver	43	44	45	46	47	48	49	50	51	52
WCVI	OCNN	ESCP	0.81	1.00	1.00	1.00	1.00					
WCVI	SJDF	OCNN	0.60	0.82	0.99	0.99	1.00					
LFGS	OCNN	SJDF	0.94	1.00								
LFGS	OCNS	SJDF	0.00	0.00	0.00	0.00	0.00	0.05	0.12	0.46	0.74	1.00
LFGS	SJDF	GEOS	0.39	0.31	0.28	0.13	0.14	0.03	0.11	0.11	0.44	1.00
LFGS	GEOS	ESCP	0.45	0.45	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
NPSD	OCNN	SJDF	0.03	0.35	0.67	1.00						
NPSD	OCNS	SJDF	1.00									
NPSD	GEOS	SJDF	0.27	0.23	0.12	0.00	0.00	0.00	0.00	0.00	0.00	1.00
NPSD	SJDF	NSND	0.31	0.25	0.21	0.17	0.11	0.09	0.06	0.09	0.12	1.00
NPSD	NSND	ESCP	1.00	1.00	1.00	0.73	0.73	0.73	0.76	0.76	0.49	1.00
SPSD	OCNN	SJDF	0.98	1.00								
SPSD	OCNS	SJDF										
SPSD	GEOS	SJDF	0.29	0.25	0.16	0.00	0.00	0.00	0.00	0.00	0.33	1.00
SPSD	SJDF	SSND	0.32	0.41	0.32	0.20	0.07	0.02	0.15	0.15	0.46	1.00
SPSD	SSND	ESCP	1.00	0.76	0.50	0.30	0.20	0.13	0.00	0.22	0.56	1.00
NWAC	OCNN	OCNS	0.67	1.00								
NWAC	OCNS	WCTM	0.67	0.67	0.67	0.67	0.33	0.33	0.67	1.00	1.00	1.00
NWAC	SJDF	OCNS	0.21	0.24	0.23	0.23	0.12	0.03	0.07	0.17	0.47	1.00
NWAC	WCTM	ESCP	0.17	0.13	0.15	0.18	0.08	0.19	0.27	0.57	0.78	1.00
CRIV	OCNS	CRTM	1.00	1.00	1.00	1.00						
CRIV	SJDF	OCNS	0.44	0.76	0.90	1.00						
CRIV	CRTM	ESCP	0.11	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.10	1.00

The following example illustrates the relationship between the $\gamma_{s,a,b,t}$ and the $m_{i,j}$. Table 3 lists the dispersion rate (and “Non-Dispersion Rate”) parameters for the South Puget Sound stock during week 40.

Table 3. Dispersion and non-dispersion (= 1 - dispersion) rate parameters for the South Puget Sound stock during week 40 used in the PSC Selective Fishery Model.

Donor Region	Receiving Region	Dispersion Rate	Non-Dispersion Rate
Ocean North	Strait Juan de Fuca	0.67	0.33
Ocean South	Strait Juan de Fuca	0.79	0.21
Georgia Strait	Strait Juan de Fuca	0.03	0.97
Strait Juan de Fuca	South Puget Sound	0.21	0.79
South Puget Sound	Escapement	0.54	0.46

It is assumed that fish that do not disperse from a donor region remain in the donor region. There are six areas counting the “Escapement” area (1 = OCNN; 2 = OCNS; 3 = SJDF; 4 = GEOS; 5 = SSND; and 6 = ESCP). The corresponding State Space Model migration matrix representing this movement pattern is:

$$M_{40} = \begin{bmatrix} 0.33 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0.21 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0.97 & 0 & 0 & 0 \\ 0.67 & 0.79 & 0.03 & 0.79 & 0 & 0 \\ 0 & 0 & 0 & 0.21 & 0.46 & 0 \\ 0 & 0 & 0 & 0 & 0.54 & 1.00 \end{bmatrix}$$

Note that values along the diagonal represent the non-dispersion rates (i.e., the fraction of the cohort that remains in the region).

