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(ORNL/NUREG/TM-422)

**PREREM: An Interactive Data
Preprocessing Code for INREM II**
Part I: User's Manual
Part II: Code Structure

M. T. Ryan
D. E. Fields

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Division of Safeguards, Fuel Cycle, and Environmental
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Printed in the United States of America. Available from
National Technical Information Service
U.S. Department of Commerce
5285 Port Royal Road, Springfield, Virginia 22161

Available from
GPO Sales Program
Division of Technical Information and Document Control
U.S. Nuclear Regulatory Commission
Washington, D.C. 20555

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NUREG/CR-1478
(ORNL/NUREG/TM-422)

Dist. Category NRC-RH

Health and Safety Research Division

PREREM: AN INTERACTIVE DATA PREPROCESSING CODE FOR INREM II

PART I: USER'S MANUAL

PART II: CODE STRUCTURE

Edited by

M. T. Ryan
D. E. Fields

NUREG/CR--1478

TI86 002778

Manuscript Completed: April 3, 1981

Date Published: May 1981

Research sponsored by U. S. Nuclear Regulatory Commission
Division of Safeguards, Fuel Cycle, and Environmental Research
Under Interagency Agreement DOE 40-550-75
NRC FIN No. B0188 (J. Foulke, Project Monitor) and
NRC FIN No. B0410 (E. Conti, Project Monitor)

Prepared by the
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ACKNOWLEDGEMENTS

We wish to thank J. C. Pleasant for writing the INCON computer code. This code performed some of the tasks of the interactive portion of PREREM and served as a basis for our approach. We are indebted to D. Holly for her assistance in coding part of the decay chain algorithm and S. R. Glandon for coding the name check algorithms. D. C. Kocher helped greatly in providing us with the radionuclide data set used for the decay chain determination. Further, we wish to thank K. F. Eckerman, G. G. Killough, and D. C. Kocher for their helpful suggestions regarding this work. We would also like to acknowledge W. C. Minor for her excellent clerical assistance.

ABSTRACT

PREREM is an interactive computer code developed as a data pre-processor for the INREM-II (Killough, Dunning, and Pleasant, 1978a) internal dose program. PREREM is intended to provide easy access to current and self-consistent nuclear decay and radionuclide-specific metabolic data sets. Provision is made for revision of metabolic data, and the code is intended for both production and research applications.

Documentation for the code is in two parts. Part I is a user's manual which emphasizes interpretation of program prompts and choice of user input. Part II stresses internal structure and flow of program control and is intended to assist the researcher who wishes to revise or modify the code or add to its capabilities.

PREREM is written for execution on a Digital Equipment Corporation PDP-10 System and much of the code will require revision before it can be run on other machines. The source program length is 950 lines (116 blocks) and computer core required for execution is 212 K bytes. The user must also have sufficient file space for metabolic and S-factor data sets. Further, 64 100 K byte blocks of computer storage space are required for the nuclear decay data file. Computer storage space must also be available for any output files produced during the PREREM execution.

INTRODUCTION

PREREM is a conversational computer code that allows a user to prepare the input files for the internal radiation dosimetry computer code INREM-II (Killough, Dunning, and Pleasant, 1978a). The PREREM code was developed to give users access to a current and internally consistent set of metabolic models and nuclear decay data for more than 250 radionuclides in an easily accessible form. The preparation of input data sets for INREM-II is exacting, and PREREM is capable of creating these data sets. The user is required to be familiar with basics of computer operation and the terminology of internal dosimetry and to answer a few simple questions regarding the particular dosimetry assessment that is being considered. PREREM is intended for execution on a Digital Equipment Corporation PDP-10 System, and much of the code will require revision before attempting to run on other machines. The user must also have sufficient space for his data sets. The computer or machine storage minimal data requirement is for the nuclear decay data file, S-factor files, and metabolic data files. File space must also be available for any output files produced during the PREREM execution.

INREM-II is a powerful and widely used code (Killough, Dunning, and Pleasant, 1978a) for calculating internal dose resulting from radionuclide inhalation or ingestion. Data required for execution of INREM-II include detailed specifications of radionuclide decay chains including half-lives and branching fractions and metabolic data for relevant organs for the parent radionuclide and all daughter products. Also required are dose-equivalent values per microcurie-day of residence, or S-factors (Dunning, Pleasant, and Killough, 1977) for major organs. These input data are extensive, and manual preparation of an input data set is an exacting and formidable task. PREREM has been developed as a data preprocessor for the INREM-II internal dose program in order to provide users with easy access to these data.

PREREM: An Interactive Data Preprocessing Code for INREM-II
Part I. User's Manual

M. T. Ryan, D. E. Fields, D. E. Dunning, Jr., and J. C. Pleasant

1.1 Metabolic and S-factor Data Files

Before discussing the conversational input for PREREM, it is important to discuss the structure, content, and naming protocol for S-factor and metabolic data sets.

The S-factor data sets have been produced from decay data by Kocher (in press) and contain a set of source-target organ cross-irradiation values (S-factors). The details of the organization of these data sets have been documented previously (Dunning, Pleasant, and Killough, 1977; 1980). Basically, the file consists of a lead card which contains the radionuclide name in the form RN-NNNm which allows for the two-character element name, up to three numbers for the radionuclide mass number, and provision for an "m" or blank space for metastable or ground states, respectively. The 22 by 24 source-target organ matrix of S-factors follows this name card. The column and row labels are given in Table 1.

The metabolic data set consists of a name card, cards containing target-organ retention function data, and notes concerning the references used to compile the metabolic data and the date of file preparation. A typical example is given for sodium in Table 2. This file structure was intentionally adopted because it is similar to the input file structure required by the INREM-II code. Basically, the file consists of a radionuclide name card, cards containing nuclear decay data, cards containing target organ names and masses, and cards containing the retention function data for those target organs. A detailed discussion of these data are given in the documentation for INREM-II (Killough, Dunning, and Pleasant, 1978a, 1978b; Dunning et al., 1979).

The metabolic file naming protocol, while complicated, is intended to be informative to the user. In many cases the metabolic data file applies to all isotopes of a given element whether the isotopes are parent or daughter species in decay chains. In this case, where a single formulation of metabolic data applies to all isotopes of the element, the metabolic file name is given by the element's two-letter abbreviation followed by the extension .MET. For example, the file names for sodium and strontium would be NA.MET and SR.MET, respectively.

Table 1. S-factor file matrix labeling scheme

Columns (Source organs)	Rows (Target organs)
Adrenals	Adrenals
Bladder contents	Bladder wall
Stomach contents	Stomach wall
Small intestine contents	Small intestine wall
Upper large intestine contents	Upper large intestine wall
Lower large intestine contents	Lower large intestine wall
Kidneys	Kidneys
Liver	Liver
Lungs	Lungs
Respiratory lymph	Respiratory lymph
Muscle	Muscle
Ovaries	Ovaries
Pancreas	Pancreas
Cortical bone	Bone
Cancellous bone	Red marrow
Red marrow	Yellow marrow
Yellow marrow	Endosteal cells
Skin	Skin
Spleen	Spleen
Testes	Testes
Thyroid	Thymus
Total body	Thyroid
	Uterus
	Total body

Table 2. Metabolic model file structure for sodium

NA ^a				
3 ^b				
ABSORBED ^c	0.700E+05	BONE	0.500E+04	OTHER
0.100E+01	1 ^d			0.363E+05
0.100E+01	0.150E+02			
0.300E00	1 ^e			
0.100E+01	0.150E+02			
0.700E+00	1 ^f			
0.100E+01	0.15E+02			
SODIUM MODEL FROM NRPB-R82 ^g				
8/15/80 ^h				

^aElement name.

^bNumber of organs for which retention functions are given (except respiratory and gastrointestinal tract compartments).

^cTarget organs and masses for which retention function are given (except respiratory and gastrointestinal tract compartments).

^dRetention function for absorbed.

^eRetention function for bone.

^fRetention function for other.

^gNotes on information source for metabolic data.

^hDate of file preparation.

A difficulty arises for radionuclides that can be considered either as a parent or a daughter in a radioactive decay series, provided that prompt excretion is to be considered. For example, thorium has two metabolic files named THP.MET and THD.MET. The content of these files is given in Tables 3 and 4, respectively. The difference is that prompt excretion is allowed if a thorium isotope is the inhaled or ingested parent radionuclide. The THP.MET file has a compartment deposition fraction of 0.1, which assigns 0.1 of the absorbed material to prompt excretion with a retention half-time of 0.5 day. When a thorium isotope is a daughter species of a parent for which prompt excretion is allowed, then the THD.MET file should be used. The fraction assigned to prompt excretion for thorium in this case is zero because it is assumed that daughter atoms born in the body do not undergo prompt excretion.

A further complication arises if radioisotopes of a given element can be considered either as a daughter of a parent for which prompt excretion is considered or as a daughter of a parent for which prompt excretion is not considered. Bismuth is an example of this possibility. Three metabolic files are given for bismuth: BIP.MET is to be used when a bismuth isotope is considered as the parent radionuclide; BIDEX.MET is to be used when a bismuth isotope is to be considered as a daughter radionuclide of a parent for which prompt excretion occurs; and BIDNEX.MET is to be used when a bismuth isotope is considered as a daughter of a parent for which prompt excretion does not occur. Tables 5, 6, and 7 list BIP.MET, BIDEX.MET, and BIDNEX.MET, respectively. While this naming protocol and file complexity may seem awkward, it provides easy access to files tailored to fit specific needs without requiring editing by the user.

Table 3. Thorium metabolic data file (thorium as parent species)

TH						
8	PLUS PROMPT EXCRETION					
ABSORBED	0.700E+05BONE	0.500E+04LIVER	0.180E+04KIDNEYS	0.310E+03		
SPLEEN	0.180E+03TESTES	0.350E+02OVARIES	0.110E+02OTHER	0.339E+05		
0.100E+01	3					
0.100E+00	0.500E+00	0.200E+00	0.700E+03	0.700E+00	0.800E+04	
0.100E+00	1 ^a					
0.100E+01	0.500E+00					
0.700E+00	1					
0.100E+01	0.800E+04					
0.400E-01	1					
0.100E+01	0.700E+03					
0.136E-02	1					
0.100E+01	0.700E+03					
0.789E-03	1					
0.100E+01	0.700E+03					
0.153E-03	1					
0.100E+01	0.700E+03					
0.482E-04	1					
0.100E+01	0.700E+03					
0.158E+00	1					
0.100E+01	0.700E+03					
THORIUM MODEL FROM ICRP CO; THORIUM AS PARENT.						
9/1/80						

^aA prompt excretion compartment with a compartment deposition fraction of 0.1.

Table 4. Thorium metabolic data file (thorium as daughter species)

TH					
8	PLUS PROMPT EXCRETION				
ABSORBED	0.700E+05BONE	0.500E+04LIVER	0.180E+04KIDNEYS	0.310E+03	
SPLEEN	0.180E+03TESTES	0.350E+02OVARIES	0.110E+02OTHER	0.339E+05	
0.100E+01	2				
0.300E+00	0.700E+03	0.700E+00	0.800E+04		
0.000E+00	1 ^a				
0.100E+01	0.500E+00				
0.700E+00	1				
0.100E+01	0.800E+04				
0.400E-01	1				
0.100E+01	0.700E+03				
0.221E-02	1				
0.100E+01	0.700E+03				
0.128E-02	1				
0.100E+01	0.700E+03				
0.249E-03	1				
0.100E+01	0.700E+03				
0.784E-04	1				
0.100E+01	0.700E+03				
0.784E-04	1				
0.100E+01	0.700E+03				
0.256E+00	1				
0.100E+01	0.700E+03				

THORIUM MODEL FROM ICRP CO; THORIUM AS DAUGHTER ISOTOPE.
9/1/80

^a Prompt excretion compartment with a compartment deposition fraction of 0.0.

Table 5. Bismuth metabolic data file (bismuth as parent species)

BI					
8	PLUS PROMPT EXCRETION				
ABSORBED	0.700E+05BONE	0.500E+04LIVER	0.180E+04KIDNEYS	0.310E+03	
SPLEEN	0.180E+03TESTES	0.350E+02OVARIES	0.110E+02OTHER	0.339E+05	
0.100E+01	2				
0.600E+00	0.600E+00	0.400E+00	0.500E+01		
0.300E+00	1 ^a				
0.100E+01	0.500E+00				
0.350E-01	2				
0.600E+00	0.600E+00	0.400E+00	0.500E+01		
0.126E-01	2				
0.600E+00	0.600E+00	0.400E+00	0.500E+01		
0.400E-00	2				
0.600E+00	0.600E+00	0.400E+00	0.500E+01		
0.126E-02	2				
0.600E+00	0.600E+00	0.400E+00	0.500E+01		
0.245E-03	2				
0.600E+00	0.600E+00	0.400E+00	0.500E+01		
0.770E-04	2				
0.600E+00	0.600E+00	0.400E+00	0.500E+01		
0.251E+00	2				
0.600E+00	0.600E+00	0.400E+00	0.500E+01		
BISMUTH MODEL FROM NRPB-R82; BISMUTH AS PARENT NUCLIDE.					
9/1/80					

^aPrompt excretion compartment with a compartment deposition fraction of 0.3.

Table 6. Bismuth metabolic data file (bismuth as a daughter species of a parent with prompt excretion)

BI					
8	PLUS PROMPT EXCRETION				
ABSORBED	0.700E+05BONE	0.500E+04LIVER	0.180E+04KIDNEYS	0.310E+03	
SPLEEN	0.180E+03TESTES	0.350E+02OVARIES	0.110E+02OTHER	0.339E+05	
0.100E+01	2				
0.600E+00	0.600E+00	0.400E+00	0.500E+01		
0.000E+00	1 ^a				
0.100E+01	0.500E+00				
0.698E-01	2				
0.600E+00	0.600E+00	0.400E+00	0.500E+01		
0.251E-01	2				
0.600E+00	0.600E+00	0.400E+00	0.500E+01		
0.400E-00	2				
0.600E+00	0.600E+00	0.400E+00	0.500E+01		
0.251E-02	2				
0.600E+00	0.600E+00	0.400E+00	0.500E+01		
0.489E-03	2				
0.600E+00	0.600E+00	0.400E+00	0.500E+01		
0.154E-03	2				
0.600E+00	0.600E+00	0.400E+00	0.500E+01		
0.502E+00	2				
0.600E+00	0.600E+00	0.400E+00	0.500E+01		
BISMUTH MODEL FROM NRPB-R82; BISMUTH AS DAUGHTER OF EXCRETION PARENT.					
9/1/80					

^a Prompt excretion compartment with a compartment deposition fraction of 0.0.

Table 7. Bismuth metabolic data file (bismuth as a daughter species of a parent with no prompt excretion)^a

BI					
8					
ABSORBED	0.700E+05	BONE	0.500E+04	LIVER	0.180E+04
KIDNEYS	0.310E+03				
SPLEEN	0.180E+03	TESTES	0.350E+02	OVARIES	0.110E+02
OTHER	0.339E+05				
0.100E+01	2				
0.600E+00	0.600E+00	0.400E+00	0.500E+01		
0.698E-01	2				
0.600E+00	0.600E+00	0.400E+00	0.500E+01		
0.251E-01	2				
0.600E+00	0.600E+00	0.400E+00	0.500E+01		
0.400E-00	2				
0.600E+00	0.600E+00	0.400E+00	0.500E+01		
0.251E-02	2				
0.600E+00	0.600E+00	0.400E+00	0.500E+01		
0.489E-03	2				
0.600E+00	0.600E+00	0.400E+00	0.500E+01		
0.154E-03	2				
0.600E+00	0.600E+00	0.400E+00	0.500E+01		
0.502E+00	2				
0.600E+00	0.600E+00	0.400E+00	0.500E+01		
BISMUTH MODEL FROM NRPB-R82; BISMUTH AS DAUGHTER OF NON-EXCRETION PARENT.					
9/1/80					

^a No prompt excretion compartment is required.

