

Program Documentation

No. 21

Biological Impact of an Oil Spill (BIOS) Model Documentation

Part 1: Fish Migrations and Exposure to Contamination

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1. Introduction

The BIOS (Biological Impact of an Oil Spill) model, a **multispecies** ecosystem simulation, was developed at the request of the Outer Continental Shelf **Environmental Assessment Program (OCSEAP)**, as part of their **eastern Bering Sea oil impact study**. This document is intended as a technical reference for the **migration subroutines of BIOS**; descriptions of the overall model structure are included for clarification when needed.

BIOS simulates uptake of oil contaminants from exposure to contaminated water and sediments as well as from the consumption of contaminated food. Sixteen species groups are included in the model (Table 1). Salmon appears seasonally in the Bering Sea; the impact of an oil **spill** on salmon has been **modelled** by Dr. Nicholas Bax of Compass Systems, inc. (**pers. comm.**). BIOS includes depuration of contaminants and effects of fish migrations on the ecosystem.

The model has been applied to three locations in the Bering Sea (Figure 1): offshore of Port **Moller**, Port Heiden, and Cape Newenham. Computed oil concentrations at each model grid point for 15 days following a hypothetical oil spill were provided by Rand Corporation. Two scenarios were simulated at each location: a **"blowout" occurring during** a period of high winds and strong tidal mixing, and a tanker **diesel** spill occurring during a time of weak winds and tidal mixing.

We have attempted to determine the maximum impact of an oil spill on the ecosystem. **Wind and tide conditions which would maximize the amount of oil entering the water column were determined by Science Applications, Inc.** **Avoidance of oil by mobile fish species is not included**, allowing maximum **exposure to oil**. Finally, the migrations of selected fish species across