Proportional Migration (PM) Model

The PM model does not have specific geographic objects. However, fishery definitions act as de facto geographic objects. For example, the sport fisheries are generally defined by statistical reporting area, such as “Area 7”, “Area 8”, “Buoy 10”, etc. There are 45 fisheries/geographic areas in this model.

There are three gear types used to define fisheries and each gear type partitions the geographic range differently. For example, within the troll gear group there is a Northwest Vancouver Island and a Southwest Vancouver Island and within the sport gear group there is only one fishery for all of the West Coast of Vancouver Island. This methodology assumes that fish available for the WCVI sport fishery are not the same fish that are also available for the two WCVI troll fisheries. In other words, the model tacitly assumes that there are three distinct geographic regions off WCVI. In terms of the notation used in this report, the subscript r indexes both geographic regions and their associated fisheries.

There is no explicit movement of fish between fishing regions. However, the fisheries are assumed to have a geographic and temporal ordering such that the fish available in a given fishery and time are received only from designated donor fishing regions (designated by the set $D_{r,t}$). Note that several receiving regions may share some of the donor regions. For example, region 2 may receive fish from regions 1 and 2 and region 3 may receive fish from regions 2 and 3.

The model expresses changes in fishery mortalities relative to a base year. For a given base year and stock, the model begins with input data for three parameters (obtained from run reconstructions): $c_{r,t}$, $h_{r,t}$ and $E_{r,t}$. The harvest rates ($h_{r,t}$) are assumed to be fishery and time specific, but not stock specific. That is, the same $h_{r,t}$ term is applied to all stocks harvested in region (fishery) r at time t .

The region and time specific abundances at the start of time interval $[t-1,t)$ are computed by

$$n_{r,t-1} = \frac{c_{r,t}}{h_{r,t}} \cdot EV$$

where EV is a stock and year specific “Environmental Variability” scalar. For the base year $EV = 1$. For years other than the base year, these initial abundances are adjusted by the EV scalars to reflect the brood year strength relative to the base year. These scalars have the same effect as EV scalars in the PSC chinook model.

Note that the regional abundances are determined solely from the input data for that region and time step. Thus, it is possible for the total abundance for a stock to be greater at time t than at time $t-1$. That is,

$$\sum_r n_{r,t} \stackrel{?}{>=} < \sum_r n_{r,t-1} .$$

The survivors after the fishing process during the period $[t-1,t)$ are computed by

$$ns_{r,t-1} = n_{r,t-1} - c_{r,t}$$

The model simulates the impacts of changes in region specific harvest rates as follows (primes in the notation indicate variables under the new harvest management scenario). Let $E'_{r,t}$ be the new effort level in region r at time t . Let the associated new harvest rate be some function of the base period effort, base period harvest rate, and the new effort level. That is,

$$h'_{r,t} = f(h_{r,t}, E_{r,t}, E'_{r,t})$$

This function may be a simple linear scaling, such as

$$h'_{r,t} = h_{r,t} \cdot \frac{E'_{r,t}}{E_{r,t}}$$

In the first time step the new harvest rate is applied to the original abundance ($n_{r,0}$) to get the new catch:

$$c'_{r,1} = h'_{r,1} n_{r,0}$$

New survivors in the first time step are computed by

$$ns'_{r,1} = n_{r,0} - c'_{r,1}$$

Thus, during the first time step we have

$$c_{r,1} = h_{r,1} n_{r,0}$$

$$c'_{r,1} = h'_{r,1} n_{r,0}$$

and we can write

$$\frac{c_{r,1}}{h_{r,1}} = \frac{c'_{r,1}}{h'_{r,1}}.$$

Solving for the new catch we get

$$c'_{r,1} = c_{r,1} \frac{h'_{r,1}}{h_{r,1}}$$

Thus, the new regional catches in the first time step are just the old regional catches scaled up or down by the ratio of the new and old harvest rates. Note that the scaling is based on the relative harvest rates, not the effort levels. If a non-linear relationship is used to relate effort and harvest rate, doubling the effort may not necessarily double the harvest rate and the catch.