1.2 PREREM Execution on the PDP-10 Computer

In order to execute PREREM, the user must have the PREREM.FOR source file in his user area. The user must also recall the metabolic and S-factor files that will be needed for the radionuclide(s) being considered. The naming protocol for S-factor files consists of the radionuclide abbreviation and mass number followed by the extension .SFC. For example the S-factor files names for ^{22}Na and ^{105}Rh would be NA22.SFC and Rh105M.SFC, respectively. The file DECAF.DAT, containing the nuclear decay data must also be copied in the user's PDP-10 area. These files are stored on DECTAPES, and library listings of all files are given in Appendix A. To recall the nuclear decay data file for example, the user types

```
.File_R-DNNNN, DECAF.DAT
```

where NNNN is the 4-digit DECTAPE identification number on which the respective files are stored. If, for example the radionuclide under consideration is ^{22}Na the commands to recall the metabolic and S-factor files, respectively, would be

```
.File_R,DNNNN,NA.MET
```

```
.File_R,DNNNN,NA22.SFC .
```

Help files are available for the use of DECTAPES in the PDP-10 HELP Library for more information. The HELP_DECTAP command calls and prints a file which gives detailed instructions about using DECTAPES. Also, the user must make two assignments of peripheral equipment, a teletype and a disk by typing

```
.ASSIGN_TTY 6
```

```
.ASSIGN_DSK_8 .
```

Once all of the metabolic and S-factor data files have been written in the user's PDP-10 area and peripheral equipment assignments have been made, PREREM can be executed by using the following command

.EX_PREREM.FOR .

The next section is designed to aid the user in the conversational section of PREREM.

1.3 Conversational Input

The questions that will be asked of the user after the PREREM execution step are discussed in this section. For purposes of illustration, each question that can be asked is listed and a typical response given.

After the execution step, the title

CONVERSATIONAL INPUT PROGRAM FOR INREM II

will be printed.

The first request is printed next.

Computer: PLEASE ENTER THE PARENT RADIONUCLIDE

Example Answer: RH-105M

The correct response is the name of the radionuclide for which the dosimetry assessment is being considered. For example, if ^{232}Th is being considered, the user types TH-232; if ^{105}Rh is being considered, the user types RH-105M. In order to avoid confusion, the radionuclide naming protocol will always follow the format given below.

<u>X</u>	<u>X</u>	-	<u>N</u>	<u>N</u>	<u>N</u>	<u>M</u>
↑	↑		↑	↑	↑	↑
1	2		3	4		

- 1) One or two letter characters for the element name
- 2) A dash
- 3) One, two, or three number characters for the radionuclide mass number
- 4) The character "M" for radionuclides for which the meta-stable state is being considered

After this question is answered, the data set DECAY.DAT (Kocher, in press) is accessed by PREREM, and the decay chain with the appropriate radioactive half-lives is generated. The decay chain is then printed, and each radionuclide is assigned an index number for easy reference. Branching fractions are also determined and stored. Three examples of the decay chain data are given below.

DECAY CHAIN ENTITIES:

INDEX NO.	RADIONUCLIDE	RAD. HALF-LIFE
1	RH-105M	.52083E-03 DAYS
2	RH-105	.35360E+02 DAYS

If the answer to the first question had been TH-232, the output would be:

DECAY CHAIN ENTITIES:

INDEX NO.	RADIONUCLIDE	RAD. HALF-LIFE
1	TH-232	.51282E+13 DAYS
2	RA-228	.20988E+04 DAYS
3	AC-228	.25542E+00 DAYS
4	TH-228	.69832E+03 DAYS
5	RA-224	.36200E+01 DAYS
6	RN-220	.64363E-03 DAYS
7	PO-216	.16898E-05 DAYS
8	PB-212	.44346E+00 DAYS
9	BI-212	.42049E-01 DAYS
10	TL-208	.21201E-02 DAYS
11	PO-212	.34491E-11 DAYS

If the answer to the first question had been Pu-239, the output would be

DECAY CHAIN ENTITIES:

INDEX NO.	RADIONUCLIDE	RAD. HALF-LIFE
1	PU-239	.88078E+07 DAYS
2	U-235	.25689E+12 DAYS
3	TH-231	.10633E+01 DAYS
4	PA-231	.13600E+08 DAYS
5	AC-227	.79471E+04 DAYS
6	FR-223	.15139E-01 DAYS
7	TH-227	.18718E+02 DAYS
8	RA-223	.11434E+02 DAYS
9	RN-219	.45833E-04 DAYS
10	PO-215	.20579E-01 DAYS
11	PB-211	.25069E-01 DAYS

12	BI-211	.14792E-02 DAYS
13	TL-207	.33125E-02 DAYS
14	PO-211	.59722E-05 DAYS

The user is then asked:

Computer: TYPE THE INDEX NO. FOR THE LAST RADIONUCLIDE WHICH
CONTRIBUTES TO DOSE

Example Answer: 2

Radioactive daughters whose half-lives are very long compared to their parents may not contribute significantly to the dose to various organs of the body. The user must indicate the index number of the last radionuclide which will contribute to the dose. For example in the case of ^{239}Pu ($T_{1/2} = 2.35 \times 10^4$ y) the first daughter product is ^{235}U (4.51×10^9 y). The half-life of ^{235}U is so long compared to the parent ^{239}Pu that only decay of ^{239}Pu contributes significantly to the total dose. Therefore, the user should enter 1 in this case. Conversely, for ^{232}Th and ^{105}Rh all of the radioactive species in the chains should be considered.

While it is difficult to give absolute criteria for deciding which is the last radionuclide that will contribute to the dose, inspection of the radioactive half-lives will usually suffice. Computer codes which solve differential equations for serial radioactive decay provide the activity of each species as a function of time. The relative amounts of each daughter product after a given decay period may provide some insight as to the last radionuclide in a series which contributes to dose. If the user does not properly truncate the decay chain, the numerical methods used in INREM-II may give erroneous results.

The next question is:

Computer: READ METABOLIC DATA FROM SOURCE FILES (Y OR N)?

Example Answer: Y

The user is given the option of accepting the metabolic models that have been prepared with available information (by typing Y for yes) or typing in a new metabolic model (by typing N for no). The

prepared files are discussed in Sect. 1.1. The questions which are given and answers that will be required if the user chooses to type in a new metabolic model (by indicating "N") are discussed separately in Appendix B.

The user will then be asked to name the metabolic files for the case being considered.

Computer: ENTER PARENT METABOLIC FILE NAME (SPECIES 1)

Example Answer: THP.MET

The user responds giving the parent radionuclide metabolic file name in the format discussed in Sect. 1.1. The user is then asked:

Computer: ENTER DAUGHTER METABOLIC FILE NAME FOR SPECIES 2

Example Answer: RADEX.MET

The user responds by typing in the metabolic file name for the second element of the decay chain being considered and so on until the metabolic file name for the last radionuclide which contributes to dose has been given.

The user is then asked to give S-factor file names. S-factors are the calculated dose equivalents to target organs per microcurie-days of residence of a radionuclide in a source organ (Dunning, Pleasant, and Killough, 1977; 1980).

Computer: ENTER THE SFACTOR FILE NAME FOR SPECIES 1

Example Answer: TH232.SFC

The user responds by typing in the parent radionuclide S-factor file name in the format discussed in Sect. 1.1. The user is then asked:

Computer: ENTER THE SFACTOR FILE NAME FOR SPECIES 2

Example Answer: RA228.SFC

The name of the S-factor file for the second radionuclide in the chain is then typed in, and so on, until the S-factor file name for the last radionuclide which contributes to dose has been given.

The user will then be asked to give the output file a name.

Computer: ENTER THE NAME OF A FILE TO RECEIVE INREM II INPUT
DATA FOR THIS CHAIN

Example Answer: TH232

The user would usually indicate the parent radionuclide name. Also, the user is asked to request or suppress a summary of the metabolic data compiled up to this point.

Computer: TYPE 1 FOR INPUT SUMMARY, 2 TO SUPPRESS

Example Answer: 1

From this point on the questions are about the specifics of route, duration, and magnitude of the exposure for which INREM-II calculates dose equivalents. Next, the user is asked:

Computer: ENTER THE NUMBER OF CASES FOR THIS RUN (1 TO 6, NO
DECIMAL)

Example Answer: 2

The total number of different exposure cases (both inhalation and ingestion) should be entered here. Assume for this example, the user indicates "2" for the number of cases. The user will then be prompted:

Question: ENTER THE INTAKE MODE FOR CASE (1) (G FOR INGESTION,
H FOR INHALATION) AND THE TIME (DAYS) FOR ENDING THE
INTEGRATION
MODE TIME
---- ----

Example Answer: H_1.825E+04

The user must indicate "G" or "H" as indicated followed by at least one space and then followed by the time for which the dose integration is to be carried out. This is usually 1.825×10^4 days (50 years) but any time period may be chosen.

Next the user is asked about the intake rate function. Information regarding the length and duration of the intake period is required.

Question: ENTER THE NUMBER OF TIME INTERVALS FOR THE INTAKE RATE FUNCTION

and

Question: FOR EACH OF THE (M) TIME INTERVALS, ENTER THE INTERVAL START TIME (DAYS) AND THE INTAKE RATE (MICROCURIES/DAY)

<u>INTERVAL START TIME</u>	<u>RATE</u>
----------------------------	-------------

The response to the second question depends upon the response to the previous question. Typically, one intake is used, but any number up to 30 "steps" may be used. The corresponding number of time intervals for one intake period is "2." The information required in answer to the second of these two questions is

Interval Starting Time	Rate
0.0	1.0
1.0	0.0

This means that from day "0" to day "1," the intake rate is 1.0 $\mu\text{Ci/day}$ and from day "1.0" to the end of the integration period (indicated previously) the intake rate is 0.0 $\mu\text{Ci/day}$. A second example is

Interval Starting Time	Rate
0.0	2.74×10^{-3}
365.0	0.0

This indicates that from day "0" to day "365," the intake is $2.74 \times 10^3 \mu\text{Ci/day}$ ($1/365 \mu\text{Ci/d}$), and from day 365 to the end of the integration period the intake rate is 0.0 $\mu\text{Ci/day}$.

If "H" was given in answer to the question about the intake mode indicating that the mode of exposure for the current case is inhalation, the user will be prompted by the following questions.

Question: ENTER PARTICLE SIZE (MICROMETER) FOR CASE (M)

Question: ENTER DE OR SP RESPECTIVELY, FOR DEFAULT OR SPECIAL LUNG PARAMETERS FOR (*RADIONUCLIDE NAME*)

Question: ENTER THE SOLUBILITY CLASS (D,W,Y) FOR (*RADIONUCLIDE NAME*) (This prompt will be printed, if "DE" was indicated in the previous question.)

Question: SPECIAL LUNG PARAMETERS FOR (*RADIONUCLIDE NAME*) FOR EACH OF THE 9 PATHWAYS A-I, ENTER THE BIOLOGICAL HALF-TIME (DAY) AND THE COMPARTMENTAL FRACTION BIOLOGICAL HALF-TIME COMPARTMENTAL FRACTION (This prompt will be printed if "SP" was indicated above.)

Question: FOR EACH OF THE *N* SPECIES OF THIS CHAIN, ENTER THE UPTAKE FRACTION f_1 (SEPARATE NUMBERS BY COMMAS OR BLANKS)

Question: ENTER 1 TO RETURN TO BEGINNING OF CASE (*M*) FOR MAKING CORRECTIONS, 2 TO CONTINUE

The user may indicate any particle size (AMAD = Activity Median Aerosol Diameter) in the range of 0.1 to 20 microns in response to the first of these six questions. If default (DE) lung parameters are indicated in the next question, the International Commission on Radiological Protection (ICRP) Task Group on Lung Dynamics lung clearance parameters (Morrow et al., 1966; ICRP, 1979) will be assumed. The user will then be prompted to indicate the solubility class of the species being considered. If special (SP) lung parameters were indicated in response to the previous question, the user will be asked to type in 9 compartment fractions and 9 biological half-times for the nine lung removal pathways as defined in the Task Group Lung Model (Morrow et al., 1966; ICRP, 1979). These special lung parameters are usually specified, for example, for gaseous radionuclides. Typical values for these special lung parameters are documented and discussed in Table A13 of Appendix A. The next question asks for the gastrointestinal uptake fraction, f_1 , for each of the radionuclides in the chain. These values are clearly part of radionuclide specific metabolic data, but since f_1 may vary with solubility class, they are not included in the metabolic data files. A reference table for suggested f_1 values is provided in Table A14 of Appendix A. The next question allows the user to return to the beginning of the case being considered to correct any typing errors that may have occurred.

If "G" was given in answer to the question about the intake mode indicating that the mode of exposure for the current case is ingestion, the user will be prompted by the following questions.

Question: ENTER THE NUMBER OF TIME INTERVALS FOR THE INTAKE RATE FUNCTION

Question: FOR EACH OF THE M TIME INTERVALS, ENTER THE INTERVAL START TIME (DAYS) AND THE INTAKE RATE (MICROCURIES/DAY)

<u>INTERVAL START TIME</u>	<u>RATE</u>
----------------------------	-------------

Question: FOR EACH OF THE N SPECIES OF THE SUBCHAIN, ENTER THE UPTAKE FRACTION F_1 (SEPARATE NUMBERS BY COMMAS OR BLANKS)

Question: ENTER 1 TO RETURN TO BEGINNING OF CASE (M) FOR MAKING CORRECTIONS, 2 TO CONTINUE

The responses to these questions are the same as indicated previously. The user will then be prompted to give any comments regarding the INREM-II input file.

Question: IF COMMENTS REGARDING THIS CHAIN ARE TO BE PRINTED, ENTER THEM. FOLLOWING THE LAST COMMENT LINE, ENTER A DOLLAR SIGN IN COLUMN 1 OF THE NEXT LINE

The user may include any notes regarding the file preparation that may be appropriate such as preparer's name, preparation date, special data used, etc. To end the comment the user must carriage return, then type a dollar sign (\$) in column "1" and then carriage return again.

A file with the name indicated by the user with the extension .DAT will then be created in the PDP-10 user area.

