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**INREM II: A Computer Implementation
of Recent Models for Estimating the Dose
Equivalent to Organs of Man from an
Inhaled or Ingested Radionuclide**

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ABSTRACT

This report describes a computer code, INREM II, which calculates the internal radiation dose equivalent to organs of man which results from the intake of a radionuclide by inhalation or ingestion. Deposition and removal of radioactivity from the respiratory tract is represented by the ICRP Task Group Lung Model. A four-segment catenary model of the GI tract is used to estimate movement of radioactive material that is ingested or swallowed after being cleared from the respiratory tract. Retention of radioactivity in other organs is specified by linear combinations of decaying exponential functions. The formation and decay of radioactive daughters is treated explicitly, with each radionuclide species in the chain having its own uptake and retention parameters, as supplied by the user.

The dose equivalent to a target organ is computed as the sum of contributions from each source organ in which radioactivity is assumed to be situated. This calculation utilizes a matrix of S-factors (rem/ μ Ci-day) supplied by the user for the particular choice of source and target organs. Output permits the evaluation of crossfire components of dose when penetrating radiations are present.

INREM II is coded in FORTRAN IV and has been compiled and executed on an IBM-360 computer.

1. INTRODUCTION

This report describes and documents a computer code, INREM II, which is designed to read dosimetric and metabolic information about the radionuclides in a chain and calculate the resultant dose equivalent to various organs of a reference adult human being following inhalation or ingestion of the first (or parent) nuclide of the chain. Written in FORTRAN IV for the IBM-360 or 370, INREM II implements contemporary dynamic models for internal dose estimation. The ICRP Task Group Lung Model¹ is used to estimate the deposition and retention of inhaled particulates and their absorption into the blood and clearance into the GI tract. A four-segment model of the GI tract with first-order mass transport and absorption of activity permits calculation of residence times of radionuclides in the tract and the dynamics of their assimilation from that site. Residence times of activity in other organs are computed from retention functions that are linear combinations of decaying exponential functions. The code combines its estimates of $\mu\text{Ci-days}$ residence of activity in those source organs for which retention data are available with dosimetric factors (S-factors, in units of $\text{rem}/\mu\text{Ci-day}$) to calculate dose equivalent to prescribed target organs, thereby permitting the accounting for cross-irradiation effects when penetrating radiations are present. Source-target dose matrices are printed to facilitate the assessment of contributions of cross-irradiation to a target organ's total dose.

The residence times of the radioactive daughters are calculated with consideration of their differential transfer among the body's compartments. This approach permits each nuclide in the chain to be cleared from the lungs, absorbed from the GI tract, and taken up and retained by other organs in accordance with its own properties.

The models are described in the text of the report, and the logic, data preparation, and operation of the computer code are discussed. A complete listing of the source code is included in the Appendix.

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1.1 Internal Dosimetry

In calculations performed with INREM II it is assumed that the nuclide taken into the body (the parent) is the first in a chain of N radioactive species ($N \geq 1$; this formulation is always intended to include the special case of a chain with only one radionuclide, which decays to a stable element). Dynamics of decay and the formation of radioactive daughters will be described in Sect. 1.2.

Let $A_{ik}(t)$ denote the activity (μCi) of the i th species of the chain ($1 \leq i \leq N$) in an organ indexed by subscript k , represented as a function of the time, t (days), since the intake of the parent species into the body. The time integral of this activity

$$\lambda_{ik}(T) = \int_0^T A_{ik}(t) dt \quad \mu\text{Ci-days} \quad (1.1)$$

is fundamental to the dose estimates to be described. The integral (1.1) is a measure of the total number of transformations of the i th species that occur in the k th organ during the time interval 0 to T and therefore is a measure of the total energy emitted by transformations of that species in the organ. The problem is to estimate the fraction of this energy that is absorbed by the k th organ (the source organ) and (possibly) other organs.

The "S-factor" $S_i(X + Y)$ ($\text{rem}/\mu\text{Ci-day}$) is defined as the average dose equivalent rate to target organ X due to 1 μCi of the radionuclide species i uniformly distributed in source organ Y . An extensive tabulation of S-factors was initiated by W. S. Snyder and his colleagues.^{2,3} Dunning et al.⁴ have provided additional S-factors using the methods described in ORNL-5000 and Monte Carlo data from that report, using nuclear decay data prepared by Koccher.⁵ The S-factors in both tabulations are broken down into components according to emission type, viz., alpha, alpha recoil, electron (β^+ , β^- , Auger, conversion), photon (gamma, X ray), and spontaneous fission (neutron, fission fragment, and prompt and delayed electron and photon). Thus the total S-factor is expressed as

$$S_i(X + Y) = \sum_{\delta} S_i^{\delta}(X + Y) \quad \text{rem}/\mu\text{Ci-day},$$

where the sum on the right is understood to contain nonzero terms only for those emission types, δ , which are present in transformations of the i th species. INREM II utilizes the total S-factors, which it reads as input data. For further information concerning the definition and computation of the S-factors, the reader is referred to the previously cited reports.

For the estimation of dose equivalent, we consider mutually exclusive source organs $Y_1, Y_2, \dots, Y_M$, which may be assumed to partition all of the body's radioactivity which results from the intake. The average dose equivalent to target organ X due to radionuclide species i in these source organs is

$$D_i(X) = \sum_{k=1}^M D_i(X + Y_k) \quad \text{rem}, \quad (1.2)$$

where

$$D_i(X + Y_k) = S_i(X + Y_k) \tilde{\Lambda}_{ik} \quad \text{rem}, \quad (1.3)$$

where $\tilde{\Lambda}_{ik}$ is the $\mu\text{Ci-days}$ residence of species i in source organ Y_k , as defined by Eq. (1.1). The S-factor in Eq. (1.3) is the sum of the S-factors for those emission types present in the decay of species i . We note that the assumption of uniform distribution of activity in each source organ is implicit in these definitions, as is the averaging of the dose equivalent over the tissue of the target organ.

In calculations involving intake of a radionuclide by inhalation, INREM II always estimates the $\mu\text{Ci-days}$ residence for parent and daughters in the respiratory tract (lungs and respiratory lymph nodes) and the GI tract (contents of stomach, small intestine, upper large intestine, and lower large intestine). For intake by ingestion, the $\mu\text{Ci-days}$ residences in the GI tract are always calculated. It is usual that uptake and retention data for at least one other source organ will permit the

explicit computation of the $\mu\text{Ci-days}$ residences for parent and daughters in that organ, but seldom are such data available for more than a few such organs (e.g., bone, liver, and kidneys).

In order to account for the activity not residing in specific source organs as indicated by explicit metabolic data, one may conceive of a complementary compartment which we denote by Y_{OTHER} . In terms of our previous notations, suppose we have computed the $\mu\text{Ci-days}$, $\bar{A}_{ik}$, in the source organs Y_k , $k = 1, \dots, P < M$, where M denotes the total number of organs that we distinguish (ORNL-5000 considers 22 source organs, of which the total body is one). The remaining organs, $Y_{P+1}, \dots, Y_M$ are considered to make up Y_{OTHER} . The present version of INREM II accords no special status to the "organ" Y_{OTHER} , which is to say that it is handled the same in the calculations as the organs for which explicit uptake and retention data are available (except respiratory and GI tract, which are special cases). The user must supply uptake and metabolic data and S-factors for Y_{OTHER} , and it is suggested that the latter be calculated from the equation

$$S_i(X + Y_{\text{OTHER}}) = \left[\sum_{k=P+1}^M m_k S_i(X + Y_k) \right] \left[\sum_{k=P+1}^M m_k \right]^{-1} \text{ rem}/\mu\text{Ci-day}, \quad (1.4)$$

where m_k denotes the mass of source organ Y_k . With this definition, $S_i(X + Y_{\text{OTHER}})$ corresponds to a distribution of activity in Y_{OTHER} which is uniform with respect to mass. This is activity that is not accounted for by the explicit metabolic information which is usually available for the few organs where the concentration tends to be higher. The total dose to X from species i due to activity taken into the body is therefore estimated to be

$$D_i(X) = \sum_{k=1}^P D_i(X + Y_k) + D_i(X + Y_{\text{OTHER}}) \text{ rem}. \quad (1.5)$$

1.2 Dynamic Retention Models

Retention and translocation of radioactivity in the body are represented by a set of conceptual compartments, which correspond to a system of ordinary differential equations. Figure 1.1 depicts the assumed movement of activity among the various compartments as it is carried by various mechanical and physiological processes. More detailed views of the respiratory and GI-tract submodels will be shown in Sects. 1.2.1 and 1.2.2. Following inhalation of a radioactive particulate, part of the activity is absorbed into the blood from the respiratory tract. Mechanical processes move another part of the inhaled activity up from the respiratory passages and into the GI tract, from which a further fraction is absorbed into the blood. Ingestion bypasses the respiratory tract, but the submodel used for the GI tract is the same.

Superimposed on the dynamics of translocation and retention is the formation of radioactive daughters for certain radionuclides taken into the body. The daughters may have different chemical and physical properties from those of the parent and therefore may behave differently in the body. If one considers a chain of radionuclide species, indexed $i = 1, \dots, N$, in a compartment of the body, we assume that each species has associated with it a function, $R_i(t)$, which equals the fraction of activity in the organ at time zero that survives the organ's removal processes and radioactive decay t days later.

