Program Documentation
No. 22

DOCUMENTATION OF THE BIOLOGICAL IMPACT OF AN OIL SPILL MODEL, BIOS

Part 2: Fish Feeding and Contamination through Consumption - Subroutine FEDOIL

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1. Introduction

The Biological Impact of an Oil Spill model, BIOS, is a multispecies ecosystem simulation that quantitatively analyzes the expected impact of hypothetical oil spill scenarios on fishery resources in the eastern Bering Sea, It was developed at the request of the Outer Continental Shelf Environmental Assessment Program (OCSEAP), and is a part of their eastern Bering Sea oil impact study. This program documentation is intended to serve as a technical reference for the BIOS computations of the subroutine FEDOIL, which simulates the uptake of oil contaminants through feeding and the consumption of oil contaminated food.

A full description of the OCSEAP study and its relation to the BIOS model can be found in Laevastu and Fukuhara (1984). Details of the BIOS computations for simulating fish migrations, uptake of oil contaminants from exposure to oil contaminated water and sediments, and deputation of oil contaminants is given in Swan .(1984). The theory and underlying assumptions of the subroutine FEDOIL, with examples of results, is given in Gallagher (1984).

As general background, BIOS is a gridded model that simulates uptake of oil contaminants in selected marine species resulting from exposure to oil contaminated water and sediments and the consumption of oil contaminated food. The model includes sixteen marine species or species groups (Appendix Table 1), simulates the expected impacts of two hypothetical oil spill scenarios (see Laevastu and Fukuhara, 1984, for details), and has been applied to three locations (Port Moller, Port Heiden, and Cape Newenham) in the Bristol Bay region of the eastern Bering Sea (Figure 1).