In subsequent time steps, the new harvest rate is not applied to the original local abundance. Instead, the original local abundance is scaled up or down to reflect the total changes in fishing mortality in the donor regions during the previous time step. The scaling factor is the ratio of the new survivors to original survivors (from the donor areas) during the previous time step, and the new abundance is computed as follows:

$$n'_{r,t} = n_{r,t} \cdot \frac{\sum_{r \in D_{r,t}} ns'_{r,t-1}}{\sum_{r \in D_{r,t}} ns_{r,t-1}}$$

where the new survivors at time $t-1$ are computed by

$$ns'_{r,t-1} = n_{r,t-1} - c'_{r,t}.$$

If we separate the original (base) variables from the adjusted variables we can write

$$n'_{r,t} = \frac{n_{r,t}}{\sum_{r \in D_r} ns_{r,t-1}} \cdot \sum_{r \in D_r} ns'_{r,t-1}$$

Note that this equation is quite similar to the equation for the elements of the new abundance vector in the State Space Model formulation, namely:

$$n_{r,t} = \sum_{j=1}^R m_{r,j} nS_{j,t-1}$$

Recall that $m_{r,j}$ is the fraction of the fish located in donor region j moving into region r . If one assumes a constant migration rate during the interval $[t-1,t)$ from all donor regions j into region r (call the constant $K_{r,t} = m_{r,j}$ for all j), the migration rate terms can be moved outside the summation sign:

$$n_{r,t} = K_{r,t} \sum_{j=1}^R nS_{j,t-1}$$

For the PM model, we can set

$$K_{r,t} = \frac{n_{r,t}}{\sum_{r \in D_r} nS_{r,t-1}}$$

In the PM model the term $K_{r,t}$ must be thought of as a migration index, rather than a migration rate. It is the ratio of the fish located in region r at the start of time period t to the total potential donor fish for region r at the end of time period $t-1$. Since the abundances for different time periods are computed independently, this ratio can be greater than one and does not represent a movement of fish from one area to another.

Regardless of the biological interpretation of the $K_{r,t}$ terms, the important point is that the mathematical computations of the PM Model can be conducted using the matrix formulation of the State Space Model by substituting the $K_{r,t}$ terms in the appropriate position of the migration matrix. For time t , each $K_{r,t}$ term is placed in each column of the r^{th} row that corresponds to a donor region for region r .

The State Space Model formulation of the PM model is best explained with an example. Consider a case of three fisheries (regions) and two time steps. Assume that for the second time step the donor regions are as follows:

<u>Receiving Region</u>	<u>Donor Regions</u>
1	1
2	1 and 2
3	2 and 3

Then from the input data we have:

$$K_{1,2} = \frac{n_{1,2}}{nS_{1,1}}$$

$$K_{2,2} = \frac{n_{2,2}}{ns_{1,1} + ns_{2,1}}$$

$$K_{3,2} = \frac{n_{3,2}}{ns_{2,1} + ns_{3,1}}$$

In terms of the matrix computations we have

$$\begin{bmatrix} n'_{1,2} \\ n'_{2,2} \\ n'_{3,2} \end{bmatrix} = \begin{bmatrix} K_{1,2} & 0 & 0 \\ K_{2,2} & K_{2,2} & 0 \\ 0 & K_{3,2} & K_{3,2} \end{bmatrix} \begin{bmatrix} ns'_{1,1} \\ ns'_{2,1} \\ ns'_{3,1} \end{bmatrix}$$

where the \mathbf{ns}'_1 abundance vector represents the fish surviving the new harvest regime during the first time step. In practice \mathbf{ns}'_1 vector would be computed by multiplying a new survival matrix (with the diagonal elements representing the new survivals determined from the original and new effort levels) times the original abundance vector.