We may express the activities $A_i(t)$ of the radionuclides in terms of the functions R_i as follows:^{*}

$$A_i(t) = A_i(0) R_i(t) + \int_0^t \left[p_i(\tau) + \lambda_i^R \sum_{j=1}^{i-1} B_{ij} A_j(\tau) \right] \times R_i(t-\tau) d\tau \quad \mu\text{Ci} , \quad (1.6)$$

^{*}The summations in Eq. (1.6) and subsequent equations of this report are defined as zero when the lower limit exceeds the upper limit.

Fig. 1.1. Schematic representation of radioactivity movement as modeled by the INREM II code.

where

$\lambda_i^R = (\ln 2)/T_i^R$, where T_i^R = radioactive half-life (days) of species i ,

B_{ij} = radioactive branching ratio from species j to species i ,
 $j < i$,

$p_i(t)$ = rate ($\mu\text{Ci/day}$) at which activity of species i enters the compartment at time t .

We assume that the retention function $R_i(t)$ can be adequately represented by a linear combination of decaying exponential terms:

$$R_i(t) = \sum_{s=1}^{L_i} c_{is} \exp[-(\lambda_i^R + \lambda_{is}^B)t], \quad (1.7)$$

where

λ_{is}^B = rate coefficient (day^{-1}) for biological removal of species i from the compartment.

For correct interpretation of Eq. (1.6), R_i should satisfy $R_i(0) = 1$. Usually the coefficients c_{is} in Eq. (1.7) are positive, but on occasion better fits to data from experiments or compartmental analyses are obtained by allowing mixed signs.

1.2.1 Particulates in the respiratory tract: the ICRP Task Group Lung Model

Our submodel of particulate deposition and retention in the respiratory tract, based on the ICRP Task Group Lung Model,¹ is shown schematically in Fig. 1.2. The clearance parameters indicated in the figure were adopted from ICRP Publication 19 (ref. 6). The three clearance classes, D, W, and Y, correspond to rapid, intermediate, and slow absorption, respectively, of material deposited in the respiratory passages. The model identifies four major respiratory regions: nasal-pharynx (N-P), tracheo-bronchial tree (T-B), pulmonary region (P), and lymphatic tissue (L). Fractional depositions of inhaled particulates in

COMPARTMENT		CLASS					
		D		W		Y	
		T	F	T	F	T	F
N-P	a	0.01	0.5	0.01	0.1	0.01	0.01
(D ₃ = 0.30)	b	0.01	0.5	0.4	0.9	0.4	0.99
T-B	c	0.01	0.95	0.01	0.5	0.01	0.01
(D ₄ = 0.08)	d	0.2	0.05	0.2	0.5	0.2	0.99
	e	0.5	0.8	50	0.15	500	0.05
P	f	n.a.	n.a.	1.0	0.4	1.0	0.4
(D ₅ = 0.25)	g	n.a.	n.a.	50	0.4	500	0.4
	h	0.5	0.2	50	0.05	500	0.15
L	i	0.5	1.0	50	1.0	1000	0.9

Fig. 1.2. The ICRP Task Group Lung Model for particulates (refs. 1 and 6). The columns D, W, and Y correspond, respectively, to rapid, intermediate, and slow clearance of the inspired material. The symbols T and F denote the biological half-time (days) and coefficient, respectively, of a term in the appropriate retention function [Eqs. (1.8) through (1.12)]. The values shown for D₃, D₄, and D₅ correspond to activity median aerodynamic diameter (AMAD) = 1 μ m. Differential equations for pathways a, b, ..., i are (1.13) through (1.24).

the first three of these regions are given by the fractions D_3 , D_4 , and D_5 , respectively (the sum of these is less than one, with the shortfall accounting for prompt exhalation). These fractions are functions of the activity median aerodynamic diameter (AMAD) of the inspired particles; a functional relationship (for AMAD > 0.1 μm) suggested to W. S. Snyder by P. E. Morrow and presented in graphical form in Appendix VI of the Reactor Safety Study⁷ has been adopted in the INREM II calculations (Fig. 1.2.1-2).

The schematic presentation of the Task Group Lung Model, as set forth in the Task Group Report,¹ has been variously interpreted for purposes of a mathematical formulation, particularly when radioactive progeny are formed. The interpretation followed in INREM II is based on retention functions for the major regions, which are defined as follows:

Nasal-pharynx

$$R_i^{N-P}(t) = \underbrace{F_{a,i} e^{-\lambda_{a,i} t}}_{\text{to blood}} + \underbrace{F_{b,i} e^{-\lambda_{b,i} t}}_{\text{to GI}} \quad (1.8)$$

Tracheo-bronchial tree

(i) activity deposited directly

$$R_{1,i}^{T-B}(t) = \underbrace{F_{c,i} e^{-\lambda_{c,i} t}}_{\text{to blood}} + \underbrace{F_{d,i} e^{-\lambda_{d,i} t}}_{\text{to GI}} \quad (1.9)$$

(ii) activity in transit from pulmonary region (pathways f and g)

$$R_{2,i}^{T-B}(t) = \underbrace{e^{-\lambda_{d,i} t}}_{\text{to GI}} \quad (1.10)$$

Pulmonary region

$$R_i^P(t) = \underbrace{F_{e,i} e^{-\lambda_{e,i} t}}_{\text{to blood}} + \underbrace{F_{f,i} e^{-\lambda_{f,i} t} + F_{g,i} e^{-\lambda_{g,i} t}}_{\text{to T-B}} + \underbrace{F_{h,i} e^{-\lambda_{h,i} t}}_{\text{to lymph}} \quad (1.11)$$

Lymphatic tissue

$$R_1^L(t) = \underbrace{F_{i,1} e^{-\lambda_{i,1}^R t}}_{\text{to blood}} + \underbrace{(1 - F_{i,1}) e^{-\lambda_1^R t}}_{\text{remains in lymph (class Y materials)}} \quad (1.12)$$

In these equations, $\lambda_{v,1} = \lambda_1^R + \lambda_{v,1}^B$, where $\lambda_{v,1}^B = (\ln 2)/T_{v,1}^B$ and $T_{v,1}^B$ is the biological half-time (Fig. 1.2) associated with clearance pathway v ($= a, b, \dots, i$). The clearance class (D, W, Y) depends on chemical properties of species 1. The pathway fractions, $F_{v,1}$, are also shown in Fig. 1.2 for the three clearance classes.

Application of Eq. (1.6) to these retention functions permits us to write equations for the activity of species 1 in these major compartments. But for various reasons, it is more practical to use Eq. (1.6) and Eqs. (1.8) through (1.12) to derive a set of differential equations for the activities $A_{a,1}, \dots, A_{l,1}$ cleared by pathways $a, \dots, l$, respectively. These equations follow:

$$\begin{aligned} \dot{A}_{a,1} = & -\lambda_{a,1} A_{a,1} + F_{a,1} \lambda_1^R \sum_{j=1}^{i-1} B_{1j} (A_{a,j} + A_{b,j}) \\ & + F_{a,1} D_3 H_1(t) , \end{aligned} \quad (1.13)$$

$$\begin{aligned} \dot{A}_{b,1} = & -\lambda_{b,1} A_{b,1} + F_{b,1} \lambda_1^R \sum_{j=1}^{i-1} B_{1j} (A_{a,j} + A_{b,j}) \\ & + F_{b,1} D_3 H_1(t) , \end{aligned} \quad (1.14)$$

$$\begin{aligned} \dot{A}_{c,1} = & -\lambda_{c,1} A_{c,1} + F_{c,1} \lambda_1^R \sum_{j=1}^{i-1} B_{1j} (A_{c,j} + A_{d,j}) \\ & + F_{c,1} D_4 H_1(t) , \end{aligned} \quad (1.15)$$

$$\begin{aligned}\dot{A}_{d,i} = & -\lambda_{d,i} A_{d,i} + F_{d,i} \lambda_i^R \sum_{j=1}^{i-1} B_{ij} (A_{e,j} + A_{d,j}) \\ & + F_{d,i} D_4 H_1(t) ,\end{aligned}\quad (1.16)$$

$$\begin{aligned}\dot{A}_{e,i} = & -\lambda_{e,i} A_{e,i} + F_{e,i} \lambda_i^R \sum_{j=1}^{i-1} B_{ij} (A_{e,j} + A_{f,j} + A_{g,j} + A_{h,j}) \\ & + F_{e,i} D_5 H_1(t) ,\end{aligned}\quad (1.17)$$

$$\begin{aligned}\dot{A}_{f,i} = & -\lambda_{f,i} A_{f,i} + F_{f,i} \lambda_i^R \sum_{j=1}^{i-1} B_{ij} (A_{e,j} + A_{f,j} + A_{g,j} + A_{h,j}) \\ & + F_{f,i} D_5 H_1(t) ,\end{aligned}\quad (1.18)$$

$$\begin{aligned}\dot{A}_{g,i} = & -\lambda_{g,i} A_{g,i} + F_{g,i} \lambda_i^R \sum_{j=1}^{i-1} B_{ij} (A_{e,j} + A_{f,j} + A_{g,j} + A_{h,j}) \\ & + F_{g,i} D_5 H_1(t) ,\end{aligned}\quad (1.19)$$