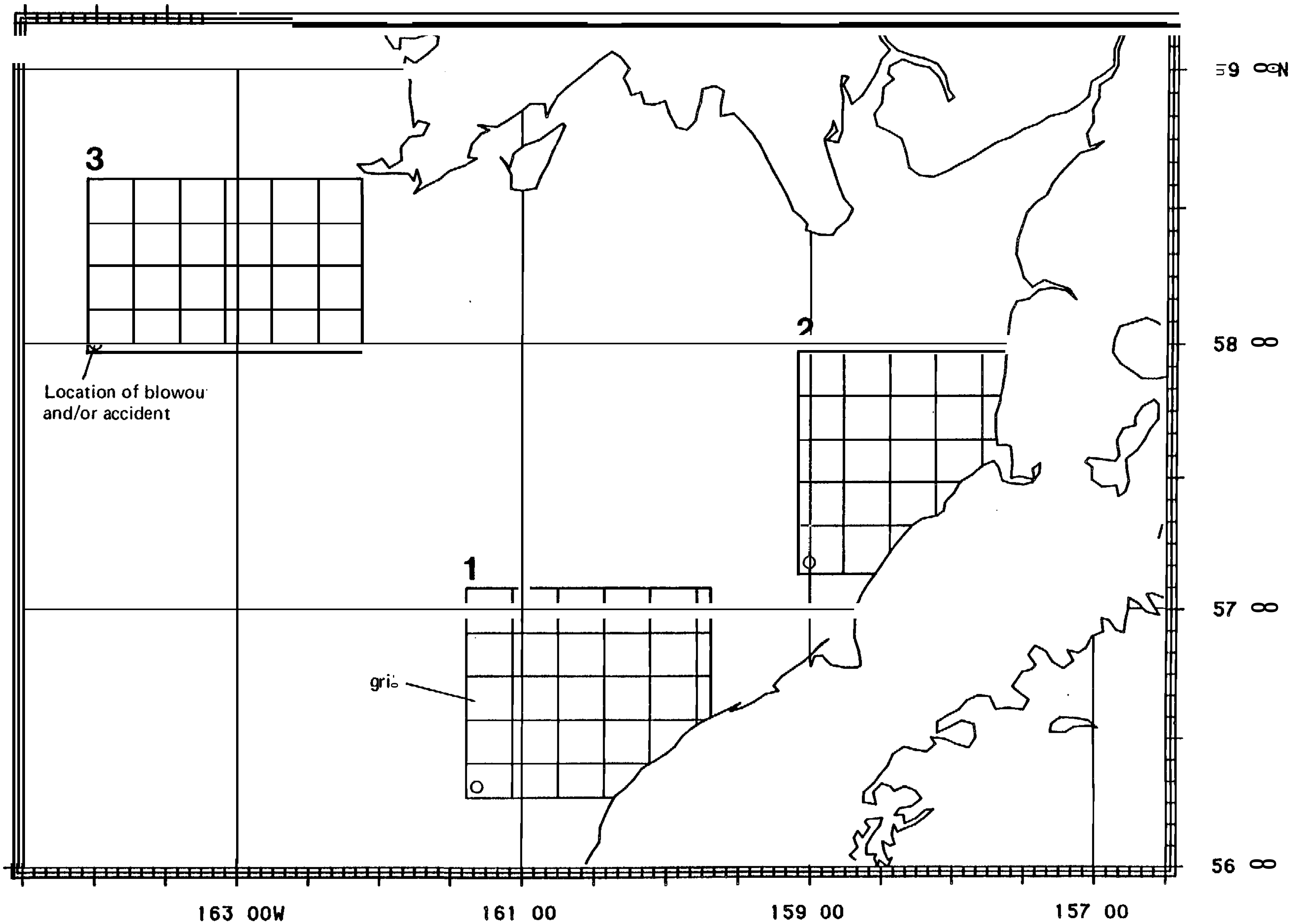


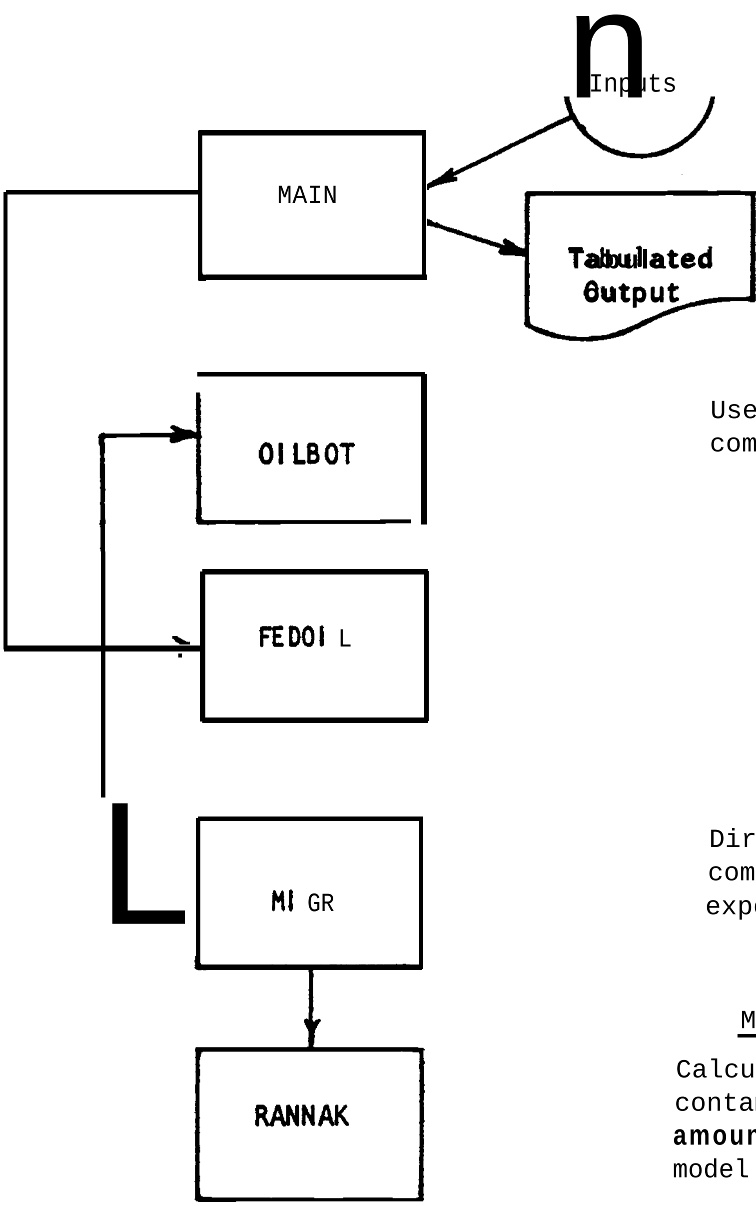
Figure --Locations of hypothetical oi spi s, and computational grids in Bristol Bay.

Input data on oil spill concentrations at each model grid point for each scenario and location were provided by Rand Coporation in conjunction with Science Applications, Inc. (SAI); details are provided elsewhere (see Laevastu and Fukuhara, 1984, for references). Input biomass data for each species or species group for the three oil spill locations are given in Appendix Table 1. A list of the parameters and values used in the FEDOIL computations is provided in Appendix Table 2. Appendix Table 4 gives a list of symbols and abbreviations.

2. Sequence of BIOS Model Computations

The BIOS model is comprised of four sections as shown in Figure 2 (this is an update of the model as described in Swan, 1984). The main program controls the model flow; the subroutine OILBOT computes the "oil on the bottom"; the subroutine FEDOIL computes uptake of oil contaminants due to consumption of oil contaminated food; and the subroutines MIGR and RANNAK simulate fish migrations, uptake of oil contaminants due to exposure to oil contaminated water and sediments, and deputation.