The specific element formulas for the \mathbf{n}'_2 vector are:

$$n'_{1,2} = n_{1,2} \cdot \frac{ns'_{1,1}}{ns_{1,2}}$$

$$n'_{2,2} = n_{2,2} \cdot \frac{ns'_{1,1} + ns'_{2,1}}{ns_{1,1} + ns_{2,1}}$$

$$n'_{3,2} = n_{3,2} \cdot \frac{ns'_{2,1} + ns'_{3,1}}{ns_{2,1} + ns_{3,1}}$$

Thus, it is possible to cast the PM model in the general matrix framework as follows:

- Use the regional abundances at the start of the first time step for the initial abundance vector;
- Use the input catch and harvest rate data to compute the $K_{r,t}$ terms;
- Use the input and adjusted effort data to create new survival matrices;
- Place the $K_{r,t}$ terms in the appropriate location in the migration matrices;
- Perform the matrix computations in chronological order.

It is clear from the above formulae that the PM model makes the tacit assumption that for a given cohort and time step, fish migrate from all donor regions *at the same rate*. This is very different from the PSC Selective Fishery Model that estimates separate migration rates for each donor area. Recall from the PSC example for week 40 for the SPSD stock that fish migrate into the SJDF area from four other areas at very different rates: OCCN = 0.67; OCNS = 0.79; GEOS = 0.03; and SJDF = 0.79. The PM model would require that fish would enter the SJDF area at the same rate from each of the four areas.

We also note that if the set of donor regions for each area and time step ($D_{r,t}$) is the entire set of possible regions, the PM model is virtually identical to a single pool model in which the original regional harvest rates are defined with respect to the total abundance of the cohort at any given time (instead of local abundance within a region). That is, under a single pool model the pooled harvest rate ($ph_{r,t}$) is defined as:

$$ph_{r,t} = \frac{c_{r,t}}{\sum_r n_{r,t-1}}.$$

The catch equation is:

$$c_{r,t} = ph_{r,t} \sum_r n_{r,t-1}.$$

The base regional catches are the same under both formulations of the harvest rate (PM and Single Pool), so we can write:

$$ph_{r,t} \sum_r n_{r,t-1} = h_{r,t} n_{r,t-1}$$

and

$$ph_{r,t} = h_{r,t} \frac{n_{r,t-1}}{\sum_r n_{r,t-1}}$$

Thus, the base harvest rate in a single pool model is equal to the base local harvest rate in the PM model scaled by the fraction of the total cohort abundance located in the region.

Recall that during the first time step of the PM model, the local abundances are not adjusted before applying the adjusted harvest rates and the adjusted catches are just scaled by the ratio of the new to the old harvest rate:

$$c_{r,1} = c_{r,1} \frac{h'_{r,1}}{h_{r,t}}$$

For the single pool model, the same is true. Here we have

$$c_{r,1} = ph_{r,1} \sum_r n_{r,0}$$

$$c'_{r,1} = ph'_{r,1} \sum_r n_{r,0}$$

Thus, we can write

$$\frac{c_{r,1}}{ph_{r,1}} = \frac{c'_{r,1}}{ph'_{r,1}}$$

and

$$c'_{r,1} = c_{r,1} \frac{ph'_{r,1}}{ph_{r,t}}$$

Thus, at the first time step the regional catches are scaled up and down to reflect the changes in the harvest rates. If the set of donor regions for each area and time step is the entire set of possible regions, then the same will be true for all time steps.

Fishery Regulation Analysis Model (FRAM)

This model is similar to the PSC Chinook Model in that it has no specific geographic areas, but does partition the fisheries into preterminal and terminal categories, and also includes separate extreme terminal areas. This model uses monthly time steps. At each time step the maturation algorithm is called, but it is unclear whether or not a maturation calculation actually occurs at each time step. Need further clarification on this.

The Terminal Area Management Modules (TAMMs) used in FRAM do not have any migration components. The harvest rates in the extreme terminal areas are all defined with respect to the abundance of fish entering the extreme terminal area.