$$\begin{aligned}\dot{A}_{h,i} = & -\lambda_{h,i} A_{h,i} + F_{h,i} \lambda_i^R \sum_{j=1}^{i-1} B_{ij} (A_{e,j} + A_{f,j} + A_{g,j} + A_{h,j}) \\ & + F_{h,i} D_5 H_1(t) ,\end{aligned}\quad (1.20)$$

$$\begin{aligned}\dot{A}_{i,i} = & -\lambda_{i,i} A_{i,i} + F_{i,i} \left\{ \lambda_i^R \sum_{j=1}^{i-1} B_{ij} (A_{i,j} + A_{j,j}) \right. \\ & \left. + \lambda_{h,i}^B A_{h,i} \right\} ,\end{aligned}\quad (1.21)$$

$$\dot{A}_{j,1} = -\lambda_1^R A_{j,1} + (1 - F_{i,1}) \left\{ \lambda_1^R \sum_{j=1}^{i-1} B_{ij} (A_{i,j} + A_{j,j}) + \lambda_{h,1}^B A_{h,1} \right\}, \quad (1.22)$$

$$\dot{A}_{k,1} = -\lambda_{d,1} A_{k,1} + \lambda_1^R \sum_{j=1}^{i-1} B_{ij} A_{k,j} + \lambda_{f,1}^B A_{f,1}, \quad (1.23)$$

$$\dot{A}_{l,1} = -\lambda_{d,1} A_{l,1} + \lambda_1^R \sum_{j=1}^{i-1} B_{ij} A_{l,j} + \lambda_{g,1}^B A_{g,1}. \quad (1.24)$$

For an initial intake of 1 μCi , depositions of species 1 (the parent) in the N-P, T-B, and P regions are D_3 , D_4 , and D_5 μCi , respectively, with $i - D_3 - D_4 - D_5$ μCi being exhaled. The amount of each daughter inhaled is assumed to be zero. The function $H_1(t)$ is the rate ($\mu\text{Ci/day}$) at which species 1 is inhaled at time t , and the previous remark implies $H_1(t) = 0$ when $i > 1$. Initial conditions for all species and compartments are zero:

$$A_{v,i}(0) = 0, \quad v = a, \dots, l, \quad i = 1, \dots, N.$$

To simulate an acute intake of a radionuclide, the function $H_1(t)$ can be defined by the user to be nonzero over a brief initial interval and zero elsewhere. For example, the 50-year dose commitment from an initial intake of 1 μCi can be obtained by defining

$$H_1(t) = \begin{cases} 1 \mu\text{Ci/day}, & 0 \leq t < 1 \text{ day} \\ 0 \mu\text{Ci/day}, & 1 \leq t \leq 18,250 \text{ days.} \end{cases}$$

In general, $H_1(t)$ may be defined by the user as a step function of time (i.e., a function which is constant on each of a set of subintervals which partition its domain of definition). User instructions for preparing data to define $H_1(t)$ are given in Sect. 2.1.

The μCi -days residences in the four major respiratory compartments are computed from the following equations:

$$\lambda_{N-P,i} = \lambda_{a,i} + \lambda_{b,i} , \quad (1.25)$$

$$\lambda_{T-B,i} = \lambda_{c,i} + \lambda_{d,i} + \lambda_{k,i} + \lambda_{l,i} , \quad (1.26)$$

$$\lambda_{P,i} = \lambda_{e,i} + \lambda_{f,i} + \lambda_{g,i} + \lambda_{h,i} , \quad (1.27)$$

$$\lambda_{L,i} = \lambda_{i,i} + \lambda_{j,i} , \quad (1.28)$$

where

$$\lambda_{v,i} = \int_0^T A_{v,i}(t) dt \quad \mu\text{Ci-days},$$

$$v = a, \dots, l . \quad (1.29)$$

The interpretations of the ICRP Task Group Lung Model expressed by Eqs. (1.13) through (1.28) are similar to those adopted by Snyder, Ford, and Watson⁸ and implemented in the TIMED computer code by Watson.⁹ The principal difference lies in the use of the intake rate function $H_1(t)$ for inhalation (and a counterpart for ingestion) rather than restriction of the calculation to a single acute intake.

The time-varying rate of absorption of activity from the respiratory tract into the blood is used to determine the uptake to other organs. This rate is

$$\dot{A}_{LB,i} = \lambda_{a,i}^B A_{a,i} + \lambda_{c,i}^B A_{c,i} + \lambda_{e,i}^B A_{e,i} + \lambda_{i,i}^B A_{i,i} , \quad (1.30)$$

where $A_{LB,i}$ may be interpreted as the cumulative activity of species i (μCi) absorbed into the blood. As before, $\lambda_{v,i}^B$ is the rate coefficient

for biological removal of the material from the respiratory tract by pathway v . The equation expressing the rate at which activity of species i is transmitted from respiratory to GI tract is

$$\dot{A}_{LG,i} = \lambda_{b,i}^B A_{b,i} + \lambda_{d,i}^B A_{d,i} + \lambda_{k,i}^B A_{k,i} + \lambda_{l,i}^B A_{l,i}, \quad (1.31)$$

where $A_{LG,i}$ is the cumulative activity of species i entering the GI tract from the respiratory tract. The equation governing the subsequent transfer from GI tract to blood is given in Sect. 1.2.2.

1.2.2 The gastrointestinal tract

The gastrointestinal (GI) tract is irradiated following the intake of radioactivity either by inhalation or ingestion. In the former case, particulate matter deposited in the respiratory tract and cleared from there by way of pathways b , d , k , and l enters the GI tract, as is indicated schematically in Fig. 1.3. Moreover, the dynamics of absorption of activity from the GI tract into the blood must be examined to determine the availability to other organs.

The four-segment catenary model of the GI tract adopted for use in these calculations (Fig. 1.3) is equivalent to the one described by Bernard.¹⁰ It assumes exponential outflow of activity from each segment into the next or out of the system. Outflow rate coefficients have been calculated from the transit times suggested by Eve¹¹ and are shown in the figure. Absorption of activity into the blood is usually assumed to be confined to the small intestine, but INREM II permits the user to specify absorption from any combination of the four segments at differential rates.

The differential equations for activity (μCi) and μCi -days residence of species i in the stomach (S), small intestine (SI), upper large intestine (ULI), and lower large intestine (LLI) follow:

$$\begin{aligned} \dot{A}_{S,i} = & -(\lambda_S + \lambda_i^R + \lambda_{S,i}^B) A_{S,i} + \lambda_i^R \sum_{j=1}^{i-1} B_{ij} A_{S,j} + (1 - \theta) G_i(t) \\ & + \theta (\lambda_{b,i}^B A_{b,i} + \lambda_{d,i}^B A_{d,i} + \lambda_{k,i}^B A_{k,i} + \lambda_{l,i}^B A_{l,i}), \end{aligned} \quad (1.32)$$

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Fig. 1.3. Schematic representation of radioactivity movement among respiratory tract, GI tract, and blood, as simulated by INREM II.

$$\begin{aligned} \dot{A}_{SI,i} = & -(\lambda_{SI} + \lambda_i^R + \lambda_{SI,i}^{ab}) A_{SI,i} + \lambda_S A_{S,i} \\ & + \lambda_i^R \sum_{j=1}^{i-1} B_{ij} A_{SI,j} , \end{aligned} \quad (1.33)$$

$$\begin{aligned} \dot{A}_{ULI,i} = & -(\lambda_{ULI} + \lambda_i^R + \lambda_{ULI,i}^{ab}) A_{ULI,i} + \lambda_{SI} A_{SI,i} \\ & + \lambda_i^R \sum_{j=1}^{i-1} B_{ij} A_{ULI,j} , \end{aligned} \quad (1.34)$$

$$\begin{aligned} \dot{A}_{LLI,i} = & -(\lambda_{LLI} + \lambda_i^R + \lambda_{LLI,i}^{ab}) A_{LLI,i} + \lambda_{ULI} A_{ULI,i} \\ & + \lambda_i^R \sum_{j=1}^{i-1} B_{ij} A_{LLI,j} , \end{aligned} \quad (1.35)$$

where

$A_{\sigma,i}$ = activity (μCi) of species i in the segment σ ($= S, SI, ULI,$ or LLI) of the GI tract,

λ_{σ} = outflow rate coefficient (day^{-1}) for activity in segment σ of the GI tract (calculated from transit times of Eve;¹¹ see Fig. 1.2),

λ_i^R = radioactive decay rate coefficient (day^{-1}) for nuclide species i ,

$\lambda_{\sigma,i}^{ab}$ = rate coefficient (day^{-1}) for absorption of nuclide species i from segment σ ($= S, SI, ULI,$ or LLI) into the blood,

B_{ij} = branching ratio of nuclide species j to species i ,

$\theta = 0$ or 1 according as intake of the parent nuclide occurs by ingestion or inhalation,

$G_i(t)$ = ingestion rate ($\mu\text{Ci/day}$) of species i at time t .