At the start of each daily model time step, the main program reads in the appropriate oil concentrations (in parts per billion (ppb)) for the selected scenario and location. These oil concentration data are read in for each grid point ((N,M), location specific and defined in the computer code), and are the "water soluable fraction" (WSF) that includes the dissolved and emulsified oil in the water. The main program then calls the subroutine OILBOT to compute the "oil on the bottom" (TARS) that includes the weathered and sedimentized oil that accumulates in a nepheloid layer at the sediment-water interface and in the sediments (details are given in Laevastu and Fukuhara, 1984). The model then returns to the main program and calls the subroutine FEDOIL.



Main Program

Directs sequence of model calculations, reads input, and prints output.

Oil on the Bottom Subroutine

Uses WSF oil concentration data to compute the "oil on the bottom", TARS.

Feeding Subroutine

Computes uptake of contaminants through consumption of oil contaminated food.

Main Migration Subroutine

Directs sequence of migration computations, computes uptake of contaminants from exposure to oil, and calculates deputation.

Migration Calculation Subroutine

Calculates actual migration and redistributes contamination over model grid. Calculates amount of contaminated b omass caving the model region.

Figure 2.--Sequence of BIOS model computations.

Upon completion of the FEDOIL computations described in detail below, the model returns to the main program, which then calls the subroutine MIGR. Details of subroutine MIGR and its associated subroutine RANNAK are given in Swan (1984), and will not be repeated here. After completing the MIGR computations, the model returns again to the main program. The main program then prints selected outputs, increments the model time step, and repeats the sequence of subroutine calls for the new time step.

3. Details and Technical Specifications of Subroutine FEDOIL

Subroutine FEDOIL is called once during each time step (LL) of the simulation and computes the uptake of oil contaminants due to consumption (CONOIL) for each species (J). It then adds this value to the current level of oil contaminants (OILCON) in the given species. After completing the computations for all species, FEDOIL returns to the main program. A general flow diagram of the subroutine is given in Figure 3.

FEDOIL first sets general constants for use in subsequent subroutine equations, and then begins to loop through the species specific computations for feeding. The first step in computing the uptake of contaminants is to determine the species specific food coefficient ($TOH_{LL,J}$) of the given time step (LL).

The food coefficient ($TOH_{LL,J}$) for each species group (J) is computed as a function of percent body weight daily. The basic rates of percent body weight daily (TJ_J, given as a fraction), are prescribed by month (t) and adjusted for seasonal variation via the harmonic function:

$$TOH_{LL,J} = TJ_J + [0.35(TJ_J) \cos (ALP(t) - GKAP)] \qquad (1)$$

where ALP is the phase speed and equals 30°; t is the month of the simulation; LL is the daily time step of the simulation (i.e., TOH is held constant over a month); and GKAP is the phase lag and equals 175°. This equation is taken from Laevastu and Larkins (1981), and is discussed in detail in Gallagher (1984).