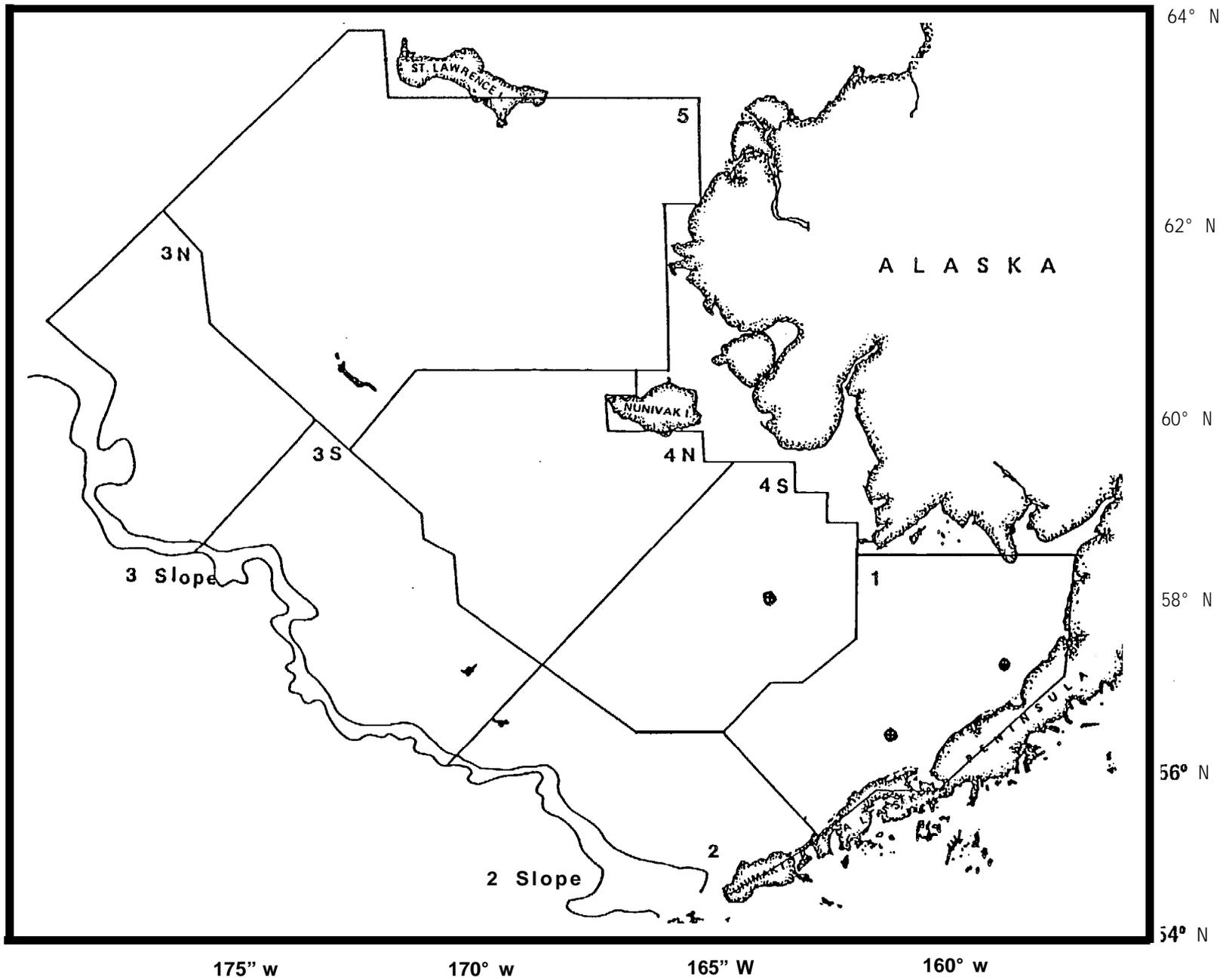


Figure 1 --- Locations of hypothetical oil spills in the eastern Bering Sea.

Table 1.--BIOS model species groups

Species number	Species name
1	Herri ng juveni l es
2	Herri ng adul ts
3	Pol l ock juveni l es
4	Pol l ock adul ts
5	Paci fi c cod juveni l es
6	Hal i but juveni l es
7	Yellowfin sole juveni l es
8	Other flatfish juveni l es
9	Yellowfin sole adul ts
10	Other flatfish adul ts
11	Paci fi c cod adul ts
12	Ki ng and Bai rdi crab juveni l es
13	Ki ng and Bairdi crab adul ts
14	Mobi l e epifauna
15	Sessile epifauna
16	Infauna

the model grid maximizes the spatial extent of contaminated food. Contaminated fish may also migrate beyond the **model** grid (i.e., beyond the location of the **oil** spill), and their effect on the entire eastern Bering Sea ecosystem may be examined by tracing their possible migration routes until deputation is complete.

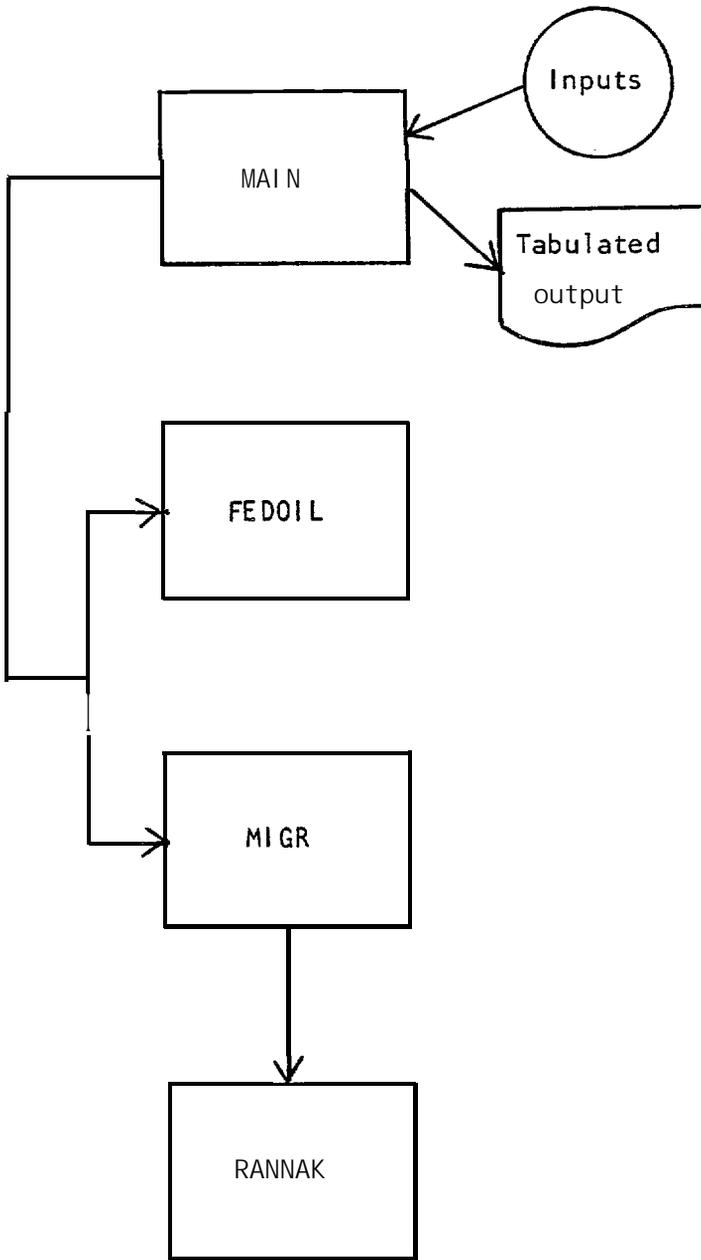
2. Sequence of Model Calculations

The BIOS model is comprised of three **sections, as shown in Figure 2. The main program controls the model** flow, the feeding subroutine computes uptake of contaminants through consumption, and the migration subroutines simulate fish migrations and uptake of contaminants by exposure to oil in the water or sediments.