Initial conditions for the GI segments are zero:

$$A_{S,i}(0) = A_{SI,i}(0) = A_{ULI,i}(0) = A_{LLI,i}(0) = 0.$$

The intake rate function for ingestion, $G_1(t)$, is zero for $i > 1$. The user defines $G_1(t)$, by appropriate input data, as a step function of time. Note that when $\theta = 1$ (inhalation), all activity enters the GI tract from the respiratory tract through the last term in Eq. (1.32). In the case of ingestion, that term is zero, but $G_1(t)$ has a coefficient of unit ($\theta = 0$), and the intake is determined by $G_1(t)$.

The coefficient $\lambda_{\sigma,i}^{ab}$ ($\sigma = S, SI, ULI, LLI$) for the rate of absorption of species i into the blood from segment σ of the GI tract is derived from an absorption fraction $f_{\sigma,i}$ by the equation

$$f_{\sigma,i} = \lambda_{\sigma,i}^{ab} \int_0^{+\infty} \exp[-(\lambda_{\sigma} + \lambda_{\sigma,i}^{ab})t] dt, \quad (1.36)$$

which expresses the requirement that the fraction $f_{\sigma,i}$ of each mass unit of species i entering segment σ would be absorbed from that segment into the blood if none were lost to radioactive decay [the latter process is already taken into account in Eqs. (1.32) through (1.35)]. Integration and solution for $\lambda_{\sigma,i}^{ab}$ give

$$\lambda_{\sigma,i}^{ab} = \lambda_{\sigma} f_{\sigma,i} / (1 - f_{\sigma,i}). \quad (1.37)$$

In most calculations, absorption of activity into the blood is assumed to be confined to the small intestine, in which case the resultant fractional absorption, $f_{SI,i}$, is representative of the entire GI tract:

$$f_{SI,i} = f_{1,i}, \quad f_{S,i} = f_{ULI,i} = f_{LLI,i} = 0.$$

The notation f_1 has commonly been employed in ICRP literature^{12,13} to denote fractional absorption of the activity of a radionuclide from the GI tract as a whole.

We note that $f_{\sigma,i} = 1$ is inadmissible in Eq. (1.37). The INREM II code imposes an upper bound of 0.95 on each of the fractions $f_{\sigma,i}$, substituting this value if it is exceeded by the user's input. This practice, while arbitrary, is consistent with the premise that experimental data may well err by five percent or more in their indication of total absorption of an element from the GI tract.

The rate of absorption of species i from the GI tract into the blood is given by the equation

$$\begin{aligned} \dot{A}_{GB,i} = & \lambda_{S,i}^{ab} A_{S,i} + \lambda_{SI,i}^{ab} A_{SI,i} + \lambda_{ULI,i}^{ab} A_{ULI,i} \\ & + \lambda_{LLI,i}^{ab} A_{LLI,i} \end{aligned} \quad (1.38)$$

The rate $\dot{A}_{GB,i}$ is used, together with $\dot{A}_{LE,i}$ of Eq. (1.30) in the case of intake by inhalation, to compute the availability of species i to other organs.

1.2.3 Other organs

The dynamics of activity of a radionuclide species in an organ other than the respiratory or GI tract are assumed to be characterized by a fractional retention function of the form specified by Eq. (1.7). In general, we assume that $R_i(0) = 1$, i.e., that the coefficients, c_{is} , sum to unity. This assumption permits us to interpret the retention function as representing the fractional survival of each μCi deposited in the organ with respect to radioactive decay and the organ's removal processes. The integral in Eq. (1.6) then convolutes this fractional survival with the rate of formation of species i from the decay of progenitors in the organ plus the flow of activity into the organ from other parts of the system. With this interpretation, there is no sojourn of activity in an explicit blood compartment; rather, each μCi entering the blood from respiratory or GI tract is immediately allocated among several competing organs, with the remainder assigned to OTHER if the user supplies data for such a compartment. The fractional allocation to an organ is denoted

$f'_{2,i}$, where for the time being we have omitted a subscript for the specific organ. Therefore, we may rewrite Eq. (1.6) as

$$\begin{aligned} \dot{A}_i(t) = \int_0^t \left\{ f'_{2,i} [\theta \dot{A}_{LB,i}(\tau) + \dot{A}_{GB,i}(\tau)] + \lambda_i^R \sum_{j=1}^{i-1} B_{ij} A_j(\tau) \right\} \\ \times R_i(t - \tau) d\tau \quad \mu Ci, \end{aligned} \quad (1.39)$$

with $\dot{A}_{LB,i}$ and $\dot{A}_{GB,i}$ defined by Eqs. (1.30) and (1.38), respectively. Therefore, the quantity in brackets represents the rate at which species- i activity moves into the blood from the GI tract and (in case of intake by inhalation, viz., $\theta = 1$) the lungs; the fraction $f'_{2,i}$ of it is assumed to flow without delay into the organ. The initial level in the organ is set equal to zero.

The differential equations corresponding to Eq. (1.39) [when R_i is given by Eq. (1.7)] are

$$\begin{aligned} \dot{A}_{is} = -(\lambda_i^R + \lambda_{is}^B) A_{is} + c_{is} \left\{ \lambda_i^R \sum_{j=1}^{i-1} B_{ij} \sum_{r=1}^{L_j} A_{jr} \right. \\ \left. + f'_{2,i} [\theta \dot{A}_{LB,i} + \dot{A}_{GB,i}] \right\}, \quad s = 1, \dots, L_i, \end{aligned} \quad (1.40)$$

with initial conditions

$$A_{is}(0) = 0, \quad s = 1, \dots, L_i. \quad (1.41)$$

This formulation does not attempt to deal explicitly with recirculation to the blood of daughters formed in the organ and redistribution of the effluents among the competing organs. Snyder, Ford, and Watson⁸ have proposed one possible scheme for treating this process, which is implemented in the TIMED code of Watson.⁹

We define a retention function, $R_{i,ab}(t)$, to represent retention in the body of all radioactivity of species i that is absorbed into the

blood from the respiratory and GI tracts. If for each of the organs Y_k , $k = 1, \dots, P$ (assumed not to include respiratory or GI tract) we have a retention function $R_{i,k}(t)$ and a blood-to-organ transfer fraction $f'_{2,i,k}$, then we may write the equation

$$R_{i,ab}(t) = \sum_{k=1}^P f'_{2,i,k} R_{i,k}(t) + f'_{2,i,OTHER} R_{i,OTHER}(t) \quad (1.42)$$

for the fraction of activity surviving in the body t days after absorption into the blood. If $R_{i,ab}$ is available as part of the retention data for species i , this relation may be used to calculate the retention function and uptake fraction for the compartment Y_{OTHER} :

$$R_{i,OTHER}(t) = \left[R_{i,ab}(t) - \sum_{k=1}^P f'_{2,i,k} R_{i,k}(t) \right] \left[f'_{2,i,OTHER} \right]^{-1} \quad (1.43)$$

and

$$f'_{2,i,OTHER} = 1 - \sum_{k=1}^P f'_{2,i,k} \quad (1.44)$$

It is important that relations (1.42) and (1.44) be kept in mind when retention data are organized for the calculation.

For each radionuclide in a given chain, INREM II inputs a retention function $R_{i,ab}(t)$ for absorbed activity, but no use is made of it in the calculation.

It sometimes happens that the set of organs for which retention data are available is not the same for all nuclides in a chain. In such cases, the set of organs for each species must be enlarged so that a common set is obtained for the entire chain. When data are lacking for species i in organ k , it is suggested that the retention function $R_{i,OTHER}(t)$, as defined by Eqs. (1.43) and (1.44) be used, with the blood-to-organ transfer fraction

$$f'_{2,i,k} = \frac{m_k}{m_{\text{OTHER}}} f'_{2,i,\text{OTHER}} \quad (1.45)$$

This choice corresponds to the assumption of a uniform distribution of activity in Y_{OTHER} with respect to mass. It is appropriate only if higher concentrations of species i are accounted for by the explicit retention data assumed to be available for some organs.

1.3 Solution of the Differential Equations

The differential equations (1.13) through (1.24), (1.32) through (1.35), and (1.40) may be viewed as a single linear system with constant coefficients and expressed in matrix form as

$$\frac{d\vec{A}}{dt} = \vec{C}\vec{A} + \vec{I}(t), \quad \vec{A}(0) = \vec{0}, \quad (1.46)$$

where $\vec{C}$ is a constant $K \times K$ matrix, $\vec{A}$ is a vector (or $K \times 1$ matrix) of activities of the N radioactive species in the various compartments, $\frac{d\vec{A}}{dt}$ is the time derivative of $\vec{A}$, and $\vec{I}(t)$ is a vector function of t whose components are intake rates for the compartments. The number K of equations comprising the system is given by

$$K = \theta(12N) + 4N + \sum_{i=1}^N \sum_{j=1}^P L_{ij}, \quad (1.47)$$

where

$\theta = 0$ for intake by ingestion and 1 for intake by inhalation,

N = number of radionuclides in the chain,

P = number of organs in addition to lungs and GI tract that are considered in the calculation (including Y_{OTHER} if it is present),

L_{ij} = number of exponential terms in the retention function for species i and organ j .