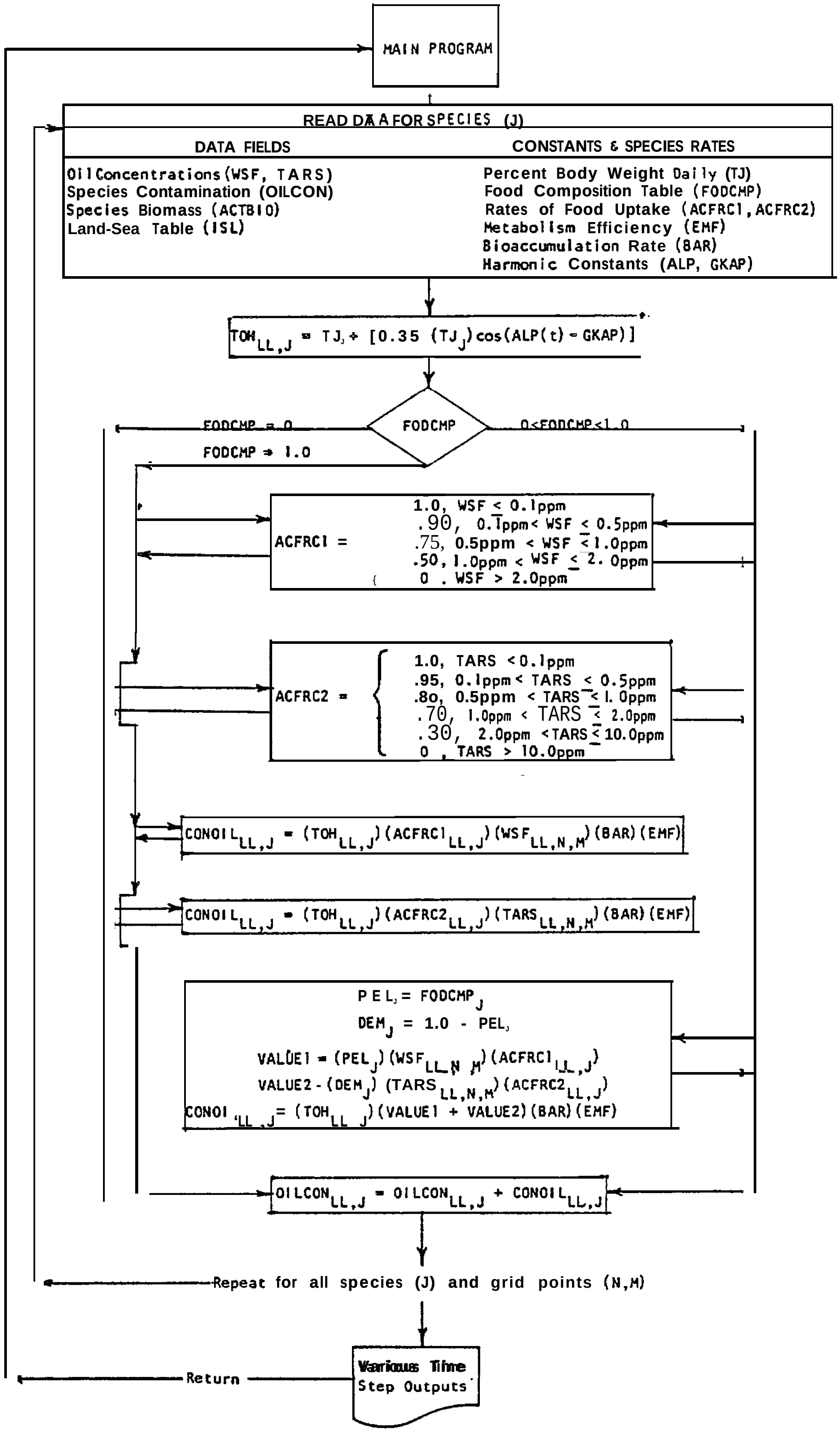


Figure 3.--Flow diagram of subroutine FEDOIL

After computing $TOH_{LL,J}$, the subroutine next checks the percent composition of pelagic food items ($FODCMP_J$) in the diet of the given species in order to determine which of several equations to use in computing the value of CONOIL. As a first approximation, the general food composition data for each species or species group are assumed to be comprised of either general pelagic food, general demersal food, or a combination of both.

If the diet of a given species (J) is composed only of pelagic food items (i.e., FODCMP=1.0), then the amount of oil contaminants taken up through feeding during time step LL, $CONOIL_{LL,J}$, is given by:

$$CONOIL_{LL,J} = (TOH_{LL,J})(ACFRCI_{LL,J})(WSF_{LL,N,M})(BAR)(EMF) \quad (2)$$

'here $ACFRCI_{LL,J}$ is the actual fraction of a species diet that may be consumed and is a function of oil concentration, $WSF_{LL,N,M}$ (see Appendix Table 3); BAR is the bioaccumulation ratio between oil concentration in the environment and oil concentration in the food items in a species diet; EMF is the efficiency of metabolism of oil contaminated food items; and other parameters are as previously given. (The preliminary values for parameters BAR and EMF are 50.0 and 0.75, respectively. See Laevastu and Fukuhara (1984) and Gallagher (1984) for a full discussion.)

Equation 2 is a reasonable approximation given the additional assumptions that 1) a species biomass is constant across the grid and for the duration of the simulation due to the limited temporal and spatial scales of the study; and 2) that in computing the amount of oil contaminants taken up during feeding, no attempt is made to try to estimate species specific growth *or* consumption rates; instead, each species (J) is assumed to get its full food requirement (food ration) for each time step of the simulation (i.e., there is no starvation). This topic is discussed in detail in Gallagher (1984).

if the diet of a given species (J) iscomposedonly of demeral food items (i.e. , FODCMP=0) , then the amount of oil contaminants taken up through feeding during time step LL, $CONOIL_{LL,J}$, is given by:

$$CONOIL_{LL,J} = (TOH_{LL,J})(ACFRC2_{LL,J})(TARS_{LL,N,M})(BAR)(EMF) \quad (3)$$

'here $ACFRC2_{LL,J}$ is the actual fraction of a species diet that may be consumed and is a function of oil concentration, $TARS_{LL,N,M}$ (see Appendix Table 3) , and other parameters are as previously given.

if the diet of a given species (J) is composed of both pelagic and demersal food items (i.e., $0<FODCMP<1.0$), then the amount of oil contaminants taken up through feeding during time step LL, $CONOIL_{LL,J}$, is given by:

$$CONOIL_{LL,J} = (TOH_{LL,J})(VALUE1 + VALUE2)(BAR)(EMF) \quad (4)$$

where

$$VALUE1 = (PEL_J)(WSF_{LL,N,M})(ACFRC1_{LL,J}) \quad (5)$$

and

$$VALUE2 = (DEM_J)(TARS_{LL,N,M})(ACFRC2_{LL,J}) \quad (6)$$

and where PEL_J is the fraction of pelagic food items in a species diet and is equal to FODCMP; DEM_J is the fraction of demersal food items in a species diet and is equal to $(1.0 - PEL_J)$; and other parameters are as previously given.