At the start of each daily **model** time step, the main program reads in the concentrations of oil (in parts per billion). Two values are read **at** each gridpoint: the "**watersoluble** fraction", including oil dissolved or in **suspension** in the water column, and the "tars" (weathered **oil**), which concentrate at the sediment-water interface and within the sediments. The tars are computed in a separate model (**Laevastu & Fukahara, 1984**).

After reading the oil concentrations, the main program calls the feeding subroutine, FEDOIL, which is described in detail in Gallagher, 1984. The feeding subroutine calculates the uptake of contaminated food, updates the fish contamination values, and returns to the main **program, which** then calls **the first migration subroutine, MIGR.**

Subroutine **MIGR** loops through the species list and assigns various parameters. Species-specific choices include: whether or not the species migrates (a function of season), the migrating fraction of the biomass, the migration velocity



Main Program

Di rects sequence of model **calculations**, **reads input and prints Output.**

Feedi na Subroutine

Computes uptake of contaminants through consumption of contaminated food.

Main Migration Subroutine

Di rects sequence of migration computations. Sets species-speci fi c parameters and veloci ties, calculates uptake from exposure to oil and **deputation.**

Mi grati on Cal culati on Subrouti ne

Calcu lates actual migration and redi stribute contamination over model grid. Calcu lates amount of contaminated biomass leaving the model region.

Figure 2. --Sequence of BIOS model cal cul ati ons.

and direction, and uptake and deputation rates. If the species is migrating, MIGR calls RANNAK, which performs the actual migration calculations. On return to **MIGR**, uptake and/or deputation are calculated, species contamination arrays are updated and selected results are printed. After all species have **been considered**, MIGR returns to the main program, which prints selected outputs, increments the time step and continues through the next day's calculations.

3. Technical Specifications of Migration Subroutines

The model calculations for the two migration subroutines, **MIGR** and **RANNAK**, are diagrammed in Figure 3. **MIGR** is only called once each model time step (LL) ; **RANNAK** is called once for each migrating species (**J**) during each time step. If a species does not migrate (**IFMIG = 0**), **MIGR** calculates the uptake **and/or** deputation of oil over one day (as described below) and continues on to the **next species**.

If a species does migrate, **MIGR** assigns the species-specific migrating fraction and migration speed and direction. The model is presently designed to simulate either alongshore or cross-shore migration (**MIGDIR = 1** for cross-shore migration and = 0 for **alongshore** migration). In addition, migration can either be toward shallow (KE = 1) or deep (KE = 2) water. The migration velocity is assumed constant over the model grid for any one species. Mean velocities (in km/day) are calculated from biomass distributions estimated from fisheries survey data. The model can be easily modified to include spatial variations of migration velocities.

The **areal** extent of each model led region is on the order of the station spacing in survey cruises. However, the finer model grid spacing (2 km) is

MIGR

Loops through each species (J)
Checks: Does species migrate?