The quantity needed for dose estimates is

$$\vec{\tilde{A}}(t) = \int_0^t \vec{\dot{A}}(\tau) d\tau, \quad (1.48)$$

where $\vec{\tilde{A}}(t)$ is a K-vector whose components are time-integrated activities ($\mu\text{Ci-days}$) of each of the N species in all compartments. Various sums of these components, as indicated in Sects. 1.2.1, 1.2.2, and 1.2.3, are then used in the dose computations.

Solution of the system (1.46) and subsequent integration of the activity levels [Eq. (1.48)] can be accomplished in various ways. Numerical integration by a discrete-variable method is possible but not entirely straightforward in practice because of the size of the system for certain calculations and the "stiffness" property of the differential equations for some sets of time constants that are encountered. Watson⁹ has implemented such an approach for a similar, though not identical, formulation and gives some discussion of the latter problem.

The INREM II code uses an alternative approach based on solving parts of the system in closed form and approximating certain continuous transfers of activity by discrete counterparts. We give some general indications of this approach in the following paragraphs.

We consider a subsystem of (1.46) governed by the differential equations

$$\dot{A}_{ik} = -(\lambda_i^R + \lambda_{ik}^B)A_{ik} + c_{ik}\lambda_i^R \sum_{j=1}^{i-1} B_{ij} \sum_{r=1}^{L_j} A_{jr} + p_i, \\ k = 1, \dots, L_i, \quad (1.49)$$

with arbitrary initial conditions. The inflow rates p_i are constants. The subsystem described by these equations can be interpreted as a biological compartment in which the fractional retention of species i is governed by the function

$$R_i(t) = \sum_{k=1}^{L_i} c_{ik} \exp[-(\lambda_i^R + \lambda_{ik}^B)t]. \quad (1.50)$$

The explicit solutions, $A_{ik}(t)$, of Eq. (1.49) are calculated by a subroutine, MULCOM. We express these solutions as

$$A_{ik}(t) = \begin{cases} D_{1k} + H_{1k} \exp(-\lambda_{1k} t) & \text{if } i = 1, \\ D_{ik} + H_{ik} \exp(-\lambda_{ik} t) + \sum_{j=1}^{i-1} \sum_{m=1}^{L_j} G_{ikjm} \exp(-\lambda_{jm} t) & \text{if } i > 1, \end{cases} \quad (1.51)$$

where the coefficients D_{ik} , H_{ik} , and G_{ikjm} may be calculated from the following recursions:

$$D_{ik} = \begin{cases} c_{1k} p_1 / \lambda_{1k} & \text{if } i = 1, \\ (c_{ik} / \lambda_{ik}) \left[\lambda_i^R \sum_{j=1}^{i-1} B_{ij} \sum_{m=1}^{L_j} D_{jm} + p_i \right] & \text{if } i > 1, \end{cases} \quad (1.52)$$

$$H_{ik} = \begin{cases} A_{1k}(0) - D_{1k} & \text{if } i = 1, \\ A_{ik}(0) - D_{ik} - c_{ik} \lambda_i^R \sum_{j=1}^{i-1} \sum_{m=1}^{L_j} (E_{ijm} + B_{ij} H_{jm}) \\ \quad \times (\lambda_{ik} - \lambda_{jm})^{-1} & \text{if } i > 1, \end{cases} \quad (1.53)$$

and

$$G_{ikjm} = c_{ik} \lambda_i^R (E_{ijm} + B_{ij} H_{jm}) (\lambda_{ik} - \lambda_{jm})^{-1}, \quad i > 1, \quad (1.54)$$

where

$$E_{ijm} = \begin{cases} \sum_{r=j+1}^{i-1} B_{ir} \sum_{\mu=1}^{L_r} G_{r\mu jm} & \text{if } j \leq i-2 \\ 0 & \text{if } j = i-1. \end{cases} \quad (1.55)$$

Computer storage requirements are reduced by retaining only the D_{ik} , H_{ik} , and E_{ijm} and generating the G_{ikjm} as needed. To exercise this option, we use the following recursion to calculate the E_{ijm} :

$$E_{ijm} = \begin{cases} 0 & \text{if } i = 2 \\ \sum_{r=j+1}^{i-1} B_{ir} \lambda_r^R \sum_{\mu=1}^{L_r} c_{r\mu} (E_{rjm} + B_{rj} H_{jm}) (\lambda_{r\mu} - \lambda_{jm})^{-1}, & \\ \text{for } j = 1, \dots, i-2, \text{ and } i > 2. \end{cases} \quad (1.56)$$

The order of computation is with increasing i , and for each i , a feasible order is D_{ik} , E_{ijm} (if $i > 2$), and then H_{ik} ; the G_{ikjm} may be calculated as soon as the E_{ijm} are available.

We note that the appearance of the factor $(\lambda_{ik} - \lambda_{jm})^{-1}$ in Eqs. (1.53) and (1.54) and $(\lambda_{r\mu} - \lambda_{jm})^{-1}$ in Eq. (1.54) requires the assumption that the λ_{ik} are distinct. In practice it is possible to separate equal pairs by a small percentage of their common values; this expedient is usually preferable to attempting to derive and implement general expressions that allow for all possible degeneracies.

The total interval of integration $[0, T]$ is subdivided into a number Q of subintervals $I_q = [t_{q-1}, t_q]$, $q = 1, \dots, Q-1$, and $I_Q = [t_{Q-1}, t_Q]$, with $t_0 = 0$ and $t_Q = T$. Several criteria will be imposed on this partition of the total interval, the first of which is that the intake rate function $[H_1(t)$ for inhalation or $G_1(t)$ for ingestion] is constant on each subinterval. A second criterion is that the user choose the number of subintervals to satisfy himself that their lengths $|I_q|$, $q = 1, \dots, Q$, permit continuous flows of activity from donor to receptor compartments to be approximated satisfactorily by pulses.

We illustrate this second point by considering an organ other than respiratory or GI tract. For the interval I_q , we write the differential equations as

$$\dot{A}_{is}^q = -(\lambda_i^R + \lambda_{is}^B) A_{is}^q + c_{is} \lambda_i^R \sum_{j=1}^{i-1} B_{ij} \sum_{r=1}^{L_j} A_{jr}^q, \quad s = 1, \dots, L_i, \quad (1.57)$$

with initial conditions

$$A_{is}^q(t_{q-1}) = A_{is}^{q-1}(t_{q-1}) + c_{is} f_{2,i}' [\theta A_{LB,i}^q + A_{GB,i}^q]. \quad (1.58)$$

Equation (1.57) is analogous to (1.40) with the continuous inflow rate for the interval I_q replaced by an initial pulse [Eq. (1.58)]. The number $A_{is}^{q-1}(t_{q-1})$ is the activity remaining from the previous subinterval (or zero if $q = 1$); more precisely, it is the limit of $A_{is}^{q-1}(t)$ as $t \rightarrow t_{q-1}^-$ because of the exclusion of the right endpoint of I_{q-1} . The cumulative activities $A_{LB,i}^q$ and $A_{GB,i}^q$ may be defined as

$$A_{LB,i}^q = \int_{t_{q-1}}^{t_q} \dot{A}_{LB,i}(t) dt, \quad (1.59)$$

$$A_{GB,i}^q = \int_{t_{q-1}}^{t_q} \dot{A}_{GB,i}(t) dt, \quad (1.60)$$

where the integrands are given by Eqs. (1.30) and (1.38), respectively.

Other transfers that are represented in an analogous fashion are depicted schematically as follows:

$$\left. \begin{array}{l} b \rightarrow S \\ d \rightarrow S \\ f \rightarrow k \rightarrow S \\ g \rightarrow l \rightarrow S \\ h \rightarrow L \end{array} \right\} \rightarrow SI \rightarrow ULI \rightarrow LLI$$

Equation (1.57) with initial condition (1.58) is a special case of the system (1.49), with all $p_i = 0$, and therefore can be solved by subroutine MULCOM.

A second type of subsystem occurs in this solution scheme. We illustrate by considering the computational counterparts of Eqs. (1.13) and (1.14) for pathways a and b of the N-P. The equations for interval I_q are

$$\begin{aligned} \dot{A}_{a,i}^q = & -\lambda_{a,i} A_{a,i}^q + F_{a,i} \lambda_i^R \sum_{j=1}^{i-1} B_{ij} (A_{a,j}^q + A_{b,j}^q) \\ & + F_{a,i} D_3 H_i(t) , \end{aligned} \quad (1.61)$$

$$\begin{aligned} \dot{A}_{b,i}^q = & -\lambda_{b,i} A_{b,i}^q + F_{b,i} \lambda_i^R \sum_{j=1}^{i-1} B_{ij} (A_{a,j}^q + A_{b,j}^q) \\ & + F_{b,i} D_3 H_i(t) \end{aligned} \quad (1.62)$$

with initial conditions

$$A_{a,i}^q(t_{q-1}) = A_{a,i}^{q-1}(t_{q-1}) , \quad (1.63)$$

$$A_{b,i}^q(t_{q-1}) = A_{b,i}^{q-1}(t_{q-1}) , \quad (1.64)$$

where, as before, $A_{a,i}^{q-1}(t_{q-1})$ and $A_{b,i}^{q-1}(t_{q-1})$ are intended to mean the limits as t tends to t_{q-1} from the left, or zero if $q = 1$.