1.4 INREM-II Job Submission

The following job control language can be used to submit the data file to INREM-II for execution using the IBM system job control language (JCL). The file named INREM.SUB is stored on a DECTAPE (D4884) as indicated in Appendix A. There are several unique features to this submission file named INREM.SUB which are discussed below.

```

//UIDNNN JOB (MMMMM) X-10 LOCATION
/*ROUTE_ PUNCH LOCAL
/*ROUTE_ PRINT LOCAL OR REMOTENN
/*CLASS CPU91=IM,I0=2,LINES=10
//EXEC FORTH CLG,PARM.GO=EU=-1,REGION.GO=270K
//LKED.INREM2 DD DSN=T.GGK06944.INR4.DISP=(SHR.KEEP),UNIT=SPDA
//LKED.STEPIN DD DSN=T.GGK06944.STEP4,DISP=(SHR,KEEP),UNIT=SPDA
//LKED.SYSIN DD *
INCLUDE INREM2
INCLUDE STEPIN
/*
//GO.FT06F001 DD SYSOUT=A,
//      DCB=(RECFM=YBA,LRECL=137,BLKSIZE=1100)
//GO.FT16F001 DD SYSOUT=A,
//      DCB=(RECFM=YBA,LRECL=137,BLKSIZE=1100)
//GO.FT07F001 DD SYSOUT=B
//GO.FT05F001 DD *
=RNAME.DAT
//
ENDINPUT

```

The user identification code UIDNNN, the charge number MMMMM, and the location on the job card must be defined by the user. The user must also change (using TECO, EDITS, or any of the PDP-10 editing codes) the data file name RNAME.DAT to the PREREM output file name discussed in Sect. 4. If the user has created more than one data file for submission to INREM-II, the user can submit them all at once by adding them to the data set list as follows:

```

//GO.FT05F001 DD *
=RNAME1.DAT
=RNAME2.DAT
=RNAME3.DAT
=etc.
//

```

The INREM output will be placed in output location indicated on the ROUTE_ PRINT card.

PREREM: An Interactive Data Preprocessing Code for INREM-II
Part II. Code Structure

D. E. Fields, M. T. Ryan, D. E. Dunning, Jr., and J. C. Pleasant

2.1 Subroutine Structure

The subroutine structure of PREREM is outlined in Fig. 1. The Main Program orders the flow of control. It also prompts for and accepts much of the user input. If the user chooses to use metabolic data from a source other than data files, then prompts are printed from the Main Program. Nearly all of the data initialization is performed here.

Subroutine CHAIN, called by the Main Program, structures the nuclear decay chain algorithms. When given the name of a parent radionuclide, CHAIN repeatedly searches a nuclear data base (accessed as logical unit 8) for elements of the decay chain. The data base consists of card images, one for each isotope, containing isotope name, half-life, daughter radionuclides, and the branching fractions to each daughter. These data are returned to the Main Program.

Subroutine FIND, called by CHAIN, performs the search on the radionuclide data base for the parent radionuclide card image. When this record is located, FIND stores the data in arrays and prints parent and daughter names at the user's terminal to keep him apprised of program progress. If the record is not found in the data base, a message to this effect is printed at the user's terminal. The format of this message is "(parent name) IS AN INVALID NAME." This prompt will most likely result from an incorrect entry of the parent radionuclide name. As explained in the user's manual, this name must be specified as the chemical symbol followed by the nuclide mass number, separated by a hyphen.

Subroutine NMOVE is called by CHAIN, and itself calls CDAYS. Its purpose is to compute certain radionuclide indices used in the Main Program and to determine elements of array BR. These elements specify the branches of the decay chain. Values of the elements are the branching fractions for transitions between nuclides.

Subroutine CDAYS is called by NMOVE. CDAYS converts half-life values, which may have been specified in the nuclide data file in units of either years, days, hours, minutes, or seconds, to units of days.

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Fig. 1 Subroutine structure of PREREM code.

Subroutine PEEK is called from CHAIN. PEEK takes the next nuclide name to be searched for from the last in/first out stack ISTK. This stack is written onto by POKE.

Subroutine POKE, called from CHAIN, writes values of nuclide names and branching fractions onto vectors ISTK and FSTK. These vectors are used as last in/first out stacks by subroutines PEEK and POKE.

Subroutines PEEK and POKE perform tests on values of array indices computed therein. Should future modifications to the radio-nuclide data set (logical unit 8) lead to decay chains of uncondensed length greater than the size of the stack vectors IDAU and FDAU, error messages will be printed. The "uncondensed length" of the chain may be greater than the number of radionuclides because of the manner in which daughters are referenced by the code. Messages printed by PEEK and POKE are, respectively, "ATTEMPT TO PEEK OUTSIDE STACK BOUNDS" and "ATTEMPT TO POKE VALUE INTO FULL STACK." These messages indicate the need to redimension program arrays. We do not anticipate that the need for this user response will occur.

Subroutine IFILE is a DEC PDP-10 system subprogram, called from the Main Program, that assigns a specified PDP-10 file name to a given logical unit number for data input. This subprogram is called several times for various metabolic and S-factor input files.

Subroutine META is called from the Main Program. META reads metabolic data files specified in the Main Program, using formats similar to those used for writing metabolic data in PREREM output. If the file specified by the user is not the correct file for the next nuclide in the chain, the message "DAUGHTER RADIONUCLIDE NAME NOT FOUND" or "PARENT RADIONUCLIDE NAME NOT FOUND" is printed at the user's terminal. These messages alert the user to an incomplete nuclear data file.

Subroutine OFILE is a DEC PDP-10 system subprogram called from the Main Program. OFILE assigns a PDP-10 file name specified by the user to a logical unit number. The unit number is referenced in PREREM for data input.

Subroutine SUMMRY is called from the Main Program. Its purpose is to print a summary nuclear and metabolic data file for user inspection. This file summarizes data provided in an interactive user mode so the user may check the values.

Subroutine SURCH, called from the Main Program, receives a vector, NARR, containing radionuclide or organ names, from the Main Program. It also receives a number N, and a name, NAM. The vector is searched for a name agreeing with NAM, and if this value is found, the index IND is returned. Only the first N elements of the vector are searched. If the name being searched for is not found, the message "ERROR..SURCH FAILED TO FIND NAME (name)" is output to the user's terminal.

Subroutine NAME, along with subroutine CHECK, takes a user specified radionuclide abbreviation and mass number and tests it against the element name in the metabolic data file. The radionuclide is separated into individual characters and recombines them into a string that does not contain the mass number or any blanks. Next, the element names contained in the metabolic file are stored as variable IBNAME and run through the same decoding and recombination process used above. The two results are then compared. If the two strings (one in INNAME and the other in KNAME) match, then the subroutine returns to its calling location and processing continues normally. If the strings do not match, then control is transferred to an error message subroutine and processing halts.

DECODE and ENCODE are system utility programs invoked by statements in FORTRAN-10 that allow formatted transfers of information within a program (Digital Equipment Corporation, 1977). The DECODE statement is analogous to a READ statement in normal I/O and the ENCODE is analogous to a WRITE statement. However, there are several differences. The DECODE and ENCODE have built-in iterative capability. For example, DECODE (10, 100, NAMNUC(I)) IBUF reads what is in NAMUNC(I) according to the format given at statement 100 and puts that information into IBUF (which is an array dimensioned to hold 10 double precision computer words). Suppose the statement repeats itself 10 times. If the format is 10A1, the first character in NAMNUC(I) is put into IBUF(1), the second character is put into IBUF(2), and so on. The

PDP-10 word length for single precision variables is 5 characters. This is extended to 10 characters for double precision variables, hence the array IBUF is dimensioned to 10, the number of characters in the ENCODE and DECODE statements is 10, and the formats are 10A1.

2.2 Functional Description of PREREM Main Program

Figure 2 consists of a condensed version of the flow diagram for the PREREM Main Program. At this level of function resolution, the flow of control is basically linear. The major departure from linearity arises from the user's need to examine and perhaps to alter metabolic data that had been incorrectly entered. The user might also need to update values entered from an old metabolic data file. All user input is received by the Main Program.

PREREM output is from the Main Program and from subroutines CHAIN, SURCH, SUMMRY, META, FIND, PEEK, and POKE. Much of this output, however, consists of error messages and explanatory notes—if execution proceeds normally, the user will receive output from the Main Program and subroutines CHAIN and SUMMRY.

2.3 Data Requirements

Data input for the PREREM code is either via the user's keyboard or from standard data files that have been previously prepared. These files are of three basic types: metabolic, S-factor, and radionuclide decay. The spatial requirement for the nuclear decay data file, DECAY.DAT is 494 card images (64 blocks). Metabolic data may be input either interactively or by specifying file names of metabolic data files, for radionuclides of interest, as prompted by the code. Each metabolic file is approximately 25 card images. The user may at this point in program execution request a summary data file for study and possible modification, or he may specify an S-factor data file which contains 66 card images. S-factors may not be input interactively.

Fig. 2. Function diagram of PREREM.

2.4 Code Listing

A FORTRAN listing of the PREREM code is given in Table 8. The Main Program is listed first, followed by the subroutines in alphabetical order. Subprograms IFILE, OFILE, ENCODE, AND DECODE are PDP-10 utility programs (Digital Equipment Corporation, 1977) and are not included in this table.

Table 8. FORTRAN listing of the computer code PREREM

```

C PREREM. CONVERSATIONAL INPUT PROGRAM FOR INPEM II PRE 0
C REVISED 10/79-2/80 PRE 5
C BY D.E. FIELDS & M.T. RYAN PRE 10
C TO DETERMINE RADIONUCLIDE CHAIN AND OPTIONALLY PRE 15
C READ METABOLIC DATA FILE PRE 20
C PRE 25
C PRE 30
C THIS PROGRAM ASSISTS THE USER OF THE INPEM II CODE IN THE PREPARATION PRE 35
C OF INPUT DATA. IN ORDER TO PREPARE INPUT DATA FOR A GIVEN NUCLIDE CHA PRE 40
C THE USER MUST SUPPLY THE PHYSICAL AND METABOLIC DATA FOR EACH SPECIES PRE 45
C IN THE CHAIN AS WELL AS SOURCE AND TARGET INFORMATION. THIS PROGRAM PRE 50
C READS THIS INFORMATION AND THEN PREPARES INPUT DATA FOR ANY SUBCHAI PRE 55
C (INCLUDING THE ENTIRE CHAIN) WHICH THE USER SPECIFIES. PRE 60
C PRE 65
C DOUBLE PRECISION NAMNUC(25),NAMSOU(22),NAMTRG(24),NAMDAU,NAMT, PRE 70
C 1 NAMS,NMTRG(24),NMSOU(22),NAM1,NAM2,NAM3,NAM4,LTNE(8),NAMOTH, PRE 75
C 1 INFIL,IPARF,IDAUF,OUFIL PRE 80
C INTEGER OUT PRE 85
C COMMON NAMNUC,NSPEC,TR,NAMSOJ,NS,SMASS,NT,TMASS,NAMTRG, BRANCH, PRE 90
C 1 F2PRIM,C,TB,NC,ISOP,ITAR PRE 95
C COMMON NSI,NSOI,OMASS,F2EXC PRE 100
C DIMENSION BRANCH(25,25),TR(25),NDAU(25),F2PRIM(25,16), TR(25,5,15) PRE 105
C 1 ,C(25,5,16),N(25),SFAC(25,24,22),SMASS(24),TMASS(24), NC(25,15), PRE 110
C 1 MODE(6),TEND(6),T(6,30),P(6,30),TBLUNG(9,25), FLUNG(9,25), PRE 115
C 1 ISOL(25),SFAC(25,24,22),FI(25),PAR(25),ISOR(22), ITAR(24), PRE 120
C 1 MSOP(22),F2EXC(25),KSOL(3),CORRED(25), COREND(25),CANRED(25), PRE 125
C 1 CANEND(25),SURVOL(25) PRE 130
C LOGICAL CK(25) PRE 135
C PRE 140
C THE FOLLOWING QUANTITIES ARE MASSES (G) OF THE PRE 145
C PRE 150
C SOURCE ORGANS.. LUNGS, RES LYM, S CONT, SI CONT, PRE 155
C ULI CONT, LLI CONT PRE 160
C PRE 165
C TARGET ORGANS.. LUNGS, RES LYM, S WALL, SI WALL, PRE 170
C ULI WALL, AND LLI WALL PRE 175
C PRE 180
C PRE 185
C DATA SMASS/14.0,200.0,250.0,400.0,220.0,135.0,310.0,1800.0, PRE 190
C 1 1000.0,15.0,28000.0,11.0,100.0,4000.0,1000.0,1500.0, 1500.0, PRE 195
C 1 2600.0,180.0,35.0,20.0,70000.0,10000.0,5000.0/, TMASS/14.0,45.0, PRE 200
C 1 150.0,640.0,210.0,160.0,310.0,1800.0,1000.0, 15.0,28000.0,11.0, PRE 205
C 1 100.0,5000.0,1500.0,1500.0,2000.0, 2600.0,180.0,35.0,20.0,20.0, PRE 210
C 1 80.0,70000.0/ PRE 215
C PRE 220
C THE NAMES OF THESE SPECIAL SOURCE AND TARGET ORGANS ARE PRE 225
C INITIALIZED NEXT. PRE 230
C DATA NAMSOU/10HLUNGS ,10HPES LYM ,10HS CNT , PRE 235
C 1 10HSI CNT , 10HULI CNT ,10HLLI CNT ,16*10H /, PRE 240
C 1 NAMTRG/10HLUNGS ,10HPES LYM ,10HS WALL , 10HSI WALL , PRE 245
C 1 10HULI WALL ,10HLLI WALL , 10HT BODY ,10HADREN , PRE 250
C 1 10HBL WALL ,10HKIDNEYS , 10HLIVER ,10HVARIES , PRE 255
C 1 10HPANCREAS ,10HBONE , 10HP MAP ,10HY MAP , PRE 260
C 1 10HENDOST ,10HSPLEEN , 10HTESTES ,10HTYMUS , PRE 265
C 1 10HTHYROID ,10HUTERUS , 2*10H / PRE 270
C PRE 275
C THE NAMES OF ALL SOURCE AND TARGET ORGANS FOR WHICH SFAC PRODUCES PRE 280
C S FACTORS AS INPUT TO THIS PROGRAM ARE AS FOLLOWS.. PRE 285
C PRE 290
C PRE 295
C DATA NMSOU/10HADREN ,10HBL CNT ,10HS CNT , PRE 300
C 1 10HSI CNT ,10HULI CNT ,10HLLI CNT ,10HKIDNEYS , PRE 305
C 1 10HLIVER ,10HLUNGS ,10HPES LYM ,10HMUSCLE , PRE 310