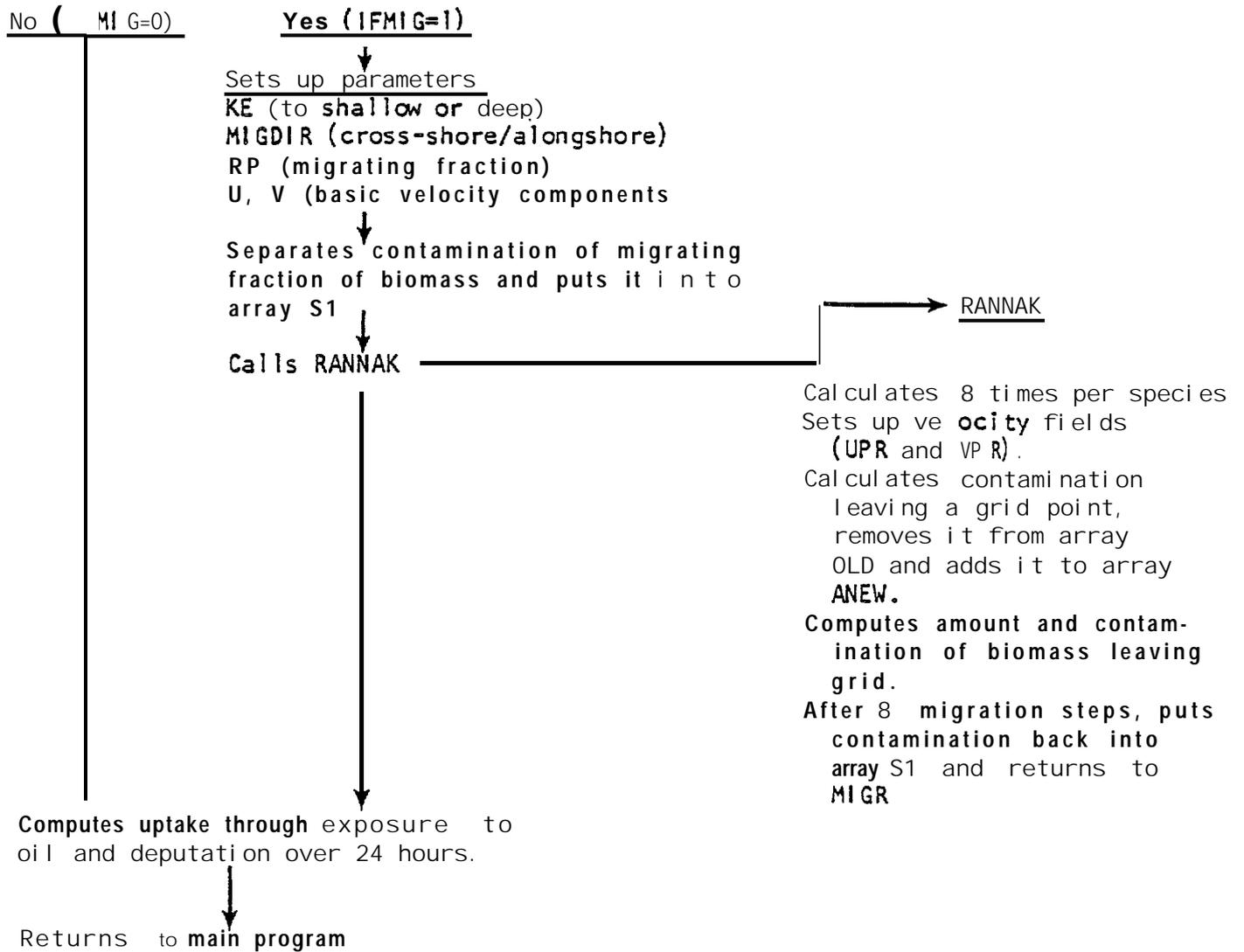


Figure 3. --Sequence of calculations in BIOS migration subroutines.

necessary to resolve maximum oil concentrations. **The biomass for each species** is therefore assumed to be constant over the grid. Initial biomass estimates were computed **using** the **DYNUMES** eastern Bering Sea ecosystem simulation model (**Laevastu** and Larkins, 1981). The simulated migrations do not redistribute the biomass over the grid. Instead, since the total duration of a model run is only ten days, it is assumed that **biomass is conserved at each grid point, but that the fish contamination is redistributed over the grid.** The contamination of each species at each grid point is stored in array 01 LCON in parts per billion (μg oil per kilogram biomass). As **MIGR** cycles through each species, the contamination for that species **is** put into array **S1**. If a species migrates, the amount of contamination in **the migrating fraction of the biomass (RP)** is stored in array S3, which is then sent as an argument to **RANNAK**, along with **J, MIGDIR** and **KE**.

RANNAK determines the velocity components from **the values of MIGDIR and KE** sent from **MIGR** and sets up arrays of the u-component (**UPR**) and v-component (**VPR**) of velocity at each grid point. The u- and v-components of velocity for each of the four possible migration patterns (**U1, V1** for cross-shore migration to shallow water; **U2, V2** for cross-shore migration to deep water; **U3, V3** for alongshore migration to shallow water; and **U4, V4** for alongshore migration to deep water) are **stored** in common block **BLKV**. If a constant velocity is used over the entire model grid, the appropriate u-component is assigned to each element of array **UPR**, and the appropriate v-component is assigned to each element of **VPR**. Specific velocities may, on the other hand, be assigned at any grid point if spatial variation is desired.

The migration calculations in **RANNAK** are performed **8 times, with a migration time step of 3 hours** ($\text{TD} = 0.125$ days) for stability. The stability criterion is:

$$U_m t_d < L \tag{1}$$

where U_m is the maximum migration speed (in km/day), t_d is the migration time step in days (TD in FORTRAN code), and L is the grid spacing in km ($AL = 2.0$ in the model).

During each of the eight migration periods, the following calculations are performed at all grid points. First, the nearest grid point in the direction of migration is determined. That is, the contamination is moved from point (N, M) to point $(N+IN, M+IM)$, where IN and IM each has a value of either -1, 0, or 1. The amount of contamination leaving a grid point in the x direction (G_x) is:

$$G_x = (C_{n,m} t_d |U|_{n,m}) / L \quad (2)$$

and in the y direction (G_y) is:

$$G_y = (C_{n,m} t_d |V|_{n,m}) / L \quad (3)$$

$C_{n,m}$ is the contamination of a species at grid point (n,m) before a migration (array **S3** in the FORTRAN code), U and V are the velocity components at the grid point (arrays UPR and VPR in the FORTRAN code), and t_d and L are as described for equation (1).