The subroutine now adds the computed amount of oil contaminants taken up through feeding ($CONOIL_{LL,J}$) to the current amount of oil contaminants already existing in the species ($OILCON_J$). These data are then stored as parts per million (ppm; i.e., milligrams (mg) of oil per kilogram (kg) of biomass), for later use in other subroutines. These procedures are then repeated for all species and all grid points for the given location and scenario. When all computations have been completed, subroutine FEDOIL prints selected outputs for the given time step (e.g., Appendix Table 5) and then returns to the main. program.

4. References

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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.

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

Niggol, Karl.

1982. Data on fish species from the Bering Sea and Gulf of Alaska. Nat'l. Mar. Fish. Serv., Northwest and Alaska Fisheries Center, Seattle, WA, NOAA Tech. Memo. NMFS F/NWC-29, 125 pp.

Swan, Nancy Pola.

1984. Biological Impact of an Oil Spill (BIOS) model documentation. Part 1: Fish migrations and exposure to containination. Nat'l. Mar. Fish. Serv., Northwest and Alaska Fisheries Center, Seattle, WA., Program Documentation No. 21, 17 pp.

5. Appendix Tables

Appendix Table 1.--List of species and input biomass data (by location) used in BIOS[1/].

No.	Species Name	Input Biomass Data[2/] Port Moller	Port Heiden	Cape Newenham
1	Herring juveniles	1409	521	1551
2	Herring adults	1121	414	1234
3	Pollock juveniles	3708	2322	3261
4	Pollock adults	11007	6893	9679
5	Pacific cod juveniles	424	279	307
6	Halibut juveniles	730	330	240
7	Yellowfin sole juveniles	722	482	711
8	Other flatfish juveniles	2004	1472	1650
9	Yellowfin sole adults	800	534	789
10	Other flatfish adults	2004	1472	1650
11	Pacific cod adults	861	461	681
12	King and Bairdi crab juveniles	664	222	432
13	King and Bairdi crab adults	1654	553	1078
14	Mobile epi fauna	5970	4995	6075
15	Sessile epifauna	13930	11655	14175
16	Infauna	19150	13750	19250

1/ The DYNUMES model (Laevastu and Larkins, 1981) was used to get initial estimates of input biomass data for the three model locations of the BIOS model. These data were in kilograms per square kilometer (kg/km^2). Complete details on methods used will be provided in the final report.

2/ The following assumptions were used to convert the data obtained from the DYNUMES model to biomass fields for use in the BIOS model.

a) Unless noted differently below, the breakdown of species biomass data into juvenile and adult fractions was based on Niggol (1982).

b) DYNUMES species group 5 (halibut) was assumed to be 100% juvenile (i.e., in these shallow waters during this season).

c) Yellowfin sole data were assumed to comprise 75% of DYNUMES species group 7 (yellowfin and rock sole).

d) DYNUMES species group 13 (Pacific and saffron cod) was assumed to be 100% Pacific cod.

e) DYNUMES species groups 7 (rock sole-25%), 6 (flathead sole, flounder), and 8 (other flatfish) were combined to make up the other flatfish group (species 8 and 9) for the BIOS model. These groups were assumed to be equally divided between juveniles and adults.

f) DYNUMES species groups 19 (king crab) and 20 (Tanner crab) were combined, and using available survey data, assumed to be comprised of 71.4% adults and 28.6% juveniles.

g) DYNUMES species group 24 (epifauna) was assumed to be 30% mobile and 70% sessile.

Appendix Table 2. --List of parameters and associated values used in the equations of subroutine FE DO IL.

No.	Species (J)	TJ[1]	Food composition[2] %PEL	Food composition[2] %DEM[3]
1	Herring juveniles	.016	100	
2	Herring adults	.010	95	5
3	Pollock juveniles	.012	95	5
4	Pollock adults	.007	72	28
5	Pacific cod juveniles	.015	81	19
6	Halibut juveniles	.012	43	57
7	Yellowfin sole juveniles	.012	20	80
8	Other flatfish juveniles	.012	20	80
9	Yellowfin sole adults	.006	15	85
10	Other flatfish adults	.006	25	75
11	Pacific cod adults	.007	30	70
12	King and Bairdi crab juvenile	.012	30	70
13	King and Bairdi crab adults	.006	10	90
14	Mobile epifauna	.019	0	100
15	Sessile epifauna	.006	0	100
16	Infauna	.006	0	100

1/ Data taken from DYNUMES model (Laevastu and Larkins, 1981).

2/ The basic food composition data is given as the percent pelagic food in a given species' diet; i.e., parameter FODCMP. Details on the estimation of FODCMP are given in Gallagher (1984).