```

Table 8 (continued)

```

1 IOHOVARIES , IOHPANCREAS , IOHCOR BONE , IOHCAN BONE , PRE 315
1 IOHR MAR , IOHY MAR , IOHSKIN , IOHSPLEEN , PRE 320
1 IOHTESTES , IOHTHYPOID , IOHABSORBED / PRE 325
DATA NMTRG/IOHADPEN , IOHBL WALL , IOHS WALL , PRE 330
1 IOHST WALL , IOHULT WALL , IOHLLT WALL , IOHKIDNEYS , PRE 335
1 IOHLIVER , IOHLUNGS , IOHPES LYM , IOHMUSCLE , PRE 340
1 IOHOVARIES , IOHPANCREAS , IOHPONE , IOH2 MAR , PRE 345
1 IOHY MAR , IOHENDOST , IOHSKIN , IOHSPLEEN , PRE 350
1 IOHTESTES , IOHTHYMUS , IOHTHYROID , IOHUTERUS , PRE 355
1 IOHT BODY / PRE 360
DATA NAMOTH/IOHOTHER / PRE 365
DATA OUT/20/, INP/21/,Y/'Y'/ PRE 370
DATA KSQL/'D', 'W', 'Y'/ PRE 375
C PRE 380
CALL IFILE(8, 'DECAY.DAT') PRE 385
C DIALOGUE PHASE 1.. READ(6,S SOURCE AND TARGET INFORMATION AND PHYSICAL PRE 390
C METABOLIC DATA FOR EACH SPECIES IN THE CHAIN PRE 395
C PRE 400
C ----- PRE 405
NT=16 PRE 410
NTRG=NT+6 PRE 415
WRITE(6,10300) PRE 420
C PRE 425
C INPUT NUMBER OF SPECIES IN CHAIN PRE 430
C PRE 435
10 WRITE(6,10400) PRE 440
READ(6,10500)NAMNUC(1) PRE 445
C PRE 450
DO 20 ISPEC=1,25 PRE 455
DO 20 JSPEC=1,25 PRE 460
20 BRANCH(ISPEC,JSPEC)=0.0 PRE 465
C PRE 470
C COMPUTE AND SET DECAY CHAIN PARAMETERS PRE 475
C PRE 480
CALL CHAIN(INDAU) PRE 485
C PRE 490
WRITE(6,10000) PRE 495
READ(6,10100)NSPEC PRE 500
MSPEC=NSPEC PRE 505
C INITIALIZE METABOLIC DATA PRE 510
30 WRITE(6,10700) PRE 515
READ(6,10800)Q PRE 520
IF (Q.NE.Y) GO TO 50 PRE 525
WRITE(6,10900) PRE 530
READ(6,11000) IPARF PRE 535
CALL IFILE(22,IPARF) PRE 540
ISPE=1 PRE 545
KSPE=ISPE PRE 550
CALL META(NMSOU,NSOU,IEXCRT,KSPE) PRE 555
KEXCRT=IEXCRT PRE 560
IF (NSPEC.EQ.1) GO TO 40 PRE 565
DO 40 ISPE=2,NSPEC PRE 570
WRITE(6,11100)ISPE PRE 575
READ(6,11000) IDAUF PRE 580
CALL IFILE(23,IDAUF) PRE 585
C PRE 590
C PRE 595
C READ METABOLIC DATA FILE PRE 600
KSPE=ISPE PRE 605
CALL META(NMSOU,NSOU,IEXCRT,KSPE) PRE 610
IEXCRT=KEXCRT PRE 615
40 CONTINUE PRE 620
C PRE 625

```

Table 8 (continued)

C	JUMP TO S FACTOR INPUT	PRE 630
	GO TO 70	PRE 635
	50 CONTINUE	PRE 640
C		PRE 645
C		PRE 650
C	INPUT NUMBER OF SOURCES OTHER THAN LUNGS, RES LYM, S CONT, ULI CONT,	PRE 655
C	AND LLI CONT.	PRE 660
C		PRE 665
	60 WRITE(6,11200)	PRE 670
	READ(6,11300)ANS	PRE 675
	NS=ANS	PRE 680
C	NSOU IS THE NUMBER OF SOURCES INCLUDING LUNGS AND G.I. TRACT	PRE 685
	NSOU=NS+6	PRE 690
C		PRE 695
C	INPUT THE NAMES OF THESE SOURCES.	PRE 700
C		PRE 705
	WRITE(6,11400)NS	PRE 710
	READ(6,11500)(NAMSOU(IS+6),IS=1,NS)	PRE 715
	WRITE(6,11600)	PRE 720
	READ(6,10600)IEXCRT	PRE 725
C		PRE 730
C		PRE 735
C		PRE 740
C		PRE 745
C	OPEN FILE CONTAINING S FACTORS	PRE 750
C		PRE 755
	70 CONTINUE	PRE 760
C		PRE 765
C		PRE 770
C		PRE 775
C	FOR EACH SPECIES IN THE CHAIN, INPUT METABOLIC DATA FOR ORGANS OTHER	PRE 780
C	THAN RESPIRATORY OR G.I. TRACT AND THEN INPUT S FACTORS.	PRE 785
	DO 220 ISPEC=1,NSPEC	PRE 790
	WRITE(6,12400)ISPEC	PRE 795
	READ(6,12500)INFIL	PRE 800
	CALL IFILE(21,INFIL)	PRE 805
	IF (Q.EQ.Y) GO TO 100	PRE 810
C		PRE 815
C		PRE 820
C	FOR EACH SOURCE OTHER THAN LUNGS AND	PRE 825
C	G.I. TRACT, INPUT BLOOD TRANSFER FRACTIONS (F2-PRIME), COMPARTMENT	PRE 830
C	DEPOSITION FRACTIONS, AND COMPARTMENT BIOLOGICAL HALF-TIMES (DAY)	PRE 835
C		PRE 840
	80 NSOU1=NSOU + 1	PRE 845
	NS1=NS + 1	PRE 850
	NAMSOU(NSOU1)=NAMOTH	PRE 855
	DO 90 IS=1,NS1	PRE 860
	ISOU=IS+6	PRE 865
	WRITE(6,11900) NAMNUC(ISPEC),NAMSOU(ISOU)	PRE 870
	READ(6,15600)F2PRIME(ISPEC,IS)	PRE 875
	WRITE(6,12000)	PRE 880
	READ(6,10600) NC(ISPEC,IS)	PRE 885
	WRITE(6,12100) NC(ISPEC,IS)	PRE 890
	NCMP=NC(ISPEC,IS)	PRE 895
	READ(6,12200) (C(ISPEC,IC,IS),TB(ISPEC,IC,IS),IC=1,NCMP)	PRE 900
	CONTINUE	PRE 905
90	F2EXC(ISPEC)=0.0	PRE 910
	IF (IEXCRT.NE.2) GO TO 100	PRE 915
	IF (ISPEC.GT.1) GO TO 100	PRE 920
	WRITE(6,12300) NAMNUC(ISPEC)	PRE 925
	READ(6,15600)F2EXC(ISPEC)	PRE 930
100	CONTINUE	PRE 935
C		PRE 940

Table 8 (continued)

```

C READ S FACTORS FOR SPECIES ISPEC (22 SOURCES, 24 TARGETS).
C
      READ(INP,12600)ICARD
      DO 110 JTRG=1,24
110      READ(INP,12700) (SFAC(ISPEC,JTRG,JSOU),JSOU=1,22)
      READ(INP,12900) CORRED(ISPEC),COREND(ISPEC),CANRED(ISPEC),
1      CANEND(ISPEC),SURVOL(ISPEC)
      CK(ISPEC)=(CORRED(ISPEC).EQ.0.).AND.(COREND(ISPEC).EQ.0.).
1      AND.(CANRED(ISPEC).EQ.0.).AND.(CANEND(ISPEC).EQ.0.)
      IF(CK(ISPEC))GO TO 101
      IF(SURVOL(1).EQ.1.)GO TO 101
      SFAC(ISPEC,15,14)=CORRED(ISPEC)
      SFAC(ISPEC,17,14)=COREND(ISPEC)
      SFAC(ISPEC,15,15)=CANRED(ISPEC)
      SFAC(ISPEC,17,15)=CANEND(ISPEC)
101      CONTINUE
C
C SELECT A SUBMATRIX SFAC OF THE MATRIX SFAC WHICH CONTAINS ENTRIES
C FOR THE CURRENT SOURCES AND TARGETS ONLY.
C
      DO 140 ITRG=1,MTPG
      DO 140 ISOU=1,NSOU
        NAMT=NAMTRG(ITRG)
        NAMS=NAMSOU(ISOU)
C
        IF (NAMS.EQ.'SKEL' )I ISOR(ISOU)=23
        IF (NAMS.EQ.'SKEL' )I GO TO 120
        IF (NAMS.EQ.'BONE' )I ISOR(ISOU)=24
        IF (NAMS.EQ.'BONE' )I GO TO 130
C SEARCH THE ARRAY NMTRG AND RETURN THE INDEX ITAR OF THE TARGET NAMT
        CALL SURCH(NMTRG,24,NAMT,ITAR(ITRG))
C SEARCH THE ARRAY NMSOU AND RETURN THE INDEX ISOR OF THE NAME NAMS.
        CALL SURCH(NMSOU,22,NAMS,ISOR(ISOU))
C DEFINE SFAC
        SFAC(ISPEC,ITRG,ISOU)=SFAC(ISPEC,ITAR(ITRG),ISOR(ISOU))
        GO TO 140
C IF SOURCE IS SKEL, CALCULATE S FACTORS FROM THOSE FOR COR BONE,
C CAN BONE, R MAR, AND Y MAR AS FOLLOWS (EQ. 30, ORNL 5000)..
120      NAM1='COR BONE'
        NAM2='CAN BONE'
        NAM3='R MAR'
        NAM4='Y MAR'
        CALL SURCH(NMSOU,22,NAM1,ISOR1)
        CALL SURCH(NMSOU,22,NAM2,ISOR2)
        CALL SURCH(NMSOU,22,NAM3,ISOR3)
        CALL SURCH(NMSOU,22,NAM4,ISOR4)
C SINCE THE FOUR TISSUES COR BONE,CAN BONE, R MAR, AND Y MAR DO NOT
C ACCOUNT FOR TOTAL SKELETON, THE COEFFICIENTS IN THE FOLLOWING
C EQUATION HAVE BEEN ADJUSTED BY MULTIPLYING EACH BY 10/8 (8/10
C IS THE RATIO OF THE SUM OF THE MASSES OF THESE FOUR TISSUES
C TO THE MASS OF SKELETON), THUS THESE COEFFICIENTS ARE 10/8 TIMES
C MASS(COR BONE)/M, MASS(CAN BONE)/M, MASS(R MAR)/M,AND
C MASS(Y MAR)/M RESPECTIVELY, WHERE M=MASS(SKEL).
        SFAC(ISPEC,ITRG,ISOU)=.5*SFAC(ISPEC,ITAR(ITRG),ISOR1) +
1      .125*SFAC(ISPEC,ITAR(ITRG),ISOR2) + .1875*SFAC(ISPEC,
1      ITAR(ITRG),ISOR3) +.1875*SFAC(ISPEC,ITAR(ITRG),ISOR4)
        GO TO 140
C IF SOURCE IS BONE, CALCULATE S FACTORS FROM THOSE FOR COR BONE,
C AND CAN BONE.
130      NAM1='COR BONE'
        NAM2='CAN BONE'
        CALL SURCH(NMSOU,22,NAM1,ISOR5)
        CALL SURCH(NMSOU,22,NAM2,ISOR6)

```

Table 8 (continued)

```

          SFAC(IISPEC,ITRG,ISOU)=0.8*SFAC(IISPEC,ITAR(ITRG),ISOR5) + PRE1260
1          0.2*SFAC(IISPEC,ITAR(ITRG),ISOR6) PRE1265
C          IF (NAMT.EQ.'R MAR' .AND. SUPV7L(1).EQ.1.0) PRE1270
C          SFAC(IISPEC,ITRG,ISOU)=0.5 * SFAC(IISPEC,ITAR(ITRG), PRE1275
C          ISOR5) + 0.5 * SFAC(IISPEC,ITAR(ITRG),ISOR6) PRE1280
140      CONTINUE PRE1285
C GENERATE AN INDEX MSOR FOR THOSE ORGANS NOT GIVEN AS SPECIFIC SOURCE PRE1290
C ORGANS. A COMPOSITE S-FACTOR IS GENERATED FOR THESE COMPLIMENTARY PRE1295
C TISSUES, CLASSIFIED AS 'OTHER' IN INREM II. PRE1300
      INDEXO=0 PRE1305
      DO 180 ISOU=1,22 PRE1310
        DO 170 I=1,NSOU PRE1315
          IF (NAMSOU(I).NE.'SKEL' .) GO TO 150 PRE1320
          IF (NMSOU(ISOU).EQ.'COR BONE' .OR.NMSOU(ISOU) PRE1325
1          .EQ.'CAN BONE' .OR.NMSOU(ISOU) PRE1330
1          .EQ.'R MAR' .OR.NMSOU(ISOU).EQ.'Y MAR' .) GO TO PRE1335
1          180 PRE1340
          GO TO 170 PRE1345
150      IF (NAMSOU(I).NE.'BONE' .) GO TO 160 PRE1350
          IF (NMSOU(ISOU).EQ.'COR BONE' .OR.NMSOU(ISOU) PRE1355
1          .EQ.'CAN BONE' .) GO TO 180 PRE1360
          GO TO 170 PRE1365
160      IF (ISOU.EQ.ISOP(I)) GO TO 180 PRE1370
170      CONTINUE PRE1375
          INDEXO=INDEXO + 1 PRE1380
          MSOR(INDEXO)=ISOU PRE1385
180      CONTINUE PRE1390
C CALCULATE COMPOSITE MASS OF 'OTHER' SOURCE ORGAN COMPLIMENT. PRE1395
      OMASS=0.0 PRE1400
      DO 190 JM=1,INDEXO PRE1405
        OMASS=OMASS + SMASS(MSOR(JM)) PRE1410
190      CONTINUE PRE1415
C CALCULATE S-FACTORS FOR EACH TARGET FROM 'OTHER'. PRE1420
      NSOU1=NSOU +1 PRE1425
      DO 210 ITRG=1,NTRG PRE1430
        SFAC(IISPEC,ITRG,NSOU1)=0.0 PRE1435
        DO 200 ISOU=1,INDEXO PRE1440
          SFAC(IISPEC,ITRG,NSOU1)=SFAC(IISPEC,ITRG,NSOU1) + PRE1445
1          SFAC(IISPEC,ITAR(ITRG),NSOU1) *SMASS(MSOR(ISOU))/ PRE1450
1          OMASS PRE1455
200      CONTINUE PRE1460
          IF (ITAR(ITRG).EQ.21.OR.ITAR(ITRG).EQ.23) SFAC(IISPEC,ITRG, PRE1465
1          NSOU1)= SFAC(IISPEC,ITAR(ITRG),22)*SMASS(22)/OMASS PRE1470
210      CONTINUE PRE1475
C PRE1480
C END ISPEC LOOP PRE1485
220      CONTINUE PRE1490
C PRE1495
C OPEN FILE TO RECEIVE INREM II INPUT DATA. PRE1500
C PRE1505
      WRITE(6,13000) PRE1510
      READ(6,12500)OUFIL PRE1515
      CALL OFILE(20,OUFIL) PRE1520
C DOES USER WANT A SUMMARY OF INPUTS? PRE1525
230 WRITE(6,13100) PRE1530
      READ(6,10600)IANS PRE1535
      IF (IANS.EQ.2) GO TO 260 PRE1540
      IF (IANS.EQ.1) GO TO 240 PRE1545
      WRITE(6,13200) PRE1550
      GO TO 230 PRE1555
240 CALL SUMMRY PRE1560
250 WRITE(6,13300) PRE1565
      READ(6,10600)IANS PRE1570

```

Table 8 (continued)