Since $t_{q-1} \leq t < t_q$, $H_i(t)$ is constant in Eqs. (1.61) and (1.62), and therefore these equations are of the form of (1.49) and can be solved by MULCOM.

In summary, MULCOM is applied separately, on each interval I_q , to each of the following groupings of compartments:

<i>1</i>	N-P	(a,b)
<i>1</i>	T-B ₁	(c,d)
<i>2</i>	T-B ₂	(k,l)
<i>1</i>	P	(e,f,g,h)
<i>2</i>	L	(i, fixed)
<i>3</i>	S	
<i>4</i>	SI	
<i>5</i>	ULI	
<i>6</i>	LLI	
<i>7</i>	each of the other organs	

The italic numerals indicate an order ranking for the use of MULCOM; solution of groups of lower number must precede those of higher number. The order is based on the movement of activity.

To save computer time, INREM II contains a mechanism to sense a point in the interval of integration when (if such a point exists) (1) all activity in donor compartments has been reduced to a negligible level and (2) the intake rate function is zero throughout the remainder of the interval of integration. These conditions are often met in long-term integrations for acute exposure (e.g., a 50-year dose commitment following a pulse intake at time zero), and in these circumstances the remaining subintervals I_q can be treated as a single final segment, permitting the integration to be completed with one final round of calls to the subroutine MULCOM. The criterion for a negligible level of activity in a compartment which corresponds to a single exponential term of a retention function is for at least eight effective half-times of the species with the longest effective half-time for that compartment to have elapsed since the most recent replenishment.

2. THE INREM II CODE

The INREM II code, defined by its source listing in the Appendix, is written in FORTRAN IV. It has been compiled with the IBM FORTRAN Level H compiler and executed on the IBM/360 Models 75 and 91.

In coding INREM II we have made a conscious effort to keep the program readable, in order to facilitate its maintenance and further development, and to help users answer questions that might lack adequate treatment in the textual documentation. A description of the general structure is given in Sect. 2.2, and the source code contains numerous comment statements. We have attempted to avoid IBM or local enhancements of FORTRAN IV, but it has not been possible to test the code on a non-IBM system. Two IBM/360-OS Assembler routines, PGMSK and ICOMPA, are invoked by modules of INREM II. PGMSK responds to underflow and loss-of-significance interrupts by setting the number in question to zero and allowing the calculation to proceed. ICOMPA permits comparisons of character strings with respect to their relative placement in the Extended Binary Coded Decimal Interchange Code (EBCDIC) collating sequence. These routines would need to be rewritten in the assembly language of the local hardware and operating system, or their functions substituted or avoided by reprogramming. Listings of these routines are included in the Appendix.

The code utilizes input unit 5 for data and unit 6 for the line printer output described and illustrated in Sect. 2.1. Unit 16 is used for additional line printer output, for which the original purpose was diagnostic, but which has been retained for its usefulness. This supplementary output is not described in this report and may be suppressed, at the user's discretion, by manipulation of the job control language.

2.1 Input, Data Formats and Output

Before examining the general logic and the numerous operational details of INREM II, we call the reader's attention to Figs. 2.1 and 2.2. These printouts were produced by a run of INREM II for the $^{99}\text{Mo} - ^{99\text{m}}\text{Tc} - ^{99}\text{Tc}$ chain. Two intake cases were considered for this chain, one for

inhalation and one for ingestion. Each case has its own intake history and mode and data related to absorption and uptake of the parent and daughter radionuclides; but all cases share the same physical data and retention functions. The version of the code described in this report permits up to six cases for each radionuclide chain. Figure 2.1 shows tabulations of those input data that are applicable to both cases. Figure 2.2 exhibits the individual cases, with input data specific to each and the resulting dose matrix for each case.

Shown first in Fig. 2.1 are physical data for the chain, namely radioactive half-lives and branching ratios. Next is uptake and retention information for each of those source organs (other than respiratory and GI tract) which are explicitly considered in the run. The "BLOOD TRANSFER FRACTION F2-PRIME" is generally written f_2' in ICRP publications^{12,13} and is used here to denote a fractional transfer coefficient.

The coefficients labeled "COMPARTMENT DEPOSITION FRACTIONS" and the "COMPARTMENT BIOLOGICAL HALF-TIMES" are best illustrated by an example. We consider the retention model shown for ^{99}Tc in the liver:

$$R_{\text{LIVER}}(t) = e^{-\frac{0.693t}{7.77 \times 10^7}} \left[0.76 e^{-\frac{0.693t}{1.6}} + 0.20 e^{-\frac{0.693t}{3.7}} + 0.04 e^{-\frac{0.693t}{22}} \right].$$

The corresponding display in the INREM II printouts has the form

COMPARTMENT DEPOSITION FRACTION	COMPARTMENT BIOLOGICAL HALF-TIME (DAYS)
.	.
.	.
.	.
0.760	1.60
0.200	3.70
4.000E-02	22.0

PHYSICAL AND CHEMICAL PARAMETERS FOR ESSENTIALLY SIGNIFICANT PROPERTIES

000100CTIVE
 000100CTIVE
 000100CTIVE
 000100CTIVE
 000100CTIVE

DATE/TIME	FROM	TO	PAGE/TOTAL
01-00	01-00	01-00	01-00
01-00	01-00	01-00	01-00
01-00	01-00	01-00	01-00

STATION	WAVELENGTH	RECEIVED	TRANSMITTED	COMPARISON	DIFFERENCE
STATION 1	100-100	1.00	1.00	0.0000	0.00
	100-100	1.00	1.00	0.0000	0.00
	100-100	1.00	1.00	0.0000	0.00
	100-100	1.00	1.00	0.0000	0.00
STATION 2	100-100	1.00	1.00	0.0000	0.00
	100-100	1.00	1.00	0.0000	0.00
	100-100	1.00	1.00	0.0000	0.00
	100-100	1.00	1.00	0.0000	0.00
STATION 3	100-100	1.00	1.00	0.0000	0.00
	100-100	1.00	1.00	0.0000	0.00
	100-100	1.00	1.00	0.0000	0.00
	100-100	1.00	1.00	0.0000	0.00
STATION 4	100-100	1.00	1.00	0.0000	0.00
	100-100	1.00	1.00	0.0000	0.00
	100-100	1.00	1.00	0.0000	0.00
	100-100	1.00	1.00	0.0000	0.00
STATION 5	100-100	1.00	1.00	0.0000	0.00
	100-100	1.00	1.00	0.0000	0.00
	100-100	1.00	1.00	0.0000	0.00
	100-100	1.00	1.00	0.0000	0.00
STATION 6	100-100	1.00	1.00	0.0000	0.00
	100-100	1.00	1.00	0.0000	0.00
	100-100	1.00	1.00	0.0000	0.00
	100-100	1.00	1.00	0.0000	0.00
STATION 7	100-100	1.00	1.00	0.0000	0.00
	100-100	1.00	1.00	0.0000	0.00
	100-100	1.00	1.00	0.0000	0.00
	100-100	1.00	1.00	0.0000	0.00
STATION 8	100-100	1.00	1.00	0.0000	0.00
	100-100	1.00	1.00	0.0000	0.00
	100-100	1.00	1.00	0.0000	0.00
	100-100	1.00	1.00	0.0000	0.00
STATION 9	100-100	1.00	1.00	0.0000	0.00
	100-100	1.00	1.00	0.0000	0.00
	100-100	1.00	1.00	0.0000	0.00
	100-100	1.00	1.00	0.0000	0.00
STATION 10	100-100	1.00	1.00	0.0000	0.00
	100-100	1.00	1.00	0.0000	0.00
	100-100	1.00	1.00	0.0000	0.00
	100-100	1.00	1.00	0.0000	0.00

5 FACTS IN MICROCOMPUTER DAYS P. 20-29

7 APRIL 1965

REF ID: A66493

[illegible]

3 FACTORS INFLUENCING WIRE-DAY! FOR PG-00

1. PURPOSE

40201 006403

1.00000	0.00000
2.00000	0.00000
3.00000	0.00000
4.00000	0.00000
5.00000	0.00000
6.00000	0.00000
7.00000	0.00000
8.00000	0.00000
9.00000	0.00000
10.00000	0.00000
11.00000	0.00000
12.00000	0.00000
13.00000	0.00000
14.00000	0.00000
15.00000	0.00000
16.00000	0.00000
17.00000	0.00000
18.00000	0.00000
19.00000	0.00000
20.00000	0.00000
21.00000	0.00000
22.00000	0.00000
23.00000	0.00000
24.00000	0.00000
25.00000	0.00000
26.00000	0.00000
27.00000	0.00000
28.00000	0.00000
29.00000	0.00000
30.00000	0.00000
31.00000	0.00000
32.00000	0.00000
33.00000	0.00000
34.00000	0.00000
35.00000	0.00000
36.00000	0.00000
37.00000	0.00000
38.00000	0.00000
39.00000	0.00000
40.00000	0.00000
41.00000	0.00000
42.00000	0.00000
43.00000	0.00000
44.00000	0.00000
45.00000	0.00000
46.00000	0.00000
47.00000	0.00000
48.00000	0.00000
49.00000	0.00000
50.00000	0.00000
51.00000	0.00000
52.00000	0.00000
53.00000	0.00000
54.00000	0.00000
55.00000	0.00000
56.00000	0.00000
57.00000	0.00000
58.00000	0.00000
59.00000	0.00000
60.00000	0.00000
61.00000	0.00000
62.00000	0.00000
63.00000	0.00000
64.00000	0.00000
65.00000	0.00000
66.00000	0.00000
67.00000	0.00000
68.00000	0.00000
69.00000	0.00000
70.00000	0.00000
71.00000	0.00000
72.00000	0.00000
73.00000	0.00000
74.00000	0.00000
75.00000	0.00000
76.00000	0.00000
77.00000	0.00000
78.00000	0.00000
79.00000	0.00000
80.00000	0.00000
81.00000	0.00000
82.00000	0.00000
83.00000	0.00000
84.00000	0.00000
85.00000	0.00000
86.00000	0.00000
87.00000	0.00000
88.00000	0.00000
89.00000	0.00000
90.00000	0.00000
91.00000	0.00000
92.00000	0.00000
93.00000	0.00000
94.00000	0.00000
95.00000	0.00000
96.00000	0.00000
97.00000	0.00000
98.00000	0.00000
99.00000	0.00000
100.00000	0.00000