At the start of each migration time step, the values in array **S3** are put into array **OLD** and the elements in **S3** are set to zero. The amount of contamination leaving a grid point is taken out of array **OLD** and put into array **ANEW**. The FORTRAN code for this operation is:

$$OLD(N,M) = OLD(N,M) - GX - GY$$

$$ANEW(N,M+IM) = ANEW(N,M+IM) + GX$$

$$ANEW(N+IN,M) = ANEW(N+IN,M) + GY$$

where GX and GY correspond to G_x and G_y in equations (2) and (3), respectively.

After the calculations have been completed at all model grid points, the resulting contamination field (the sum of arrays **OLD** and **ANEW**) is put into array **S3**. When the calculations have been performed 8 times (24 hours) the array **S3**, containing the redistributed contamination, is returned to Subroutine **MIGR**.

The uptake of contaminants from the water or sediments is simulated by a logistic formula (Wilson, 1975):

$$C_t = C_\infty (1 - e^{-rt}) \quad (4)$$

where C_t is the contamination of a species at a grid point, r is a species-specific, temperature-dependent uptake rate (on the order of 0.025) and C_∞ is the lethal contamination of the fish. Rates are estimated from available empirical data.

Deputation is simulated by an exponential decay of contamination:

$$C_t = C_{t-1} e^{-R} \quad (5)$$

where R is the species-specific expiration rate.

Contamination of the fish is stored as parts per billion ($\mu\text{g oil per kg biomass}$), and is tabulated as a contamination index (contamination in ppm multiplied by time of exposure).

In order to conserve biomass in the model, two boundary conditions were enforced. First, fish were allowed to leave the grid at the boundaries in the direction of migration. The amount of a species' biomass leaving the grid and the contamination of that biomass are calculated and stored for future use. Second, fish may leave the boundaries in the "downstream" region and an equal amount of non-contaminated fish biomass is input to those boundaries.

4. References

Gallagher, A.F.

1984. **Biological Impact of an Oil Spill** (BIOS) model documentation. Part 2: Contamination through consumption, **Nat'l.** Mar. Fish. Serv., Northwest and **Alaska** Fisheries Center, Seattle, WA., MS Program Documentation.

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1984. **Quantitative determination of the effects of oil development** in the Bristol Bay region on the commercial fisheries in the Bering Sea. **Nat'l.** Mar. Fish. Serv., Northwest and Alaska Fisheries Center, Seattle, WA., Processed Rep. 84-06, 73 pp.

Laevastu, T., and H.A. Larkins.

1981. **Marine Fisheries Ecosystem. Its quantitative evaluation and management.** Fishing News Books, **Ltd., Surrey, England, 162 pp.**

Wilson, K.W.

1975. The laboratory estimation of the biological effects of organic pollutants, **Proc. R. Soc. London Ser. B**, 189.

Appendix A: Subroutine Specifications

SUBROUTINE MIGR

Calling sequence: CALL MIGR

Common blocks used:

COMMON/BLK1/NE, ME, K, LL, ISL

COMMON/OIL/WSF, TARS

COMMON/BLKOIL/OILCON

COMMON/BLKV/RATMG, U1, U2, U3, U4, V1, V2, V3, V4

Variables (in alphabetical order)

A1: Angle (in **degrees**) of direction of cross-shore migration toward **deep** water (= $ANG1 + 180$).

A2: Angle (in degrees) of direction of alongshore migration toward deep water (= $ANG2 + 180$).

ANG1: Angle (in degrees) of direction of cross-shore migration toward shallow water.

ANG2: Angle (in degrees) of **alongshore** migration toward shallow water

CLEFT: Total biomass of a species leaving the model grid during one time step.

IFMIG: Species-specific parameter equal to 1 if the species is migrating or 0 if not.

J: Species number (see Table 1).

KE: Indicator of migration season, equal to 1 for migration to shallow water or 0 for migration to deep water.

MIGDIR: Indicator of type of migration. **MIGDIR** = 1 for cross-shore migration and **MIGDIR** = 2 for **alongshore migration**.

OLDSUM: Total biomass of a species before migration, summed over the model grid.

RATEXP: Expiration rate over 24 hours.

RATMG: Expiration rate over 3 hours.

RP: Migrating fraction of a species' biomass.

SUMNEW: Total biomass of a species after migration, summed over the **model** grid.

VEL1: Magnitude of cross-shore migration velocity (in km/day).