IF (IANS.EQ.2) GO TO 260	PRE1575
IF (IANS.EQ.1) GO TO 30	PRE1580
WRITE(6,13400)	PRE1585
GO TO 250	PRE1590
C	PRE1595
C	PRE1600
C-----	PRE1605
C INPUT NUMBER OF SPECIES IN THE SUBCHAIN.	PRE1610
C	PRE1615
260 DO 270 ISPEC=1,MSPEC	PRE1620
N(ISPEC)=ISPEC	PRE1625
270 CONTINUE	PRE1630
C	PRE1635
C OUTPUT PHASE .. WRITES INREM II INPUT DATA FOR THE CURRENT SUBCHAIN	PRE1640
C	PRE1645
WRITE(OUT,13600)MSPEC	PRE1650
C WRITE NAMES OF NUCLIDES	PRE1655
DO 280 ISPEC=1,MSPEC	PRE1660
NISPEC=N(ISPEC)	PRE1665
WRITE(OUT,13700) NAMNUC(NISPEC),TR(NISPEC)	PRE1670
280 CONTINUE	PRE1675
C IF NUMBER OF SPECIES IN SUBCHAIN IS 1, SKIP BRANCHING RATIOS SEGMENT	PRE1680
IF (MSPEC.EQ.1) GO TO 310	PRE1685
C CALCULATE NUMBER OF NONZERO BRANCHING RATIOS (NBRA)	PRE1690
NBRA=0	PRE1695
DO 290 ISPEC=1,MSPEC	PRE1700
DO 290 JSPEC=1,MSPEC	
NISPEC=N(ISPEC)	PRE1705
NJSPEC=N(JSPEC)	
BRA=BRANCH(NJSPEC,NISPEC)	
IF (BRA.NE.0.0) NBRA=NBRA+1	
290 CONTINUE	PRE1715
C WRITE NUMBER OF NONZERO BRANCHING RATIOS	PRE1720
WRITE(OUT,13800) NBRA	PRE1725
C WRITE NONZERO BRANCHING RATIOS AND INDICES	PRE1730
DO 300 ISPEC=1,MSPEC	PRE1735
DO 300 JSPEC=1,MSPEC	PRE1740
NISPEC=N(ISPEC)	PRE1745
NJSPEC=N(JSPEC)	PRE1750
BRA=BRANCH(NJSPEC,NISPEC)	PRE1755
IF (BRA.NE.0.0) WRITE(OUT,13900) ISPEC,JSPEC,BRA	PRE1760
300 CONTINUE	PRE1765
C WRITE NUMBER OF SOURCES OTHER THAN LUNGS AND G.I. TRACT	PRE1770
310 IF (IEXCRT.NE.2) WRITE(OUT,14100) NS1	PRE1775
IF (IEXCRT.EQ.2) WRITE(OUT,14000) NS1	PRE1780
C FOR EACH SOURCE OTHER THAN LUNGS AND G.I. TRACT, WRITE ITS NAME AND MASS	PRE1785
WRITE(OUT,14200) (NAMSOU(IS+6),SMASS(ISOR(IS+6)),IS=1,NS1,	PRE1790
1 NAMSOU(NSOU1),OMASS	PRE1795
C WRITE NUMBER OF TARGETS OTHER THAN LUNGS AND G.I. TRACT	PRE1800
WRITE(OUT,14100) NT	PRE1805
C FOR EACH TARGET OTHER THAN LUNGS AND G.I. TRACT, WRITE	PRE1810
C ITS NAME AND MASS	PRE1815
WRITE(OUT,14200) (NAMTRG(IT+6),TMASS(ITAR(IT+6)),IT=1,NT)	PRE1820
C	PRE1825
C FOR EACH SPECIES IN THE SUBCHAIN, OUTPUT METABOLIC PARAMETERS	PRE1830
C FOR SOURCES OTHER THAN LUNGS AND G.I. TRACT	PRE1835
DO 340 ISPEC=1,MSPEC	PRE1840
DO 320 ISOU=1,NS1	PRE1845
C WRITE BLOOD TRANSFER FRACTION AND NUMBER OF COMPARTMENTS	PRE1850
WRITE(OUT,14300) F2PRIM(N(ISPEC),ISOU),NC(N(ISPEC),ISOU)	PRE1855
NCOM=NC(N(ISPEC),ISOU)	PRE1860
C FOR EACH COMPARTMENT, WRITE ITS DEPOSITION FRACTION AND BIO. HALF-TIME	PRE1865
WRITE(OUT,14400) (C(N(ISPEC),IC,ISOU),TB(N(ISPEC),IC,ISOU),	PRE1870

Table 8 (continued)

```

1      IC=1,NCOM)
      IF (IEXCRT.NE.2) GO TO 320
      IF (ISOU.GT.1) GO TO 320
      NCEXC=1
      CEXC=1.0
      TBEXC=0.5
      WRITE(OUT,14500) F2EXC(IISPEC),NCEXC,CEXC,TBEXC
320    CONTINUE
C WRITE S FACTORS FOR CURRENT SPECIES OF THE SURCHAIN
      DO 330 ITRG=1,NTRG
        WRITE(OUT,14600) (SFAC(I,N(IISPEC),ITRG,ISOU),ISOU=1,NSOU)
330    CONTINUE
C END ISPEC LOOP
340    CONTINUE
C
C CASE INFORMATION
C
350  WRITE(6,14700)
      READ(6,10600) NCASES
      WRITE(OUT,14800) NCASES
C FOR EACH CASE, DETERMINE THE INTAKE MODE AND THEN DETERMINE INFORMATION
C SPECIFIC TO THE MODE OF INTAKE
      DO 500 ICASE=1,NCASES
360    WRITE(6,14900) ICASE
        READ(6,15000) MODE(ICASE),TEND(ICASE)
C
C
C
C
C
C
C DETERMINE NUMBER OF TIME INTERVALS FOR INTAKE FUNCTION. THEN DETERMINE
C THE LEFT ENDPNTS OF THESE INTERVALS AND FUNCTION VALUES AT THESE POI
        WRITE(6,15100)
        READ(6,15200) NI
        WRITE(6,15300) NI
        READ(6,15400) (T(ICASE,INT),P(ICASE,INT),INT=1,NI)
C
C
C
C IF EXPOSURE MODE IS INGESTION, BRANCH AROUND LUNG PARAMETER SEGMENT
      IF (MODE(ICASE).EQ.'G' ) GO TO 440
C
C LUNG PARAMETERS
C
C
C
C
      WRITE(6,15500) ICASE
      READ(6,15600) AMAD
C FOR EACH SPECIES IN THE SURCHAIN, DETERMINE LUNG PARAMETERS.
370    DO 430 ISPEC=1,MSPEC
      NISPEC=N(IISPEC)
380    WRITE(6,15700) NAMNUC(NISPEC)
      READ(6,15800) PAR(NISPEC)
      IF (PAR(NISPEC).EQ.'SP' ) GO TO 420
      IF (PAR(NISPEC).EQ.'DE' ) GO TO 390
      GO TO 380
C DEFAULT LUNG PARAMETERS
390    WRITE(6,15900) NAMNUC(NISPEC)
400    READ(6,16000) ISOL(NISPEC)
      DO 410 I=1,3

```

```

PRE1875
PRE1880
PRE1885
PRE1890
PRE1895
PRE1900
PRE1905
PRE1910
PRE1915
PRE1920
PRE1925
PRE1930
PRE1935
PRE1940
PRE1945
PRE1950
PRE1955
PRE1960
PRE1965
PRE1970
PRE1975
PRE1980
PRE1985
PRE1990
PRE1995
PRE2000
PRE2005
PRE2010
PRE2015
PRE2020
PRE2025
PRE2030
PRE2035
PRE2040
PRE2045
PRE2050
PRE2055
PRE2060
PRE2065
PRE2070
PRE2075
PRE2080
PRE2085
PRE2090
PRE2095
PRE2100
PRE2105
PRE2110
PRE2115
PRE2120
PRE2125
PRE2130
PRE2135
PRE2140
PRE2145
PRE2150
PRE2155
PRE2160
PRE2165
PRE2170
PRE2175
PRE2180
PRE2185

```

Table 8 (continued)

```

      IF (ISOL(NISPEC).EQ.KSOL(1)) GO TO 430
410      CONTINUE
      WRITE(6,10200)
      GO TO 400
C SPECIAL LUNG PARAMETERS
420      WRITE(6,16100)NAMNJC(NISPEC)
      READ(6,16200)(TBLUNG(IPATH,NISPEC),FLUNG(IPATH,NISPEC),
      1      IPATH=1,9)
430      CONTINUE
C DETERMINE UPTAKE FRACTIONS F1 (G.I. TRACT TO BLOOD) FOR THIS CASE
440      WRITE(6,16300) MSPEC
      READ(6,16400) (F1(N(ISPEC)),ISPEC=1,MSPEC)
C ALLOW RETURN FOR CORRECTIONS
450      WRITE(6,16500) ICASE
      READ(6,10600) IANS
      IF (IANS.EQ.1) GO TO 360
      IF (IANS.EQ.2) GO TO 460
      GO TO 450
C WRITE CASE INFORMATION
460      WRITE(OUT,16600) MODE(ICASE),TEND(ICASE)
      WRITE(OUT,16700) NI
      WRITE(OUT,16800) (T(ICASE,INT),P(ICASE,INT),INT=1,NI)
C IF INHALATION, WRITE INHALATION PARAMETERS AND UPTAKE FRACTIONS
      IF (MODE(ICASE).EQ.'G ') GO TO 490
      WRITE(OUT,16900) AMAD
      DO 480 ISPEC=1,MSPEC
      NISPEC=N(ISPEC)
      IF (PAR(NISPEC).EQ.'DE ') GO TO 470
      WRITE(OUT,17000)
      WRITE(OUT,17100)(TBLUNG(IPATH,NISPEC),FLUNG(IPATH,NISPEC),
      1      IPATH=1,9)
      WRITE(OUT,17200) F1(NISPEC)
      GO TO 480
470      WRITE(OUT,17300) ISOL(NISPEC),F1(NISPEC)
480      CONTINUE
      GO TO 500
C WRITE UPTAKE FRACTIONS (INGESTION CASE)
490      WRITE(OUT,17400)(F1(NISPEC)),ISPEC=1,MSPEC)
500      CONTINUE
C END CASE LOOP
C
C
C READ(6, COMMENTS
      WRITE(6,17500)
      DO 520 I=1,1000
      KOL1=' '
      DO 510 J=1,8
      LINE(J)=' '
510      CONTINUE
      READ(6,17600) KOL1,LINE
      IF (KOL1.EQ.'S ') GO TO 530
      WRITE(OUT,17700)KOL1,LINE
520      CONTINUE
530      WRITE(OUT,17800)KOL1
C
540      STOP
10000      FORMAT(//,2X,'TYPE THE INDEX NO. FOR THE LAST RADIONUCLIDE ' ,
      1 'WHICH CONTRIBUTES TO DOSE',//)
10100      FORMAT(//)
10200      FORMAT(2X,'INVALID DATA...ENTER D,W,OR Y.')
10300      FORMAT('CONVERSATIONAL INPUT PROGRAM FOR INPEM II'/' ', 41(' ' ' ' //)
      1 ' )
10400      FORMAT(' PLEASE ENTER THE PARENT RADIONUCLIDE.')

```


Table 8 (continued)

10500	FORMAT(A8)	PRE2505
10600	FORMAT(I)	PRE2510
10700	FORMAT(//,2X,'READ METABOLIC DATA FROM SOURCE FILES (Y OR N)?')	PRE2515
10800	FORMAT(A1)	PRE2520
10900	FORMAT(2X,'ENTER PARENT METABOLIC FILE NAME(SPECIES 1)')	PRE2525
11000	FORMAT(A10)	PRE2530
11100	FORMAT(2X,'ENTER DAUGHTER METABOLIC FILE NAME FOR SPECIES',I2)	PRE2535
11200	FORMAT(' ENTER THE NUMBER OF SOURCES OTHER THAN LUNGS, RES LYM,/'	PRE2540
	1 ' S CONT, ULI CONT, AND LLI CONT (1 TO 18,USE DECIMAL)'/)	PRE2545
11300	FORMAT(F8.0)	PRE2550
11400	FORMAT(' ENTER THE NAMES OF THESE ',I2, ' SOURCES'/'SOURCE',/	PRE2555
	1 ' -----',/)	PRE2560
11500	FORMAT(A8)	PRE2565
11600	FORMAT('ENTER 2 IF PROMPT EXCRETION IS CONSIDERED, 1 IF NOT')	PRE2570
11700	FORMAT(' ENTER THE NUMBER OF TARGETS OTHER THAN LUNGS, RES LYM,/'	PRE2575
	1 ' S WALL, SI WALL, ULI WALL, AND LLI WALL (1 TO 18, '	PRE2580
	1 ' NO DECIMAL)'/)	PRE2585
11800	FORMAT(' ENTER THE NAMES OF THESE ',I2, ' TARGETS'/'TARGET',/	PRE2590
	1 ' -----',/)	PRE2595
11900	FORMAT(' ENTER THE BLOOD TRANSFER FRACTION FOR '/' ',A8,	PRE2600
	1 ' (SPECIES) AND ',A8, ' (SOURCE)'/)	PRE2605
12000	FORMAT(' ENTER THE NUMBER OF COMPARTMENTS FOR THIS SPECIES AND ',	PRE2610
	1 ' SOURCE (1 TO 5, NO DECIMAL)'/)	PRE2615
12100	FORMAT(' ENTER A DEPOSITION FRACTION AND A BID. HALF-TIME (DAY)',	PRE2620
	1 '/ FOR EACH COMPARTMENT FOR THIS SPECIES AND SOURCE '/' ',I2,	PRE2625
	1 ' PAIR(S) OF NUMBERS'/' DEPOSITION FRACTION',T24,'BID. HALF-TIME',	PRE2630
	1 '/ ' ',19('-''),T24,14('-'')/)	PRE2635
12200	FORMAT(2F)	PRE2640
12300	FORMAT('ENTER F2-PRIME FOR PROMPT EXCRETION FOR ',A8)	PRE2645
12400	FORMAT(' ENTER THE SFACOR FILE NAME FOR SPECIES ',I3)	PRE2650
12500	FORMAT(A10)	PRE2655
12600	FORMAT(A1)	PRE2660
12700	FORMAT(8E10.0)	PRE2665
12800	FORMAT(5E10.0)	PRE2670
12900	FORMAT(5E10.3)	PRE2675
13000	FORMAT(' ENTER THE NAME OF A FILE TO RECEIVE INREM II ',	PRE2680
	1 'INPUT DATA FOR THIS CHAIN.')	PRE2685
13100	FORMAT(' TYPE 1 FOR INPUT SUMMARY, 2 TO SUPPRESS')	PRE2690
13200	FORMAT(' ERROR.. PROGRAM EXPECTS 1 OR 2')	PRE2695
13300	FORMAT(' ENTER 1 TO RETURN TO BEGINNING OF DIALOGUE PHASE FOR/',	PRE2700
	1 ' MAKING CORRECTIONS, 2 TO CONTINUE'//)	PRE2705
13400	FORMAT(' ERROR.. PROGRAM EXPECTS 1 OR 2')	PRE2710
13500	FORMAT(20I)	PRE2715
13600	FORMAT(I2)	PRE2720
13700	FORMAT(A8,2X,E10.3)	PRE2725
13800	FORMAT(I2)	PRE2730
13900	FORMAT(2I2,E10.3)	PRE2735
14000	FORMAT(I2,T12,'PLUS PROMPT EXCRETION')	PRE2740
14100	FORMAT(I2)	PRE2745
14200	FORMAT(4(A8,2X,E10.3))	PRE2750
14300	FORMAT(E10.3,I2)	PRE2755
14400	FORMAT(8E10.3)	PRE2760
14500	FORMAT(E10.3,I2/2E10.3)	PRE2765
14600	FORMAT(8E10.3)	PRE2770
14700	FORMAT(' ENTER THE NUMBER OF CASES FOR THIS RUN '/',	PRE2775
	1 ' (1 TO 6, NO DECIMAL)'/)	PRE2780
14800	FORMAT(I2)	PRE2785
14900	FORMAT(' ENTER THE INTAKE MODE FOR CASE ',I2,	PRE2790
	1 ' (G FOR INGESTION, ' 'H FOR '	PRE2795
	1 ' INHALATION) AND THE TIME (DAYS) FOR ENDING THE ',	PRE2800
	1 ' INTEGRATION'/' MODE',T10,'TIME'/' ----',T10,'----'//)	PRE2805
15000	FORMAT(A1,F)	PRE2810
15100	FORMAT(' ENTER THE NUMBER OF TIME INTERVALS FOR THE INTAKE RATE',	PRE2815