Fig. 2.1. Output from INREM II subroutine OUTDAT, showing the data read in for the $^{99}\text{Mo} - ^{99}\text{Tc} - ^{99}\text{Tc}$ problem.

3 FACTORS INFLUENCING-04VI FOR TC-99M

Source: 205403

	STAGE
LUMES	0.2970--00
RES LUM	0.2938--00
S WALL	0.3000--00
SE WALL	0.2810--00
SLI WALL	0.3030--00
SLI WALL	0.3000--00
T WALL	0.2770--00
ACWALL	0.2730--00
BL WALL	0.2920--00
RTWALLS	0.2820--00
LUMES	0.2900--00
OUTLET	0.2900--00
PERCENTS	0.2930--00
PERC	0.2930--00
R PER	0.2900--00
T PER	0.2930--00
PERCENT	0.2770--00
SPLICE	0.2710--00
PERCENT	0.2700--00
PERCENT	0.2710--00
PERCENT	0.2700--00
PERCENT	0.2710--00

3 FACTORS (REF/MICROFILM(-DAT)) FOR TC-99

SOURCE ORGANS

[illegible]

Fig. 2.1 (continued)

CASE 1-- INHALATION

INHALATION INTAKE RATE FUNCTION (MICROCURIES/DAY)											
FROM (DAYS)		TO (DAYS)		RATE							
0.0		1.00		1.00							
1.00		1.02W 04		0.0							
AND INCPH... 1.20 D3 =0.310 D4 =0.000E-02 D5 =0.200											
G.I. UPTAKE FRACTIONS											
SOLUBILITY CLASS		STOMACH		S INT		M L INT		L L INT			
MO-99		0		0.0		0.0		0.0			
TC-99m		0		0.0		0.0		0.0			
TC-99		0		0.7		0.000		0.0			
DOSE EQUIVALENT (REM)											
SOURCE	LUNGS	RES LYP	S CONT	ST CONT	MLE C3AT	LLI CONT	BONE	LIVER	KIDNEYS	THYROID	OTHER
TARGET											
LUNGS	1.320E-01	5.063E-04	1.595E-07	1.509E-06	5.530E-08	2.046E-04	1.339E-05	1.203E-04	0.007E-04	1.017E-08	2.099E-05
RES LYP	1.320E-01	1.320E-02	1.595E-07	1.509E-06	5.530E-08	2.046E-04	1.339E-05	1.203E-04	0.007E-04	1.017E-08	2.099E-05
S. WALL	1.227E-04	2.270E-04	2.700E-04	1.000E-07	6.320E-07	0.001E-07	7.704E-04	9.000E-05	1.000E-05	2.130E-09	2.700E-05
SI WALL	1.466E-04	2.099E-07	1.206E-07	1.061E-05	7.021E-06	2.000E-06	1.070E-05	0.340E-05	1.041E-05	0.100E-10	0.132E-05
ULI WALL	2.102E-04	1.51E-07	1.400E-07	1.720E-06	1.000E-04	1.120E-06	9.930E-04	1.290E-04	1.504E-05	0.910E-10	1.090E-05
LLI WALL	1.013E-07	1.00E-04	2.000E-07	1.001E-07	5.051E-07	0.120E-07	1.010E-07	1.375E-05	0.170E-04	2.062E-12	1.017E-05
T BODY	5.575E-04	1.15E-04	0.100E-07	0.050E-07	0.521E-07	1.003E-06	1.007E-04	0.153E-04	0.350E-05	1.297E-07	1.043E-04
BONE	1.000E-05	1.101E-06	0.507E-07	0.100E-06	1.702E-07	1.050E-07	2.001E-05	2.001E-05	0.000E-05	0.000E-09	2.000E-04
BL WALL	0.137E-07	1.700E-04	0.100E-06	0.107E-07	1.035E-07	1.040E-06	7.704E-04	1.022E-05	1.095E-06	1.010E-10	1.711E-04
KIDNEYS	1.203E-04	1.300E-04	0.041E-07	1.043E-07	0.020E-07	0.020E-07	1.307E-04	1.000E-04	0.151E-03	1.50E-09	2.070E-05
LIVER	1.017E-04	2.350E-04	0.001E-07	0.002E-06	0.130E-07	0.150E-06	0.510E-04	1.000E-04	2.110E-05	9.020E-09	2.220E-05
QUARTERS	0.070E-07	1.007E-07	1.700E-07	1.000E-07	1.000E-06	0.000E-06	1.700E-04	2.000E-05	0.000E-05	2.000E-10	0.000E-04
PANCREAS	1.000E-07	1.007E-07	1.700E-07	1.000E-07	1.000E-06	0.000E-06	1.700E-04	2.000E-05	0.000E-05	2.000E-10	0.000E-04
BONE	7.704E-04	1.042E-04	1.313E-07	1.000E-06	1.550E-07	1.010E-07	1.040E-03	0.720E-05	0.523E-06	1.020E-09	0.053E-05
R. HAD	0.000E-04	1.000E-06	2.275E-07	1.050E-07	0.050E-07	1.100E-06	1.000E-04	0.000E-05	1.000E-05	1.707E-09	2.277E-04
V. HAD	0.100E-04	1.501E-06	1.031E-07	7.000E-06	2.277E-07	0.000E-07	0.702E-04	0.000E-05	0.000E-05	0.000E-09	2.007E-04
ENDOST	7.704E-04	1.042E-04	1.313E-07	1.000E-06	1.550E-07	1.010E-07	9.210E-04	0.720E-05	0.523E-06	1.020E-09	1.040E-04
SPLTER	1.001E-07	2.730E-06	1.010E-06	0.100E-06	2.730E-07	2.000E-07	1.010E-07	1.000E-05	0.020E-05	0.130E-09	3.022E-04
TESTES	1.700E-07	2.102E-04	1.713E-06	2.002E-06	7.117E-06	0.007E-06	0.701E-04	0.170E-04	0.007E-07	0.000E-11	2.000E-04
THYROID	2.071E-04	1.100E-04	0.000E-07	0.070E-06	2.100E-04	1.200E-04	0.210E-05	0.001E-05	1.000E-06	1.000E-07	1.707E-04
THYROID	1.072E-04	1.150E-04	2.002E-04	1.010E-04	5.021E-04	1.700E-04	1.110E-05	0.000E-06	0.205E-07	1.100E-06	2.000E-05
UTERUS	1.072E-07	1.170E-07	1.000E-07	0.701E-07	0.000E-07	1.722E-06	0.207E-05	2.000E-05	0.000E-06	2.000E-10	2.000E-04
DOSE EQUIVALENT (REM)											
SOURCE	TOTAL										
TARGET											
LUNGS	0.000E-03										
RES LYP	1.041E-02										
S. WALL	0.100E-04										
SI WALL	1.010E-04										
ULI WALL	1.750E-04										
LLI WALL	1.030E-04										
T BODY	7.007E-04										
BONE	0.000E-04										
BL WALL	1.701E-04										
KIDNEYS	0.001E-03										
LIVER	1.010E-02										
QUARTERS	0.000E-04										
PANCREAS	0.007E-04										
BONE	1.275E-01										
R. HAD	7.152E-04										
V. HAD	0.700E-04										
ENDOST	1.150E-03										
SPLTER	0.100E-04										
TESTES	1.070E-04										
THYROID	0.100E-04										
THYROID	1.000E-04										
UTERUS	1.000E-04										
PERCENT DOSE EQUIVALENT..											
NUCLIDE	MO-99	TC-99m	TC-99								
TARGET											
LUNGS	95.1	0.0	0.0								
RES LYP	96.7	3.1	0.0								
S. WALL	80.0	15.0	0.0								
SI WALL	46.1	11.7	0.0								
ULI WALL	77.1	22.0	0.0								
LLI WALL	90.5	0.5	0.0								
T BODY	80.6	10.0	0.0								
BONE	70.0	20.0	0.0								
BL WALL	80.7	15.0	0.0								
KIDNEYS	90.2	5.0	0.0								
LIVER	93.0	6.0	0.0								
QUARTERS	80.0	15.1	0.0								
PANCREAS	70.2	23.0	0.0								
BONE	72.0	0.0	0.0								
R. HAD	85.5	14.5	0.0								
V. HAD	70.1	20.7	0.0								
ENDOST	91.0	8.2	0.0								
SPLTER	82.0	17.2	0.0								
TESTES	91.3	8.7	0.0								
THYROID	91.3	10.7	0.0								
THYROID	91.0	21.0	0.0								
UTERUS	80.2	19.0	0.0								

Fig. 2.2. Output from INREM II subroutine OUTPUT, showing the results of the calculations for two cases (one inhalation, one ingestion) of the ^{99}Mo - $^{99\text{m}}\text{Tc}$ - ^{99}Tc problem.