3/ [pEL= FODCMP]; [DEM = 1.0 - PEL].

Appendix Table 3.--Effects of various concentrations of WSF and TARS of crude oil on the actual food uptake of selected marine species.[1]

Oil Concentration (CONC) (in ppm)	CONC≤0.1	0.1< CONC≤0.5	0.5<CONC≤1.0	1.0<CONC≤2.0	2.0<CONC≤10.0	CONC>10.0
Pelagic feeders (WSF)[2]						
ACFRC1	1.0	.90	.75	.50	0	0
Demersal feeders (TARS)						
ACFRC2	1.0	.95	.80	.70	.30	0

1/ For a more detailed analysis see Laevastu and Fukuhara (1984).

2/ Values shown are the actual fraction of a species food requirement that would be eaten under the given level of oil concentration.

Appendix Table 4.--List of symbols and abbreviations.

ACFRC1 - Fraction of species diet that may be consumed given the existing oil concentrations of WSF.

ACFRC2 - Fraction of species diet that may be consumed given the existing oil concentration of TARS.

ACTBIO - Species biomass.

ACTCON - Total amount of food items consumed by a species - since there is no starvation, it is a function of percent body weight daily (TOH) and biomass (ACTBIO).

ALP Phase speed (30° to reflect monthly adjustment).

BAR Bioaccumulation ratio.

CONOIL - Amount of oil contaminants taken up during feeding.

DEM - Fraction of species diet that is demersal food - equal to (1.0-PEL).

EMF Efficiency of metabolism of oil contaminated food items.

FODCMP - Fraction of species diet that is pelagic food (input food composition data).

GKAP - Phase lag (175° to prescribe time when function is maximum).

ISL - Land-sea table - defines land and sea areas of computational grids.

K Same as t (symbol used in computer code).

LL - Time step of the simulation (i.e., daily).

LOC - Index defining location of current simulation (symbol used in computer code).

ME - Columns used in grid array - location specific.

Appendix Table 4 (cent'd)

NE - Rows used in grid array - location specific.

OILCON - Current level of oil contaminants in a given species. .

PEL - Fraction of species diet that is pelagic food - equal to FODCMP.

RAD - Radians.

t - Month of simulation.

TARS - Oil concentration "on the bottom".

TJ - Basic species specific rate of percent body weight daily - defined on a monthly basis.

TOH - Species specific food coefficient as a function of percent body weight daily.

WSF - Oil concentration as "water soluable fraction".

Appendix Table 5. --Example of computed 'contamination index' of a species caused by uptake of oil contaminated food[1/].

Species No. 1 Biomass: 1409.00 kg/km^2	Location: Port Moller Time Step: Day 1	
Concentrations in ppb (µg/kg)	Total contaminated biomass[2/] Kilograms (kg)	Area (km^2)
Cont. Index greater than 1000.00	0.00	0.00
Cont. Index 500.00 to 1000.00	5636.00	4.00
Cont. Index 100.00 to 500.00	73268.00	52.00
Cont. Index 50.00 to 100.00	28180.00	20.00
Cont. Index 10.00 to 50.00	39452.00	28.00
Cont. Index 1.00 to 10.00	78904.00	56.00
Cont. Index 0.10 to 1.00	39452.00	28.00
Cont. Index less than 0.10	5867076.00	4164.00

1/ A full discussion of these and other output data will be given in the final report.

2/ Each grid point is a square of 4 km^2. Thus the total contaminated biomass at a grid point is equal to (ACTBIO x 4).