Table 8 (continued)

```

1      ' FUNCTION'//
15200 FORMAT(I)
15300 FORMAT(' FOR EACH OF THE ',I2,' TIME INTERVALS, ENTER THE ',
1      ' INTERVAL START TIME (DAYS) AND THE INTAKE RATE '// ' ',
1      ' (MICROCURI/DAIY)'// ' ', ' INTERVAL START TIME',T24,'PATE'// ' ',
1      ' 19(''-'), T24,4(''-')//)
15400 FORMAT(2F)
15500 FORMAT(' ENTER PARTICLE SIZE (MICROMETER) FOR CASE ',I2//)
15600 FORMAT(F)
15700 FORMAT(' ENTER DE DP SP, RESPECTIVELY FOR DEFAULT OR SPECIAL '//,
1      ' LUNG PARAMETERS FOR ',A8 ' ', ' ')
15800 FORMAT(A2)
15900 FORMAT(' ENTER THE SOLUBILITY CLASS (D,W,Y) FOR ',A8)
16000 FORMAT(A1)
16100 FORMAT(' OSPECIAL LUNG PARAMETERS FOR ',A8//,
1      ' FOR EACH OF THE 9 PATHWAYS A-I, ENTER THE BIOLOGICAL',
1      ' HALF-TIME (DAY) AND THE COMPARTMENTAL FRACTION'// BID. ',
1      ' HALF-TIME',T17,'COMPARTMENTAL FRACTION'// ' ',14(''-'), T17,22(''-')
1      //)
16200 FORMAT(2F)
16300 FORMAT(' FOR EACH OF THE ',I2,' SPECIES OF THE SJSCCHAIN, ENTER',
1      ' THE UPTAKE FRACTION F1 (SEPARATE NUMBERS BY COMMAS OR',
1      ' BLANKS)'//)
16400 FORMAT(20F)
16500 FORMAT(' ENTER 1 TO RETURN TO BEGINNING OF CASE ',I2//,
1      ' FOR MAKING CORRECTIONS, 2 TO CONTINUE')
16600 FORMAT(A2,IPE10.3)
16700 FORMAT(I2)
16800 FORMAT(8E10.3)
16900 FORMAT(E10.3)
17000 FORMAT('S')
17100 FORMAT(8E10.3)
17200 FORMAT(E10.3)
17300 FORMAT(A1/E10.3)
17400 FORMAT(E10.3)
17500 FORMAT(' IF COMMENTS REGARDING THIS SUBCHAIN ARE TO BE '//
1      ' PRINTED, ENTER THEM, FOLLOWING THE LAST COMMENT LINE, '//
1      ' ENTER A DOLLAR SIGN IN COLUMN 1 OF THE NEXT LINE'//)
17600 FORMAT(A1,7A10,A9)
17700 FORMAT(A1,7A10,A9)
17800 FORMAT(A1)
END

```

PRE2820
 PRE2825
 PRE2830
 PRE2835
 PRE2840
 PRE2845
 PRE2850
 PRE2855
 PRE2860
 PRE2865
 PRE2870
 PRE2875
 PRE2880
 PRE2885
 PRE2890
 PRE2895
 PRE2900
 PRE2905
 PRE2910
 PRE2915
 PRE2920
 PRE2925
 PRE2930
 PRE2935
 PRE2940
 PRE2945
 PRE2950
 PRE2955
 PRE2960
 PRE2965
 PRE2970
 PRE2975
 PRE2980
 PRE2985
 PRE2990
 PRE2995
 PRE3000
 PRE3005
 PRE3010
 PRE3015
 PRE3020
 PRE3025