VEL2: Magnitude of **alongshore** migration velocity (in km/day).

Arrays (in alphabetical order) ^{1/}

S1: Contamination of a species **at each grid point** before migration.

S2: Contamination of the non-migrating fraction of a species' biomass at each grid point.

S3: Contamination of the migrating fraction of a **species' biomass at each grid point.**

1/ Arrays are dimensioned (NE,ME) unless otherwise specified.

SUBROUTINE RANNAK

Calling sequence: CALL RANNAK (J, MIGDIR, KE, S3)

Arguments :

J: Species number (see Table 1).

MIGDIR: Indicator of type of migration, equal to **1 for cross-shore or 2 for alongshore migration.**

KE: indicator of migration season, equal to 1 for migration toward **shallow water or 2** for migration toward deep water.

S3: Array containing contamination of the migration fraction of species J at each grid point.

Common blocks used:

COMMON/BLK1/NE, ME, K, LL, ISL

COMMON/OIL/WSF, TARS

COMMON/BLKV/RATMG, U1, U2, U3, U4, V1, V2, V3, V4

Variables (in alphabetical order):

AL: Model grid spacing, in kilometers.

GONE : Biomass leaving a grid point.

GX: Biomass leaving a grid point in the x-direction.

GY: Biomass leaving a grid point in the y-direction.

IM: Indicator of migration between columns in the model grid. Biomass moves from point (N,M) to point (N,M+IM). If IM=1, biomass moves one column to the right; if IM=-1, biomass moves one column to the left. If IM=0 there is no x-component of migration from point (N,M).

IN: indicator of migration between rows in the model grid. Biomass moves from point (N,M) to point (N+IN,M). If IN=1, biomass moves one row down; if IN=-1, biomass moves one row up. If IN=0, there is no y-component of migration from point (N,M).

KRC: Number of migration time steps per day.

RATMG: Deputation over one migration time step.

TD: Length of migration time step (**in days**).

U: U-component of migration **velocity**.

V: V-component of migration velocity.

Arrays (in alphabetical order)

ANEW: Contamination of migrating fraction of the biomass **at** each grid point during migration.

OLD: **Contamination** of migrating fraction of the biomass at each grid **point before migration**.

S3: **Biomass containi**nation at each grid point before migration, updated after each migration **time** step, when $S3(N,M) = ANEW(N,M) + OLD(N,M)$.

UPR: U-component of migration velocity at each grid point.

VPR: V-component of migration velocity at each grid point.

Appendix B: Common Blocks

COMMON BLK1:

Statement: COMMON/B LK1/NE, ME, K, LL, ISL

NE: **Number of rows in the model grid.**

ME: **Number of columns in the model grid.**

K: Month of **model** run.

LL: Model time step (days).

ISL: Land-sea array (dimensioned NE x ME), where 0 designates a grid point over land and 1 designates a grid point over water.

COMMON OIL:

Statement: COMMON/OIL/WSF, TARS

WSF: Array dimensioned NE x ME containing the subsurface oil concentration (in ppm) at each model grid point.

TARS: Array dimensioned NE x ME containing the concentration of oil on the **bottom (in ppm) at each model grid point.**

COMMON BLKOIL:

Statement: COMMON/BLKOIL/OILCON

OILCON: Array dimensioned J x NE x ME containing the contamination of each species (in ppb: $\mu\text{g oil per kg biomass}$) at each model grid point.

COMMON BLKV

Statement: COMMON/BLKV/RATMG, U1, U2, U3, U4, V1, V2, V3, V4

RATMG: Species-specific deputation over a 3-hour migration time step.

U1: U-component of migration velocity for cross-shore migration toward shallow water.

U2: U-component of migration velocity for cross-shore migration toward deep water.

U3: U-component of migration velocity for a longshore migration toward **shallow** water.

U4: U-component of migration velocity for **alongshore** migration toward deep water.

V1: V-component of migration velocity for cross-shore migration **toward** shallow water.

V2: V-component of migration velocity for cross-shore migration toward deep water.

V3: V-component of migration velocity for **alongshore** migration toward **shallow** water.

V4: V-component of migration velocity for **alongshore** migration toward **deep** water.

C FCR TEST RUN, USE EXPIRATION RATE (RE) = 0.025

C RATEXP=EXP(-RE* 24.)
C RATEMG=EXP(-RE*3.)