6. Subroutine Listing in FORTRAN[1/]

1/ Computer code for the printing of selected outputs has been deleted.

```
C
C********************   ●******************   ●*******************   .*********
C                                   MAIN PROGRAM
C*****************************************************************************
C
$RESET FREE
$SET OWN OWNARRAYS
$SET LIST LINEINFO STACK
FILE  1(KIND=DISK,TITLE="OCSEAP/OILCON/LOC1",FILETYPE=7)
FILE  2(KIND=DISK,TITLE="OCSEAP/OILCON/LOC2",FILETYPE=7)
FILE 3(KIND=DISK,TITLE="OCSE AP/OILCON/LOC3",FILETYPE=7)
FILE 4(KIND=DISK,TITLE="OC SEAP2/LOC2/LANDSEA",FILETYPE=7)
FILE  6(KIND=PRINTER)
      COMMON/BLK1/NE,ME,K,LL,ISL
      COMMON/BLKBIO/LOC,ACTBIO(16)
      COMMON/INPBIO/BIOLC(3,16)
      COMMON/BLKOIL/OILCON(16,32,34)
      COMMON/OIL/WSF(32,34),TARS(32,34)
      DIMENSION ISL(32,34),D(32,34), TB(4)
      NE=32; ME=34; K=8; LL=1; LLMAX=10; LOC=1
C
C-------------------------------- ---------- --------0------0--0-------- ------
C     USING DEFINED  LOCATION  (I.E., LOC=1),SET ACTBIO EQUAL TO BIOLC.
C     BIOLC IS A BLOCK DATA ARRAY CONTAINING SPECIES BIOMASS DATA FOR
C     ALL THREE OIL SPILL SCENARIO LOCATIONS.
C------------------------- ----------0---------------- ---------------
C
      DO 25 J=1,16
      ACTBIO(J)=BIOLC(LOC,J)
   25     CONTINUE
C
C. . . . . . . . . . . . . . . . . . . . . . ------------------ ------------- . . . . . . . . ------
C     READ INPUT  DATA FOR ISL AND WSF
C     NHRS IS THE TIME STEP OF THE WSF DATA (I.E., 1 DAY = 24HRS)
C-------- --- . . ---- --------- --------------------- -------- -----------
C
      IF(LOC.NE.2)GO TO 51
      DO 50 N=1,NE
   50 READ(4,100)ME,(ISL(N,M),M=1,ME)
      GO TO 30
   51 DO 52 N=1,NE
      DO 52 M=1,ME
   52 ISL(N,M)=1
  100 FORMAT(*I2)
   30 READ(LOC,/)NHRS
      READ(LOC,/)((WSF(N,M),M=1,ME),N=1,NE)
C
C. - . . . --- . . . . . . . . .- --------- -------- --------------------- -------- -----
C   CHANGE OIL  CONCENTRATIONS FROM PPB TO PPM
C------------------- ----------------- ------------------------- ----
C
      DO 32 N=1,NE
      DO 32 M=1,ME
   32 WSF(N,M)=WSF(N,M)/1000.
C
C---------- . . . . . . . . . --------- --------- ------------------ -000 ---------
C     COMPUTE OIL ON THE BOTTOM
```

```
C      SEE LA EVASTU ANC FUKUHARA (1984) FOR DETAILS
C-------- --------- -------- --------------- -------- -------- -------- ------
C
       BLO=2.
C      BLO=2 CC NTINUCUS SOURCE, BLO=1 INSTANTANEOUS SOURCE.
       DL=2000.
C      TAT TIME STEP IN HOURS
       TAT=24.
       TD=20.
       T=LL*1440.
       KAL=1
C      KAL=0  NO OIL MOVEMENT ON THE BOTTOM, 1 OIL ADVECTED ON BOTTOM
C      KU - CURRENT INDEX, SEE CUR CIL; KA  TURBULENCE INDEX(NOTUSED);
C      LU  PRINT SCALING INDEX
       KU=3
       KA=1
       LU=0
       UI=0.
       VI=0 a
       CALL OILBOT(WSF,LL,TD,DL,D,TARS,TB,BLO,UI,VI,KU,KAL,T,KA,TAT)
       UI=60.
       VI=8.
       IF (KAL.NE.1) GO TO 31
       CALL CURCIL(TARS,KU,UI,VI,DL,LL,BLO,T,KAL)
  31   CONTINUE
C
C. . . . . . . . . . . . . . . . . . . . . . . . . . ---------- ------------------- -------
C      CALL FEDCIL AND MIGR
C. ----- .- . --- . . .0 ----------- -------e. --------- ------------------------
C
       CALL FEDCIL
       CALL MIGR
C
C------- . . . . . . . . --------- -------- -------- --------------- -------- -------
c      INCREMENT TIME STEP
C-------- --------- --------------- --------------- --------- -------- -----
C
    99 LL=LL+ 1
       IF(LL.LE.LLMAX) GO TO 30
c
c-------- --------- ---------------------- -------- -------- -------- ------
C                                END MAIN PROGRAM
C -------- --------- ---------------- .----- 9- ---------------- -------- -- ---
C
       STOP
       END
c
● *********U*** ● ************* ************** ● 4************ ● ***********