C
 C
 C

0
 5
 10
 15
 20
 25
 30
 35
 40
 45
 50

```

SUBROUTINE CDAYS(IDAY,HALF)
DIMENSION DIV(3)
DATA (DIV(I),I=1,3) /60.,60.,24./
N = 4
IF (IDAY.EQ.'Y') HALF = HALF * 365.
IF (IDAY.EQ.'H') N=3
IF (IDAY.EQ.'M') N=2
IF (IDAY.EQ.'S') N=1

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Table 8 (continued)

	IF (N.EQ.4) GO TO 20	55
	DO 10 I=N,3	60
	HALF = HALF/DIV(I)	65
10	CONTINUE	70
20	RETURN	75
	END	80
	SUBROUTINE CHAIN(NDAUG)	CHAI 0
	PROGRAM CHAIN	CHAI 5
		CHAI 10
	D.E. FIELDS	CHAI 15
	SEPTEMBER, 1979	CHAI 20
		CHAI 25
	CODE 'CHAIN' DETERMINES RADIOISOTOPE DECAY CHAIN AND	CHAI 30
	MAKES ENTITIES AND BRANCHING FRACTIONS AVAILABLE TO	CHAI 35
	INREM PACKAGE	CHAI 40
		CHAI 45
		CHAI 50
	DIMENSION ITIME(40),NDAUG(25)	CHAI 55
	DOUBLE PRECISION IPAR,FSTK,ISTK,ID(3),FD(3),IDAU,FDAU, IDSTK(40),	CHAI 60
1	NAMNUC	CHAI 65
	COMMON /SUB/ ISTK(40),FSTK(40),IPTR,NXTPTR	CHAI 70
	COMMON NAMNUC(25),NSPEC,TR(25),DUMB(142),BRANCH(25,25)	CHAI 75
	DATA BRANCH /625*0./, TP /25*0./	CHAI 80
	IPTR = 0	CHAI 85
	NXTPTR = 1	CHAI 90
	NSPEC = 1	CHAI 95
	LL = 1	CHAI 100
	IPAR = NAMNUC(1)	CHAI 105
	IDAU=IPAR	CHAI 110
	FDAU=0.	CHAI 115
	CALL POKE(IDAU,FDAU)	CHAI 120
10	CONTINUE	CHAI 125
	AVOID MULTIPLE LOOKUPS	CHAI 130
	DO 20 IC=1,NSPEC	CHAI 135
	IF (IPAR.EQ.NAMNUC(IC).AND.TR(IC).GE.0.1E-30) GO TO 50	CHAI 140
20	CONTINUE	CHAI 145
	CALL FIND(IPAR,ID,FD,NDAU,IDSTK,ITIME)	CHAI 150
	NDAUG(LL)=NDAU	CHAI 155
	LL=LL+1	CHAI 160
	IF (NDAU.EQ.0) GO TO 40	CHAI 165
	DO 30 N=1,NDAU	CHAI 170
	IDAU=ID(N)	CHAI 175
	FDAU=FD(N)	CHAI 180
	CALL POKE(IDAU,FDAU)	CHAI 185
30	CONTINUE	CHAI 190
40	CALL NMOVE(ITIME,IDSTK,NDAU,FD,LL,ID)	CHAI 195
	IF (NXTPTR.EQ.IPTR) GO TO 60	CHAI 200
50	CALL PEEK(IPAR)	CHAI 205
	GO TO 10	CHAI 210
		CHAI 215
	PRINT CONTENTS OF STACK	CHAI 220
60	WRITE(6,10000)	CHAI 225
	WRITE(6,10100) (I,NAMNUC(I),TR(I),I=1,NSPEC)	CHAI 230

Table 8 (continued)

NDAUS=NSPEC		CHAI	235
10000	FORMAT(/,2X,'DECAY CHAIN ENTITIES:',/,/,1X,	CHAI	240
1	'INDEX NO. RADIONUCLIDE', ' RAD. HALF-LIFE')	CHAI	245
10100	FORMAT(2X,13,8X,A10,5X,E11.5,' DAYS')	CHAI	250
	END	CHAI	255
SUBROUTINE CHEC(NAME)		CHEC	0
DOUBLE PRECISION IBUF(10),IBL,IDASH,IWORD(2),NAME		CHEC	5
COMMON/C1/IBUF		CHEC	10
DATA IBL/' ',IDASH/'-'/		CHEC	15
J=0		CHEC	20
DO 10 I=1,10		CHEC	25
IF (IBUF(I).EQ.IBL) GO TO 10		CHEC	30
IF (IBUF(I).EQ.IDASH) GO TO 20		CHEC	35
J=J+1		CHEC	40
IWORD(J)=IBUF(I)		CHEC	45
IF (J.GT.2) RETURN		CHEC	50
ENCODE(10,100,NAME,IWORD		CHEC	55
10	CONTINUE	CHEC	60
20	RETURN	CHEC	65
100	FORMAT(5A1)	CHEC	70
	END	CHEC	75
SUBROUTINE FIND(IPAR,IO,FD,NDAU,IDSTK,ITIME)		FIND	0
D.E. FIELDS		FIND	5
SEPTEMBER, 1979		FIND	10
		FIND	15
CALLED BY CODE 'CHAIN'		FIND	20
		FIND	25
CODE 'CHAIN' DETERMINES RADIONUCLIDE DECAY CHAIN AND		FIND	30
MAKES ENTITIES AND BRANCHING FRACTIONS AVAILABLE TO		FIND	35
INREM PACKAGE		FIND	40
		FIND	45
DIMENSION ITIME(40)		FIND	50
COMMON /SUB/ ISTK(40),FSTK(40),IPTR,NXTPTR		FIND	55
DOUBLE PRECISION IPAR,IO(3),FD(2),IP,IBLK,IDSTK(40),ISTK,FSTK		FIND	60
DATA IBLK/' '		FIND	65
REWIND 8		FIND	70
10	READ(8,10000,END=40) IP,(IO(I),FD(I),I=1,3),IDSTK(NXTPTR),	FIND	75
1	ITIME(NXTPTR)	FIND	80
IF (IP.NE.IPAR) GO TO 10		FIND	85
DO 20	I=1,3	FIND	90
NDUM=I-1		FIND	95
IF (ID(I).EQ.IBLK) GO TO 30		FIND	100
20	CONTINUE	FIND	105

Table 8 (continued)

NDUM=3	FIND 110
30 NDAU=NDUM	FIND 115
RETURN	FIND 120
40 WRITE(6,10100) IPAR	FIND 125
STOP	FIND 130
10000 FORMAT(A10.3(A10,F10.8),F9.1,A1)	FIND 135
10100 FORMAT(/,2X,A10,' IS AN INVALID NAME ')	FIND 140
END	FIND 145

SUBROUTINE META(NMSOU,NSOU,TEXCRT,ISPE)	META 0
CALLED BY	META 5
C INCON.. CONVERSATIONAL INPUT PROGRAM FOR INREM II	META 10
C READS INREM II INPUT METABOLIC DATA	META 15
C DECEMBER, 1979	META 20
C D.E. FIELDS	META 25
C	META 30
C	META 35
DOUBLE PRECISION NAMNUC(25),NAMSOU(22),NAMTRG(24),NANDAU,NAMT,	META 40
1 NAMS,NMTRG(24),NMSOU(22),NAM1,NAM2,NAM3,NAM4,LINE(8),NAMOTH,	META 45
1 INFIL,INAME	META 50
INTEGER OUT	META 55
COMMON NAMNUC,NSPEC,TR,NAMSOU,VS,SMASS,NT,TMASS,NAMTRG, BRANCH,	META 60
1 F2PRIM,C,TB,NC,ISOP,ITAR	META 65
COMMON NS1,NSOU1,OMASS,F2EXC	META 70
DIMENSION BRANCH(25,25),TR(25),NDAU(25),F2PRIM(25,16), TB(25,5,16),	META 75
1 ,C(25,5,16),N(25),SFAC(25,24,22),SMASS(24),TMASS(24), NC(25,16),	META 80
1 MODE(6),TEND(6),T(6,30),P(6,30),TBLUNG(9,25), FLUNG(9,25),	META 85
1 ISOL(25),SFAC(25,24,22),F1(25),PAR(25),ISOR(22), ITAR(24),	META 90
1 MSOR(22),F2EXC(25)	META 95
DATAPL/'PLUS'/	META 100
C	META 105
C	META 110
C	META 115
C IN=22 FOR PARENT, OR 23 FOR DAUGHTER RADIONUCLIDE.	META 120
C	META 125
IN=23	META 130
IF (ISPE.EQ.1) IN=22	META 135
10 READ(IN,10000,END=20) INAME	META 140
CALL NAME(INAME,ISPE,&10)	META 145
GO TO 30	META 150
20 IF (IN.EQ.23) WRITE(6,10100)	META 155
IF (IN.EQ.22) WRITE(6,10200)	META 160
STOP	META 165
C READ NUMBER OF SOURCES OTHER THAN LUNGS AND G.I. TRACT	META 170
30 READ(IN,10300) NS1,EXCTST	META 175
NS=NS1-1	META 180
TEXCRT=1	META 185
IF (EXCTST.EQ.PL) TEXCRT=2	META 190
C FOR EACH SOURCE OTHER THAN LUNGS AND G.I. TRACT, READ	META 195
C ITS NAME AND MASS	META 200
READ(IN,10400)(NAMSOU(IS+6),DUM,IS=1,NS1)	META 205
C	META 210
C FOR EACH SPECIES IN THE SUBCHAIN, INPUT METABOLIC PARAMETERS	META 215
C FOR SOURCES OTHER THAN LUNGS AND G.I. TRACT	META 220

Table 8 (continued)

C	SPECIFY NUMBER OF COMPARTMENT PARMETER SETS.	META 225
	ISPEC=ISPF	META 230
	DO 40 ISOU=1, NS1	META 235
C	READ BLOOD TRANSFER FRACTION AND NUMBER OF COMPARTMENTS	META 240
	READ(IN,10500)F2PRIM(ISPE,ISOU),NC(ISPE,ISOU)	META 245
	NCOM=NC(ISPE,ISOU)	META 250
C	FOR EACH COMPARTMENT, READ ITS DEPOSITION FRACTION AND BIO. HALF-TIME	META 255
	READ(IN,10600)(C(ISPE,IC,ISOU),TB(ISPE,IC,ISOU), IC=1,NCOM)	META 260
	IF (IEXCRT.NE.2) GO TO 40	META 265
	IF (ISOU.GT.1) GO TO 40	META 270
	READ(IN,10700)F2EXC(ISPEC),NCEXC,CEXC,TBEXC	META 275
40	CONTINUE	META 280
50	CONTINUE	META 285
60	CONTINUE	META 290
	NSOU=NS1+5	META 295
	NSOU1=NSOU+1	META 300
	NTRG=NT+6	META 305
	RETURN	META 310
10000	FORMAT(A10)	META 315
10100	FORMAT(2X,'DAUGHTER RADIONUCLIDE NAME NOT FOUND.')	META 320
10200	FORMAT(2X,'PARENT RADIONUCLIDE NAME NOT FOUND.')	META 325
10300	FORMAT(I2,9X,A4)	META 330
10400	FORMAT(4(A8,2X,E10.3))	META 335
10500	FORMAT(E10.3,I2)	META 340
10600	FORMAT(8E10.3)	META 345
10700	FORMAT(E10.3,I2/2E10.3)	META 350
	END	META 355

	SUBROUTINE NAME(IRNAME,ISPE,*)	NAME 0
	DOUBLE PRECISION NAMNUC(25),IRNAME,IBUF(10),KNAME,IWNAME	NAME 5
	COMMON NAMNUC	NAME 10
	COMMON/C1/IBUF	NAME 15
	DECODE(10,100,NAMNUC(ISPE))IBUF	NAME 20
	CALL CHEC(KNAME)	NAME 25
	DECODE(10,100,IRNAME)IBUF	NAME 30
	CALL CHEC(IWNAME)	NAME 35
	IF (IWNAME.NE.KNAME) RETURN	NAME 40
	RETURN	NAME 45
100	FORMAT(5A1)	NAME 50
	END	NAME 55

C		0
C		5
C		10
C		15

Table 8 (continued)

	SUBROUTINE NMOVE(ITIME,IDSTK,NDAU,FD,LL,IO)	20
	DIMENSION ITIME(40),IDAYS(5)	25
	DOUBLE PRECISION NAMNUC,IDSTK(40),FD(3),ISTK,FSTK,IO(3)	30
	COMMON NAMNUC(25),NSPEC,TR(25),DUMB(142),BRANCH(25,25)	35
	COMMON /SUB/ ISTK(40),FSTK(40),IPTR,NXTPTR	40
	DATA (IDAYS(I),I=1,5) / 'S','M','H','Y','D' /	45
	DO 10 I=1,NSPEC	50
	IF (NAMNUC(I).NE.ISTK(NXTPTR)) GO TO 10	55
	IP=I	60
	TR(I)=IDSTK(NXTPTR)	65
	HALF=TR(I)	70
	GO TO 20	75
10	CONTINUE	80
20	DO 30 I=1,4	85
	IF (ITIME(NXTPTR).EQ.IDAYS(I)) CALL CDAYS(ITIME(NXTPTR),HALF)	90
	TR(IP)=HALF	95
30	CONTINUE	100
	IF (NDAU.EQ.0) RETURN	105
	DO 60 J=1,NDAU	110
	DO 40 I=1,NSPEC	115
	IF (ID(J).EQ.NAMNUC(I)) GO TO 50	120
40	CONTINUE	125
C	DAUGHTER NAME NOT YET IN LIST	130
	NSPEC=NSPEC+1	135
	NAMNUC(NSPEC)=ID(J)	140
50	CONTINUE	145
	IF (NDAU.EQ.0) RETURN	150
	BRANCH(NSPEC,IP)=FD(J)	155
60	CONTINUE	160
	RETURN	165
	END	170
	SUBROUTINE PEEK(IPAR)	PEEK 0
	D.E. FIELDS	PEEK 5
	SEPTEMBER, 1979	PEEK 10
		PEEK 15
	SUBROUTINE CALLED BY CODE 'CHAIN'	PEEK 20
		PEEK 25
	CODE 'CHAIN' DETERMINES RADIOISOTOPE DECAY CHAIN AND	PEEK 30
	MAKES ENTITIES AND BRANCHING FRACTIONS AVAILABLE TO	PEEK 35
	INPEM PACKAGE	PEEK 40
		PEEK 45
	DOUBLE PRECISION IPAR,ISTK,FSTK	PEEK 50
	COMMON /SUB/ ISTK(40),FSTK(40),IPTR,NXTPTR	PEEK 55
	NXTPTR=NXTPTR+1	PEEK 60
	IF (NXTPTR.LT.40) GO TO 10	PEEK 65
	WRITE(6,10100)	PEEK 70
	STOP	PEEK 75
10	IPAR=ISTK(NXTPTR)	PEEK 80
	RETURN	PEEK 85
10000	FORMAT(2X,'ENTER SUBROUTINE PEEK')	PEEK 90
10100	FORMAT(/,2X,'ATTEMPT TO PEEK OUTSIDE OF STACK BOUNDS.')	PEEK 95
	END	PEEK 100

Table 8 (continued)

SUBROUTINE POKE(IDAU,FDAU)		POKE 0
C	D.E. FIELDS	POKE 5
C	SEPTEMBER, 1979	POKE 10
C	SUBROUTINE CALLED BY CODE 'CHAIN'	POKE 15
C		POKE 20
C	CODE 'CHAIN' DETERMINES RADIOISOTOPE DECAY CHAIN AND	POKE 25
C	MAKES ENTITIES AND BRANCHING FRACTIONS AVAILABLE TO	POKE 30
C	INREM PACKAGE	POKE 35
C		POKE 40
	DOUBLE PRECISION IDAU,FDAU,ISTK,FSTK	POKE 45
	COMMON /SUB/ ISTK(40),FSTK(40),IPTR,NXTPTD	POKE 50
	IPTR=IPTR+1	POKE 55
	IF (IPTR.LT.40) GO TO 10	POKE 60
	WRITE(6,10100)	POKE 65
	STOP	POKE 70
10	ISTK(IPTR)=IDAU	POKE 75
	FSTK(IPTR)=FDAU	POKE 80
	RETURN	POKE 85
10000	FORMAT(2X,'ENTER SUBROUTINE POKE')	POKE 90
10100	FORMAT(/,2X,'ATTEMPT TO POKE VALUE INTO FULL STACK')	POKE 95
	END	POKE 100
SUBROUTINE SUMMRY		SUMM 0
	DOUBLE PRECISION NAMNUC,NAMSOU,NAMTRG	SUMM 5
C	PRINTS A SUMMARY OF INFORMATION INPUT PRIOR TO SUBCHAIN AND CASE DATA	SUMM 10
C		SUMM 15
	COMMON NAMNUC(25),NSPEC,TR(25),NAMSOU(22),NS,SMASS(24),NT,	SUMM 20
	1 TMASS(24),NAMTRG(24),BRANCH(25,25),F2PRIM(25,16),C(25,5,16),	SUMM 25
	1 TB(25,5,16),NC(25,16),ISOR(22),ITAP(24)	SUMM 30
	COMMON NS1,NSOU1,OMASS,F2EXC(25)	SUMM 35
C	WRITE(6, NAMES AND HALF-LIVES OF NUCLIDES IN THE CHAIN	SUMM 40
	WRITE(6,10000)(NAMNUC(ISPEC),TR(ISPEC),ISPEC=1,NSPEC)	SUMM 45
C	WRITE(6, NAMES AND MASSES OF SOURCES AND TARGETS OTHER THAN LUNGS AND	SUMM 50
CT		SUMM 55
	WRITE(6,10100)(NAMSOU(IS+6),SMASS(ISOR(IS+6)),IS=1,NS),	SUMM 60
1	NAMSOU(NSOU1), OMASS	SUMM 65
	WRITE(6,10200)(NAMTRG(IT+6),TMASS(ITAP(IT+6)),IT=1,NT)	SUMM 70
	IF (NSPEC.EQ.1) GO TO 20	SUMM 75
C	WRITE(6, NONZERO BRANCHING RATIOS	SUMM 80
	WRITE(6,10300)	SUMM 85
	DO 10 ISPEC=1,NSPEC	SUMM 90
	DO 10 JSPEC=1,NSPEC	SUMM 95
	IF (BRANCH(JSPEC,ISPEC).NE.0.0) WRITE(6,10400)NAMNUC(ISPEC),	SUMM 100
1	NAMNUC(JSPEC), BRANCH(JSPEC,ISPEC)	SUMM 105
10	CONTINUE	SUMM 110

Table 8 (continued)

C WRITE(6, BLOOD TRANSFER FRACTIONS, DEPOSITION FRACTIONS, AND BIOLOG-	SUMM 115
C ICAL HALF-TIMES	SUMM 120
20 WRITE(6,10500)	SUMM 125
DD 60 ISOU=1, NS1	SUMM 130
WRITE(6,11000) NAMSOU(ISOU+6), NAMNUC(1), F2PRIM(1, ISOU), C(1,1,	SUMM 135
1 ISOU), TB(1,1, ISOU)	SUMM 140
NCOM=NC(1, ISOU)	SUMM 145
IF (NCOM.EQ.1) GO TO 40	SUMM 150
DD 30 IC=2, NCOM	SUMM 155
30 WRITE(6,10700) C(1, IC, ISOU), TB(1, IC, ISOU)	SUMM 160
40 IF (NSPEC.EQ.1) GO TO 60	SUMM 165
DD 50 ISPEC=2, NSPEC	SUMM 170
WRITE(6,10800) NAMNUC(ISPEC), F2PRIM(ISPEC, ISOU), C(ISPEC,1,	SUMM 175
1 ISOU), TB(ISPEC,1, ISOU)	SUMM 180
NCOMPA=NC(ISPEC, ISOU)	SUMM 185
IF (NCOMPA.EQ.1) GO TO 50	SUMM 190
DD 50 ICOM=2, NCOMPA	SUMM 195
WRITE(6,10900) C(ISPEC, ICOM, ISOU), TB(ISPEC, ICOM, ISOU)	SUMM 200
50 CONTINUE	SUMM 205
60 CONTINUE	SUMM 210
IF (F2EXC(1).GT.0.0) WRITE(6,10600) NAMNUC(1), F2EXC(1)	SUMM 215
RETURN	SUMM 220
10000 FORMAT('0NUCLIDE', T15, 'HALF-LIFE'//20(' ', A8, T15, 1PE10.3//))	SUMM 225
10100 FORMAT('0SOURCE', T15, 'MASS'//16(' ', A8, T15, 1PE10.3//))	SUMM 230
10200 FORMAT('0TARGET', T15, 'MASS'//18(' ', A8, T15, 1PE10.3//))	SUMM 235
10300 FORMAT(' BRANCHING RATIOS: FROM', T31, 'TO', T41, 'FRACTION'//)	SUMM 240
10400 FORMAT(' ', T21, A8, T31, A8, T40, E10.3)	SUMM 245
10500 FORMAT(' ', T27, 'BLOOD', T59, 'COMPARTMENT'// ' ', T26, 'TRANSFER', T41,	SUMM 250
1 'COMPARTMENT', T60, 'BIOLOGICAL'// ' ', T26, 'FRACTION', T42,	SUMM 255
1 'DEPOSITION', T60, 'HALF-TIME'// ' ORGAN', T14, 'NUCLIDE', T26,	SUMM 260
1 'F2-PRIME', T42, 'FRACTION', T62, '(DAYS)')	SUMM 265
10600 FORMAT(' ', 'PROMPT EXCRETION FRACTION FOR ', A8, ' = ', 1PG9.3)	SUMM 270
10700 FORMAT(' ', T41, 1PG9.3, T60, 1PG9.3)	SUMM 275
10800 FORMAT(' ', T14, A8, T25, 1PG9.3, T41, 1PG9.3, T60, 1PG9.3)	SUMM 280
10900 FORMAT(' ', T41, 1PG9.3, T60, 1PG9.3)	SUMM 285
11000 FORMAT(' ', A8, T14, A8, T25, 1PG9.3, T41, 1PG9.3, T60, 1PG9.3)	SUMM 290
END	SUMM 295

SUBROUTINE SURCH(NARR,N,NAM,IND)	SURC 0
C RECEIVES AN ARRAY OF NAMES, ARR, AND A NAME, NAM, AND RETURNS THE	SURC 5
C INDEX, IND, OF THE ARRAY ELEMENT WITH THIS NAME. THE FIRST N ELEMENTS	SURC 10
C OF THE ARRAY ARE SEARCHED.	SURC 15
C	SURC 20
DOUBLE PRECISION NARR(1),NAM	SURC 25
C	SURC 30
DD 10 I=1,N	SURC 35
IF (NAM.EQ.NARR(I)) GO TO 20	SURC 40
10 CONTINUE	SURC 45
WRITE(6,10000) NAM	SURC 50
GO TO 30	SURC 55
20 IND=I	SURC 60
30 RETURN	SURC 65
10000 FORMAT(' ERROR.. SURCH FAILED TO FIND NAME..',A10)	SURC 70
END	SURC 75

REFERENCES

- Digital Equipment Corporation. 1977. *DecSystem 10 Fortran Programmer's Reference Manual*, Order No. AA-0944E-TB.