C LOOP THROUGH EACH SPECIES
C S1=CONTAMINATION ARRAY

C DO 999 J=1,16
C DO 801 N=1,NE
C DO 801 M=1,ME
801 S1(N,M)=GILCON(J,N,M)
PFINT 802,J,LL,IONE
802 FORMAT('1 INITIAL CONTAMINATION, SPECIES-13-S TIME STEP'
&I3,10X'PAGE=I2' OF 2'/)
PRINT 803,(I,I=2,17)
803 FORMAT(16I8/)
PRINT 804,((S1(N,M),M=2,17),N=1,NE)
804 FORMAT(16F8.2)
PFINT 802,J,LL,ITWO
PRINT 803,(I,I=18,33)
PFINT 804,((S1(N,M),M=18,33),N=1,NE)
IF(J.GT.13)GO TO 70
IF(J.GT.4 .AND. J.LT.3)GO TO 70
IF(J.GT.10 .AND. J.LT.13)GO TO 70
IF(K.EQ.1 ● OR. K.GT.10)GO TO 70
MIGDIR=1

C CHECK FOR MIGRATION MONTH
C KE----INDICATOR OF SEASON.
C KE=1 (SPRING) KE=2 (AUTUMN)

800 GO TO(1,2,3,4,70,70,70,8,9, 8,70,70, 8,70,70,70)J

C HERRING JUVENILES (SPECIES 1)

1 IF(K.LT.6 .OR. K.GT.9)GO TO 70
KE=2
GO TO 58

C HERRING ADULTS (SPECIES 2)

2 KE=1
IF(K.EQ.2 .OR. K.EQ.3)GO TO 58
KE=2
IF(K.EQ.7 .OR. K.EQ.8)GO TO 58
GO TO 70

C FOLLOCK JUVENILES (SPECIES 3)

3 KE=1
IF(K.EQ.4 .OR. K.EQ.5)GO TO 58
KE=2
IF(K.EQ.9 .OR. K.EQ.10)GO TO 58
GO TO 70

C FOLLOCK ADULTS (SPECIES 4 1

4 KE=1
IF(K.GT.2 .AND. K.LT.6)GO TO 58

KE=2
IF(K.LT.7 .OR. K.GT.9)GO TO 70
GO TO 58

C
C OTHER FLATFISH JUVENILES,ADULTS (SP.8,10) AND CRAB ADULTS(CSF-13)
C

8 KE=1
IF(K.GT.2 .AND. K.LT.6)GO TO 58
KE=2
IF(K.LT.8 .OR. K.GT.10)GO TO 70
GO TO 58

C
C YELLOWFIN SCLE ADULTS (SPECIES 9)
C

9 KE=1
IF(K.GT.2 .AND. K.LT.7)GO TO 58
KE=2
IF(K.LT.8 .OR. K.GT.10)GO TO 70

C
C SEPARATE MIGRATING AND NON-MIGRATING BIOMASS
C RP MIGRATING FRACTION
C FOR TEST RUN, SET RP=0.95, ALL MIGRATING SPECIES
C

58 OLDSUM=0.;SUMNEW=0.
DO 65 N=1,NE
DO 65 M=1,ME
IF(ISL(N,M).NE.0 .AND. S1(N,M).GT.0.)GO TO 64
S1(N,M)=0.
S2(N,M)=0.
S3(N,M)=0.
GO TO 65
64 S2(N,M)=S1(N,M)*RP
S3(N,M)=S1(N,M)-S2(N,M)
OLDSUM=OLDSUM+S1(N,M)
65 CONTINUE

C
C CALCULATE MIGRATIONS
C
C CALL RANNAK (J,MIGDIR,KE,S2)
C
C S2 - SPECIES PORTION WHICH MIGRATED)
C ISL-SEA-LAND TABLE
C

C
C ADDING NONMIGRATING PORTION
SUMNEW=0.
DO 63 N=1,NE
DO 63 M=1,ME
S3(N,M)=S3(N,M)+RATEXP
IF(ISL(N,M).EQ.0)GO TO 63
S1(N,M)=S3(N,M)+S2(N,M)
SUMNEW=SUMNEW+S1(N,M)
63 CONTINUE
IFMIG=1

C
C OUTPUT OF MIGRATION RESULTS
C

CLEFT=OLDSUM-SUMNEW
PRINT 1007,OLDSUM,SUMNEW,CLEFT
1007 FORMAT(" FPM BEFORE MIGRATION="F15.6,4X"PPM AFTER "
2"MIGRATION="F15.6,4X" FPM LEAVING GRID="F15.6/)

GCTC 777

C** **

C CRKWITH PC NTH'S INITIAL EICMASS IF NC MIGRATION .