c                                 BLOCK DATA
● ************* ● ************* ● ************* ● S************ ● ***********
C
       COMMON/INFEIO/BIOLC(3,16)
       COMMON/VALUES/FCOCMP(16),TJ(16)
       DATA BIOLC/1409.,521.,1551.,1121.,414.,1234.,
      &3708.,2322.,3261.,11007.,6893.,9679.,424.,279.,307.,
      &730.,330.,240., 831.,555.,819., 2004.,1472.,1650.,
      &922.,615.,908., 2004.,1472., 1650., 861.,461.,681.,
      &664.,222.,432., 1656.,553.,1078., 5970.,4995.,6075.,
      &13930.,11655.,14175.,19150.,13750.,19250./
       DATAFCOCMF/1.00,.95,.95,.72, ● El*.42* .Z3P.2g Pm15v. 25, .30,
```

```
     *.30,.10,0.0,0.0,0.0/
      DATA TJ/.016,.010,.012,.007,.015,.012,.012,.012,.006,.006,
     *.007,.012,.006,.019,.006,.006/
      END
C
C*******************************************************************************8*******
C                                 SUBROUTINE FEDOIL
C**************************************************************************************
C
      COMMON/OIL/WSF(32,34),TARS(32,34)
      COMMON/BLKBIO/LOC,ACTBIO(16)
      COMMON/BLKOIL/OILCON(16,32,34)
      COMMON/BLK1/NE,ME,K,LL,ISL(32,34)
      COMMON/VALUES/FOODCMP(16),TJ(16)
C
C-----------------------------------------------------------------------------------
C     SET CONSTANTS
C-----------------------------------------------------------------------------------
C
      RAD=0.01745329
      ALP=30.*RAD
      GKAP=175.*RAD
      VALCA=COS(ALP*K-GKAP)
      BAR=50.
      EMF=0.75
C
C-----------------------------------------------------------------------------------
C     COMPUTE UPTAKE OF OIL CONCENTRATION DUE TO  CONTAMINATED  FOOD
C     CONCENTRATIONS ARE IN PPM AND ACTBIO IS IN KG
C     FOODCMP IS THE  % OF PELAGIC FOOD ITEMS IN A SPECIES DIET
C-----------------------------------------------------------------------------------
C
      DO 99 J=1,16
C
      TOH(J)=TJ(J)+(0.35* TJ(J)*VALCA) .
C
      DO 10 N=1,NE
      DO 10 M=1,ME
      IF(ISL(N,M).EQ. 0) GO TO 10
      ACFRC1=1.
      ACFRC2=1.
      IF(FOODCMP(J).GT.0..AND.FOODCMP(J).LT.1.0) GO TO 20
      IF(FOODCMP(J).EQ.1.0) GO TO 30
      IF(TARS(N,M).GT.10.0)ACFRC2=0.
      IF(TARS(N,M).GT.2.0.AND.TARS(N,M).LE.10.0)ACFRC2=.30
      IF(TARS(N,M).GT.1.0.AND.TARS(N,M).LE.2.0)ACFRC2=.70
      IF(TARS(N,M).GT.0.5.AND.TARS(N,M).LE.1.0)ACFRC2=.80
      IF(TARS(N,M).GT.0.1.AND.TARS(N,M).LE.0.5)ACFRC2=.95
      ACTCON=TOH(J)*ACTBIO(J)
      CONOIL=TOH(J)*ACFRC2*TARS(N,M)*BAR*EMF
      OILCON(J,N,M)=OILCON(J,N,M)+CONOIL
      GO TO 10
  213 IF(WSF(N,M).GT.2.0)ACFRC1=0.
      IF(WSF(N,M).GT.1.0.AND.WSF(N,M).LE.2.0)ACFRC1=.50
      IF(WSF(N,M).GT.0.5.AND.WSF(N,M).LE.1.0)ACFRC1=.75
      IF(WSF(N,M).GT.0.1.AND.WSF(N,M).LE.0.5)ACFRC1=.90
      IF(TARS(N,M).GT.10.0)ACFRC2=0.
      IF(TARS(N,M).GT.2.0.AND.TARS(N,M).LE.10.0)ACFRC2=.30
      IF(TARS(N,M).GT.1.0.AND.TARS(N,M).LE.2.0)ACFRC2=.70
      IF(TARS(N,M).GT.0.5.AND.TARS(N,M).LE.1.0)ACFRC2=.80
```

```
      IF(TARS(N,M).GT.0.1.AND.TARS(N,M).LE.0.5) ACFRC2=.95
      ACTCON=TCH(J)*ACTBIO(J)
      PEL=FOCCMF(J)
      DEM=1.0-PEL
      CONOIL=TCH(J)*(PEL*WSF(N,M)*ACFRC1+DEM*TARS(N,M)*ACFRC2)*BAR*EMF
      OILCON(J,N,M)=OILCON(J,N,M)+CONOIL
      GO TO 10
   30 IF(WSF(N,M).GT.2.0) ACFRC1=0.
      IF(WSF(N,M).GT.1.0.AND.WSF(N,M).LE.2.0) ACFRC1=.50
      IF(WSF(N,M).GT.0.5.AND.WSF(N,M).LE.1.0) ACFRC1=.75
      IF(WSF(N,M).GT.0.1.AND.WSF(N,M).LE.0.5) ACFRC1=.90
      ACTCON=TCH(J)*ACTBIO(J)
      CONOIL=TCH(J)*ACFRC1*WSF(N,M)*BAR*EMF
      OILCON(J,N,M)=OILCON(J,N,M)+CONOIL
   10 CONTINUE
C
   99 CONTINUE
C-----------------------------------------------------------------------
C                              END SUBROUTINE
C-----------------------------------------------------------------------
C
  999 RETURN
      END
```