- Dunning, D. E., Jr., S. R. Bernard, P. J. Walsh, G. G. Killough, and J. C. Pleasant. 1979. *Estimates of Internal Dose Equivalent to 22 Target Organs for Radionuclides Occurring in Routine Releases from Nuclear Fuel-Cycle Facilities, Vol. II*, NUREG/CR-0150 Vol. 2, ORNL/NUREG/TM-190/V2.
- Dunning, D. E., Jr., J. C. Pleasant, and G. G. Killough. 1977. *SFACTOR: A Computer Code for Calculating Dose Equivalent to a Target Organ per Microcurie-Day Residence of a Radionuclide in a Source Organ*, ORNL/NUREG/TM-85.
- Dunning, D. E., Jr., J. C. Pleasant, and G. G. Killough. 1980. *SFACTOR: A Computer Code for Calculating Dose Equivalent to a Target Organ per Microcurie-Day Residence of a Radionuclide in a Source Organ—Supplementary Report*, NUREG/CR-1523, ORNL/NUREG/TM-85/S1.
- International Commission on Radiological Protection. 1979. Publication 30, "Limits for Intakes of Radionuclides by Workers," *Annals of the ICRP*, Vol. 2, No. 3/4.
- Killough, G. G., D. E. Dunning, Jr., S. R. Bernard, and J. C. Pleasant. 1978b. *Estimates of Internal Dose Equivalent to 22 Target Organs for Radionuclides Occurring in Routine Releases from Nuclear Fuel-Cycle Facilities, Vol. I*, NUREG/CR-0150 V.1I, ORNL/NUREG/TM-190.
- Killough, G. G., D. E. Dunning, Jr., and J. C. Pleasant. 1978a. *INREM II: A Computer Implementation of Recent Models for Estimating the Dose Equivalent to Organs of Man from an Inhaled or Ingested Radionuclide*, NUREG/CR-0114, ORNL/NUREG/TM-84.
- Kocher, D. C. (in press). *Radioactive Decay Data Tables: A Handbook of Decay Data for Application to Radiation Dosimetry and Radiological Assessments*, U.S. Department of Energy.
- Morrow, P. E., D. V. Bates, B. R. Fish, T. F. Hatch, and T. T. Mercer, "Deposition and Retention Models for Internal Dosimetry of the Human Respiratory Tract," *Health Phys.* 12:173-207.

APPENDIX A

The tables in this appendix give listings of the metabolic and source files which are stored on DECTAPES. Tables A1 through A12 give listings of metabolic data files. The PREREM.FOR source program and the nuclear decay data file are stored on DECTAPE D4681 listed in Table A1. The INREM-II job submission file is located on DECTAPE D4884. The special lung parameters and the gastrointestinal tract uptake fractions are given in Tables A13 and A14, respectively.

Table A1. Directory for DECTAPE D4681

PREREM	.FOR	53	11-DEC-80
DECAY	.DAT	65	15-OCT-80
UP	.MET	02	01-SEP-80
UD	.MET	02	01-SEP-80
THP	.MET	01	01-SEP-80
THD	.MET	01	01-SEP-80
RA	.MET	02	01-SEP-80
RADEX	.MET	02	01-SEP-80
RN	.MET	02	01-SEP-80
RNDEX	.MET	03	01-SEP-80
PO	.MET	01	01-SEP-80
PODEX	.MET	01	01-SEP-80
BIP	.MET	02	01-SEP-80
BIDEX	.MET	02	01-SEP-80
BIDNEX	.MET	02	01-SEP-80
PB	.MET	02	01-SEP-80
PBDEX	.MET	02	01-SEP-80
TL	.MET	01	01-SEP-80
TLDEX	.MET	01	01-SEP-80
HG	.MET	01	02-SEP-80
HF	.MET	01	01-SEP-80

Table A2. Directory for DECTAPE D4682

NA	.MET 01	02-SEP-80
S	.MET 01	02-SEP-80
P	.MET 01	02-SEP-80
AR	.MET 01	01-SEP-80
K	.MET 01	01-SEP-80
SC	.MET 01	01-SEP-80
FE	.MET 01	02-SEP-80
MN	.MET 01	02-SEP-80
CO	.MET 01	02-SEP-80
NI	.MET 01	01-SEP-80
ZN	.MET 01	02-SEP-80
GA	.MET 01	02-SEP-80
AS	.MET 01	02-SEP-80
SR	.MET 01	02-SEP-80
YD	.MET 01	02-SEP-80
ZR	.MET 01	01-SEP-80
NB	.MET 01	01-SEP-80
TC	.MET 01	02-SEP-80
MO	.MET 01	02-SEP-80
CR	.MET 01	02-SEP-80
YP	.MET 01	02-SEP-80
KR	.MET 01	02-SEP-80

Table A3. Directory for DECTAPE D4684

BE	.MET 01	02-SEP-80
C	.MET 01	02-SEP-80
O	.MET 01	02-SEP-80
N	.MET 01	02-SEP-80
RB	.MET 01	04-SEP-80
W	.MET 01	01-SEP-80
IRP	.MET 01	02-SEP-80
RU	.MET 01	02-SEP-80
RHP	.MET 01	02-SEP-80
RHD	.MET 01	02-SEP-80
AG	.MET 01	02-SEP-80
LADEX	.MET 01	04-SEP-80
SN	.MET 01	15-SEP-80
IN	.MET 01	15-SEP-80
CSP	.MET 01	03-SEP-80
CSDEX	.MET 01	03-SEP-80
BAP	.MET 02	02-SEP-80
BADNEX	.MET 02	03-SEP-80
CSSGL	.MET 01	02-SEP-80

Table A4. Directory for DECTAPE D2185

ISGL	.MET 01	02-SEP-80
I	.MET 02	15-SEP-80
IDEX	.MET 02	15-SEP-80
XE	.MET 02	15-SEP-80
XEDX	.MET 02	15-SEP-80
TEP	.MET 01	15-SEP-80
TEDEX	.MET 01	15-SEP-80
TEDNEX	.MET 01	15-SEP-80
SBP	.MET 01	15-SEP-80
SBDEX	.MET 01	15-SEP-80
SBDNEX	.MET 01	15-SEP-80
PUP	.MET 02	08-SEP-80
PUD	.MET 02	08-SEP-80
ACP	.MET 02	08-SEP-80
ACD	.MET 02	08-SEP-80
PAP	.MET 02	08-SEP-80
PAD	.MET 02	08-SEP-80
NPP	.MET 02	08-SEP-80
NPD	.MET 02	08-SEP-80
AMP	.MET 02	08-SEP-80
AMD	.MET 02	08-SEP-80

Table A5. Directory for DECTAPE D4699

CMP	.MET	02	08-SEP-80
CMD	.MET	02	08-SEP-80
CFP	.MET	02	08-SEP-80
CFD	.MET	02	08-SEP-80
LA	.MET	01	08-SEP-80
CE	.MET	01	08-SEP-80
PR	.MET	01	08-SEP-80
NDP	.MET	01	08-SEP-80
PMP	.MET	01	08-SEP-80
SMP	.MET	01	08-SEP-80
EUP	.MET	01	08-SEP-80
GDP	.MET	01	08-SEP-80
TBP	.MET	01	08-SEP-80
NDD	.MET	01	08-SEP-80
PMD	.MET	01	08-SEP-80
SMD	.MET	01	08-SEP-80
EUD	.MET	01	08-SEP-80
GDD	.MET	01	08-SEP-80
TBD	.MET	01	08-SEP-80

Table A6. Directory for DECTAPE D4855

H3	.SFC 10	21-OCT-80
C14	.SFC 10	21-OCT-80
NA22	.SFC 10	21-OCT-80
NA24	.SFC 10	21-OCT-80
P32	.SFC 10	21-OCT-80
K40	.SFC 10	21-OCT-80
MN54	.SFC 10	21-OCT-80
FE55	.SFC 10	21-OCT-80
FE59	.SFC 10	21-OCT-80
C057	.SFC 10	21-OCT-80
C058	.SFC 10	21-OCT-80
C060	.SFC 10	21-OCT-80
ZN65	.SFC 10	21-OCT-80
RB86	.SFC 10	21-OCT-80
SR89	.SFC 10	21-OCT-80
SR90	.SFC 10	21-OCT-80
SR91	.SFC 10	21-OCT-80
Y91M	.SFC 10	21-OCT-80
Y90	.SFC 10	21-OCT-80
Y91	.SFC 10	21-OCT-80
ZR95	.SFC 10	21-OCT-80
ZR97	.SFC 10	21-OCT-80

Table A7. Directory for DECTAPE D4856

NB95	.SFC 10	21-OCT-80
NB95M	.SFC 10	21-OCT-80
NB97	.SFC 10	21-OCT-80
NB97M	.SFC 10	21-OCT-80
M099	.SFC 10	21-OCT-80
TC99	.SFC 10	21-OCT-80
TC99M	.SFC 10	21-OCT-80
RU103	.SFC 10	21-OCT-80
RU105	.SFC 10	21-OCT-80
RU106	.SFC 10	21-OCT-80
RH103M	.SFC 10	21-OCT-80
RH105	.SFC 10	21-OCT-80
RH105M	.SFC 10	21-OCT-80
RH106	.SFC 10	21-OCT-80
SN113	.SFC 10	21-OCT-80
SB127	.SFC 10	21-OCT-80
TE127	.SFC 10	21-OCT-80
TE127M	.SFC 10	21-OCT-80
TE129	.SFC 10	21-OCT-80
TE129M	.SFC 10	21-OCT-80
TE131	.SFC 10	21-OCT-80
TE131M	.SFC 10	21-OCT-80

Table A8. Directory for DECTAPE D4857

TE132	.SFC 10	21-OCT-80
I129	.SFC 10	21-OCT-80
I131	.SFC 10	21-OCT-80
I133	.SFC 10	21-OCT-80
I134	.SFC 10	21-OCT-80
I135	.SFC 10	21-OCT-80
CS134	.SFC 10	21-OCT-80
CS135	.SFC 10	21-OCT-80
CS136	.SFC 10	21-OCT-80
CS137	.SFC 10	15-OCT-80
BA137M	.SFC 10	15-OCT-80
BA140	.SFC 10	21-OCT-80
LA140	.SFC 10	21-OCT-80
CE141	.SFC 10	21-OCT-80
CE144	.SFC 10	21-OCT-80
PR143	.SFC 10	21-OCT-80
PR144	.SFC 10	21-OCT-80
I132	.SFC 10	21-OCT-80
PR144M	.SFC 10	21-OCT-80
ND147	.SFC 10	21-OCT-80
PM147	.SFC 10	21-OCT-80

Table A9. Directory for DECTAPE D4863

PB210	.SFC	10	22-OCT-80
PB211	.SFC	10	22-OCT-80
PB212	.SFC	10	22-OCT-80
PB214	.SFC	10	22-OCT-80
BI210	.SFC	10	22-OCT-80
BI211	.SFC	10	22-OCT-80
BI212	.SFC	10	22-OCT-80
BI213	.SFC	10	22-OCT-80
BI214	.SFC	10	22-OCT-80
P0210	.SFC	10	22-OCT-80
P0211	.SFC	10	22-OCT-80
P0212	.SFC	10	22-OCT-80
P0214	.SFC	10	22-OCT-80
P0215	.SFC	10	22-OCT-80
P0216	.SFC	10	22-OCT-80
P0218	.SFC	10	22-OCT-80
AT217	.SFC	10	22-OCT-80
RN219	.SFC	10	22-OCT-80
P0213	.SFC	10	22-OCT-80
RN220	.SFC	10	22-OCT-80
RN222	.SFC	10	22-OCT-80
FR221	.SFC	10	22-OCT-80

Table A10. Directory for DECTAPE D4865

RA223	.SFC 10	22-OCT-80
RA224	.SFC 20	22-OCT-80
RA226	.SFC 10	22-OCT-80
RA228	.SFC 10	22-OCT-80
AC225	.SFC 10	22-OCT-80
AC227	.SFC 10	22-OCT-80
AC228	.SFC 10	22-OCT-80
TH227	.SFC 10	22-OCT-80
TH228	.SFC 10	22-OCT-80
TH229	.SFC 10	22-OCT-80
TH230	.SFC 10	22-OCT-80
TH231	.SFC 10	22-OCT-80
TH232	.SFC 10	22-OCT-80
TH234	.SFC 10	22-OCT-80
PA231	.SFC 10	22-OCT-80
PA233	.SFC 10	22-OCT-80
U232	.SFC 10	22-OCT-80
U233	.SFC 10	22-OCT-80
U234	.SFC 10	22-OCT-80
PA234M	.SFC 10	22-OCT-80
PA234	.SFC 10	22-OCT-80

Table A11. Directory for DECTAPE D4883

U235	.SFC 10	29-OCT-80
U236	.SFC 10	29-OCT-80
U238	.SFC 10	29-OCT-80
U240	.SFC 10	29-OCT-80
NP237	.SFC 10	29-OCT-80
NP238	.SFC 10	29-OCT-80
NP239	.SFC 10	29-OCT-80
PU236	.SFC 10	29-OCT-80
PU238	.SFC 10	29-OCT-80
PU239	.SFC 10	29-OCT-80
PU240	.SFC 20	29-OCT-80
PU242	.SFC 20	29-OCT-80
PU244	.SFC 10	29-OCT-80
AM241	.SFC 10	29-OCT-80
AM242	.SFC 10	29-OCT-80
AM242M	.SFC 10	29-OCT-80
AM243	.SFC 10	29-OCT-80
NP240M	.SFC 10	29-OCT-80
NP240	.SFC 10	29-OCT-80

Table A12. Directory for DECTAPE D4884

CM242	.SFC 10	30-OCT-80
CM243	.SFC 10	30-OCT-80
CM244	.SFC 10	30-OCT-80
CM245	.SFC 10	30-OCT-80
CM246	.SFC 10	30-OCT-80
CM248	.SFC 10	30-OCT-80
CF252	.SFC 10	30-OCT-80
CM247	.SFC 10	30-OCT-80
INREM	.SUB 01	15-OCT-80
TL208	.SUB 10	05-DEC-80

Table A13. Typical values for special lung parameters^a

Compartment	Compartment deposition fraction	Biological half-time (days)
a	1.0	8.20×10^{-5}
b	0.0	1.0
c	1.0	8.20×10^{-5}
d	0.0	1.0
e	1.0	8.20×10^{-5}
f	0.0	0.0
g	0.0	0.0
h	0.0	0.0
i	1.0	2.96×10^{-3}

^aThese special lung parameters are required for the case where inert gases are inhaled. The nine compartments in the retention model are associated with the nine pathways in the ICRP Task Group II lung model and their derivation is discussed in more detail elsewhere (Dunning et al., 1979).

Table A14. Gastrointestinal uptake fraction f_1^a

Radionuclide	Inhalation solubility class	f_1
H as H_2	-	0.95
C	-	0.95
Na	D	0.95
P	D	0.80
	W	0.80
Mn	D	0.10
	W	0.10
Fe	W	0.10
	Y	0.10
Co	W	0.05
	Y	0.05
Zn	D	0.50
	W	0.50
	Y	0.50
Rb	D	0.95
Sr	D	0.20
	Y	0.01
Y	W	0.0001
Zr	W	0.002
	Y	0.002
Nb	Y	0.01
Mo	D	0.95
	Y	0.05
Tc	D	0.8
	W	0.8
	Y	0.04
Ru	Y	0.04
Rh	Y	0.04
Sb	W	0.05
Te	W	0.25
I	D	0.95
Cs	D	0.95
Ba	D	0.10
La	W	0.0001
Ce	Y	0.0001
	W	0.0001
	D	0.0001
Pr	Y	0.0001
	W	0.0001
	D	0.0001
Sm	Y	0.0001
	W	0.0001
	D	0.0001
Tl	W	0.95

Table A14. (continued)

Radionuclide	Inhalation solubility class	f_1
Pb	W	0.08
Bi	W	0.05
Po	W	0.10
	D	0.10
At	D	0.95
Rn	-	0.0
Fr	D	0.95
Ra	W	0.20
Ac	Y	0.001
	W	0.001
Th	Y	0.001
	W	0.001
Pa	Y	0.001
	W	0.001
U	Y	0.002
	W	0.05
	D	0.05
Np	Y	0.001
	W	0.001
Pu ^b	Y	0.00001
	W	0.0001
Am ^b	W	0.0005
Cm ^b	W	0.0005
Cf ^b	Y	0.0005
	W	0.0005

^a Unless otherwise noted, values are taken from D. E. Dunning, Jr. et al., NUREG/CR-150 Vols. 1 and 2.

^b These values taken from "Limits for Intakes of Radionuclides by Workers," *Annals of the ICRP*, Vol. 2, No. 3/4, 1979.

APPENDIX B

This appendix gives the computer prompts and user responses for the case when the user has opted to type in an alternate metabolic model. The computer will prompt the user as discussed in Sect. 1.3:

Computer: READ METABOLIC DATA FROM SOURCE FILES (Y OR N)?

Response: Y or N

If the user types Y (for yes) the prepared data files will be used; if the user types N (for No) the following prompts will be given.

Computer: ENTER THE NUMBER OF SOURCES OTHER THAN LUNGS, RES
LYM, S CONT, ULI CONT, AND LLI CONT (1 TO 18, USE
DECIMAL)

Response: 1 to N where N is the number of source organs for
which the user has specific retention functions.

Computer: ENTER THE NAMES OF THESE N SOURCES
SOURCE_

The user must type in the source organ names, for example, if the case being considered was CS-137 the user would type

Absorbed

Bone

The user is then asked

Computer: ENTER 2 IF PROMPT EXCRETION IS CONSIDERED, 1 IF NOT

The response for this example case would be

User: 1

The user is then asked

Computer: ENTER THE SFACTOR FILE NAME FOR SPECIES 1

The S-factor file for the first species in this case would be

User: CS137.SFC

The next several prompts ask the user to give the metabolic parameters for each source organ listed above

Computer: ENTER THE BLOOD TRANSFER FRACTION FOR CS-137
(SPECIES) AND ABSORBED (SOURCE)

User: 1.00

Computer: ENTER THE NUMBER OF COMPARTMENTS FOR THIS SPECIES
AND SOURCE (1 TO 5, NO DECIMAL)

User: 2

Computer: ENTER A DEPOSITION FRACTION AND A BIO. HALF-TIME
(DAY) FOR EACH COMPARTMENT FOR THIS SPECIES AND
SOURCE IN PAIR(S) OF NUMBERS

DEPOSITION_FRACTION BIO._HALF-TIME

User: 0.130_1.40
0.870_135.

These three prompts will be repeated for each source organ and for the compartment "OTHER." The fraction of activity which is not accounted for by explicit retention functions for specific sources organs is allocated to "OTHER" and is assumed to be distributed uniformly in the remainder of the body. Organs which do not have explicit retention functions are irradiated primarily by transformations in "OTHER."

The user is then prompted for data for the second species ^{137}Ba :

Computer: ENTER THE SFACTOR FILE NAME FOR SPECIES

User: BA137M.SFC

The question asking for blood transfer fraction, the number of compartments in a retention function and the deposition fraction and biological half-time for each compartment will be repeated for ^{137}Ba .

From this point the user is questioned in the same way discussed in Sect. 1.3 starting with the prompt:

Computer: ENTER THE NAME OF A FILE TO RECEIVE INREM II
INPUT DATA FOR THIS CHAIN

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