70 DO 66 N=1,NE
DO 66 M=1,ME
S1(N,M)=S1(N,M)+RATEXP
66 CCNTINUE
IFMIG=0

C
C UPTAKE CONTAMINATION. FOR TEST, USE UPTAKE RATE=0.025

777 DO 778 N=1,NE
DO 778 M=1,ME
S1(N,M)=S1(N,M)+CINF*(1.-RATEXP)
778 CILCON(J,N,M)=S1(N,M)

C
C IF(CIFMIG.NE.1)GCTC 779
C PRINT 1009,J,LL
1005 FORMAT(' 1CCNTAMINATION (PPM) FOR MIGRATING SPECIES #I2,2X,
& TIME STEP #I2,10X"PAGE 1 OF 2"/)

GC 70 780
779 PRINT 1005,J,LL
1005 FORMAT(' 1CCNTAMINATION (PPM) FOR SPECIES #I2,2X," TIME STEP #
& I2,10X"PAGE 1 OF 2"/)

780 PRINT 803,(I,I=2,17)
PRINT 804,((S1(N,M),M=2,17),N=1,NE)

1006 Fall??ATC-1 PAGE 2 OF 2"/)
PRINT 100E
PRINT 803,(I,I=18,33)
PRINT 804,((S1(N,M),M=18,33),N=1,NE)

999 CCNTINUE
9999 RETURN

END
SUBROUTINE RANNAK(J,MD,KE,S8)
DIMENSION UPR(32,34),VPR(32,34),S8(32,34),ISL(32,34)
Z,CCNTAP(32,34),CNEW(32,34),ANEW(32,34),OLD(32,34)
COMMON/CIL/WSFC(32,34),TARS(32,34)
COMMON/ELK1/NE,ME,K,LL,ISL
COMMON/ELKV/RATMG,U1,U2,U3,U4,V1,V2,V3,V4

C I S I SEA-LAND TABLE
C S8 - (SPECIES)
C KRC - NUMBER OF Z-DAY MIGRATIONS
AL=2.0

C SET UVELOCITY FIELD

C U,V VELOCITY COMPONENTS

C KE IS INDICATOR OF SEASON
C KE=1 IF MIGRATION IS TO SHALLOWER WATER; KE=2 FOR MIGRATION TO DEEP

C
C IF(MD.EC.2)GO TO 10
C IF(KE.EC.2)GO TO 5
C U=U1
C V=V1
C GCTC 20
5 U=U2
V=V2
GO TO 20

```

10 IF(KE.EC.2)GO TO 15
   U=U3
   V=V3
   GO TO 20
15 U=U4
   V=V4
20 TD=.125
   NEH=NE-I
   MEH=ME-1

```

```

C
C M IGRATE 8 TIMES PER DAY (T C=.125 DAYS)
C
C S8 IS MIGRATING CONTAMINATION
C
   DG 254 KFC=1.8

```

```

C
C CALCULATE MIGRATION AT EACH GRID POINT
C
   DG 133 N=1,NE
   DO 133 Y=1,NE
   OLD(N,M)=S8(N,M)
   S8(N,M)=0.
   IF(ISL(N,M).EQ.0)GO TO 133

```

```

C
C DETERMINE GRID POINT TO GO TO
C

```

```

   IF(KFC.GT.1)GO TO 1136
   IF(LL.GT.1)GO TO 1136
   UPR(N,M)=U
   VPR(N,M)=V
1136 CONTINUE
   IF(U)230,231,232
230 IM=-1
   GO TO 233
231 IM=0
   GO TO 233
232 IM=1
233 IF(V)234,235,236
234 IN=1
   GO TO 237
235 IN=0
   IF(IM.EC.0)GO TO 133
   GO TO 237
236 IN=-1

```

```

C
C GX,GY ARE AMTS LEAVING IN X,Y DIRECTION
C OLD IS ORIGINAL CONTAMINATION LEFT AT GRIDPOINT N,M
C ANEW IS FIELD OF MIGRATED CONTAMINATION
C

```

```

237 GCNE=(CLC(N,M)*TD)/AL
   GX=GCNE*ABS(U)
   GY=GCNE*ABS(V)
   IF(M.EC.NE .AND. IM.GT.0)GO TO 991
   IF(N.EC.1 .AND. IM.LT.0)GO TO 991
   IF(ISL(N,M+IM).EQ.0)GO TO 991
   ANEW(N,M+IM)=ANEW(N,M+IM)+GX
991 IF(N.EC.1 .AND. IN.LT.0)GO TO 992
   IF(N.EC.NE .AND. IN.GT.0)GO TO 992
   IF(ISL(N+IN,M).EQ.0)GO TO 992
   ANEW(N+IN,M)=ANEW(N+IN,M)+GY

```

```
992 CLD(N,M)=CLD(N,M)-GY
    OLD(N,M)=CLD(N,M)-GX
133 CCNTINLE
591 DC 751 N=1,NE
    DC 751 M=1,ME
    IF(IISL(N,M).EQ.0)GO TO 751
    S8(N,M)=OLD(N,M)+ANEW(N,M)
    S8(N,M)=S8(N,M)*RATMG
    GLD(N,M)=0.
    ANEW(N,M)=0.
751 CONTINUE
254 CCNTINLE
    RETURN
    END
```