CASE 2. INGESTION

INGESTION INTAKE RATE FUNCTION (MICROCURIES/DAY)
 FROM (DAYS) TO (DAYS) RATE
 0.0 1.00 1.00
 1.00 1.025E-04 0.0

INGESTION TRANSFER FRACTIONS (G. T. TRACT TO BLOOD)

	MO-99	TC-99M	TC-99
STOMACH	0.0	0.0	0.0
S INT	0.950	0.000	0.000
U L INT	0.0	0.0	0.0
L L INT	0.0	0.0	0.0

DOSE EQUIVALENT (RPM).

SOURCE	S CONT	SI CONT	ULI CONT	LLI CONT	ROSE	LEVER	KIDNEYS	THYROID	OTHER	TOTAL
TARGET										
LUNGS	2.221E-06	9.100E-08	3.426E-07	1.788E-07	2.100E-05	2.062E-04	6.012E-04	1.395E-04	6.005E-05	2.701E-04
RES LUN	2.221E-06	9.100E-08	3.426E-07	1.788E-07	2.100E-05	2.062E-04	6.012E-04	1.395E-04	6.005E-05	2.701E-04
S WALL	1.700E-05	1.091E-06	1.001E-06	2.930E-06	1.231E-05	1.502E-04	1.021E-05	2.270E-04	6.790E-05	1.001E-03
SI WALL	3.230E-04	2.713E-06	1.716E-05	1.560E-05	1.722E-05	1.302E-04	2.477E-05	6.145E-10	6.006E-05	6.706E-04
ULI WALL	3.900E-06	2.716E-06	1.131E-03	7.070E-06	1.540E-05	2.040E-04	2.913E-05	5.047E-10	6.007E-05	1.056E-03
LLI WALL	1.612E-06	2.164E-06	1.754E-06	2.731E-05	2.263E-05	2.211E-05	7.030E-06	2.890E-10	1.373E-05	2.046E-05
T BONY	1.730E-06	2.513E-06	9.124E-06	9.103E-06	1.707E-04	6.401E-04	7.000E-05	1.645E-07	2.645E-04	1.170E-03
ADREN	2.747E-06	1.632E-07	1.040E-06	7.759E-07	1.203E-05	1.925E-04	1.030E-04	6.766E-09	6.706E-04	1.003E-03
BL WALL	1.154E-07	6.150E-07	2.230E-06	1.062E-05	1.101E-05	1.773E-05	1.150E-04	1.761E-10	2.720E-04	1.195E-04
KIDNEYS	4.106E-06	9.804E-07	2.971E-06	1.685E-06	2.051E-05	3.140E-04	1.312E-07	1.557E-09	6.666E-05	1.351E-02
LIVER	2.440E-04	5.400E-07	2.640E-06	1.207E-07	1.921E-05	2.262E-02	1.401E-05	1.757E-03	1.646E-05	2.271E-02
OVARIES	1.100E-06	1.102E-04	1.140E-05	2.940E-05	1.910E-05	1.003E-05	1.111E-05	1.136E-10	6.079E-04	5.993E-04
PANCREAS	2.120E-04	6.330E-07	2.250E-06	1.266E-06	2.012E-05	3.645E-04	2.030E-05	2.190E-09	6.920E-04	6.600E-04
BONE	4.020E-07	2.310E-07	9.510E-07	2.763E-06	1.675E-03	7.593E-05	1.060E-05	2.901E-08	7.640E-05	2.037E-03
R BONE	1.700E-06	9.510E-07	2.905E-06	6.932E-06	6.790E-04	1.040E-04	2.733E-05	1.171E-06	1.630E-04	1.137E-03
Y BONE	1.110E-06	6.200E-07	1.361E-06	2.797E-06	7.602E-05	1.123E-04	1.291E-05	1.100E-08	6.653E-04	6.722E-04
SPLEEN	0.020E-07	2.930E-07	4.510E-07	7.263E-06	1.002E-03	7.503E-05	1.047E-05	2.901E-08	2.610E-04	1.036E-03
TESTES	1.102E-05	9.707E-07	1.407E-06	1.530E-06	1.615E-05	8.335E-05	7.630E-05	3.462E-09	6.166E-04	6.720E-04
THYROID	1.040E-07	1.215E-07	4.422E-07	1.000E-06	1.190E-05	1.057E-05	1.117E-04	5.270E-11	6.540E-04	6.907E-04
UTERUS	1.026E-07	1.915E-04	1.431E-07	7.227E-06	1.474E-05	7.164E-05	1.093E-04	1.303E-07	1.202E-04	6.156E-04
THYROID	1.050E-07	1.115E-08	1.690E-08	2.395E-08	1.704E-05	1.461E-05	6.854E-07	6.517E-04	6.616E-05	1.253E-04
UTERUS	1.121E-06	2.762E-04	1.197E-06	1.079E-05	1.472E-05	1.350E-05	7.844E-06	1.155E-10	1.501E-04	6.741E-04

PERCENT DOSE EQUIVALENT..

SOURCE	MO-99	TC-99M	TC-99
TARGET			
LUNGS	59.4	40.2	0.0
RES LUN	59.4	40.2	0.0
S WALL	94.0	5.6	0.0
SI WALL	76.0	21.2	0.0
ULI WALL	80.1	11.9	0.0
LLI WALL	94.1	5.9	0.0
T BONY	99.7	10.3	0.0
ADREN	76.7	21.3	0.0
BL WALL	84.5	15.5	0.0
KIDNEYS	94.1	5.7	0.0
LIVER	91.5	6.5	0.0
OVARIES	69.4	14.2	0.0
PANCREAS	77.1	22.9	0.0
BONE	92.3	7.7	0.0
R BONE	86.0	14.0	0.0
Y BONE	90.1	14.9	0.0
SPLEEN	92.7	7.8	0.0
TESTES	84.0	16.0	0.0
THYROID	91.8	8.4	0.0
UTERUS	85.5	14.5	0.0
THYROID	44.0	15.2	0.0
UTERUS	84.3	15.7	0.0

RETENTION FUNCTIONS AND METABOLIC DATA USED IN THIS EXAMPLE ARE
 TAKEN FROM MDS-1000 AND FROM BILLOUGH ET AL. (1978).
 THYROID RETENTION FOR MO-99 AND BONE RETENTION FOR TC-99M COMPUTED
 FROM THE RETENTION FUNCTIONS FOR "OTHER" AND THE APPROPRIATE
 MASS FRACTIONS.

5

Fig. 2.2 (continued)

The exponential factor outside the brackets corresponds to radioactive decay of the radioisotope; the inner terms account for material in the liver that would survive metabolic removal in the absence of radioactive decay. Notice that the sum of the coefficients is unity. Thus

$R_{\text{LIVER}}(t)$ represents the fraction of a deposition in the liver at time zero which remains in the liver at subsequent time t . The product $f_{2,\text{LIVER}} R_{\text{LIVER}}(t)$ is interpreted as the fraction of an initial deposition in the blood which remains in the liver at time t .

The S-factors tabulated in Fig. 2.1 were computed with the SFACTOR code of Dunning et al.⁴ from nuclear decay data compiled by Kocher⁵ and specific absorbed fractions for photon emissions from ORNL-5000 (ref. 2). The compartment labeled "OTHER" is complementary to the source organs listed, and the S-factors for this compartment satisfy Eq. (1.4). Our "BONE" factors combine the cortical and cancellous bone sources as follows:

$$S_{\text{BONE}} = \frac{m_{\text{CORT}} S_{\text{CORT}} + m_{\text{CANC}} S_{\text{CANC}}}{m_{\text{CORT}} + m_{\text{CANC}}},$$

where m denotes the mass of the indicated source.

The first case (Fig. 2.2) assumes intake by inhalation. The intake rate has been specified as the step function

$$H(t) = \begin{cases} 1 \text{ } \mu\text{Ci/day} & \text{if } 0 \leq t < 1 \text{ day} \\ 0 \text{ } \mu\text{Ci/day} & \text{if } 1 \leq t < 18,250 \text{ days (50 years),} \end{cases}$$

which closely approximates an initial pulse. The resulting dose estimates may therefore be interpreted as dose commitments (rem) per μCi of ^{99}Mo inhaled (only the parent nuclide is assumed to be present in the intake).

Corresponding to an assumed AMAD of $1 \text{ } \mu\text{m}$ for the inhaled particulate, supplied as input data, the program has computed and used the regional respiratory deposition fractions D_3 , D_4 , and D_5 shown in Fig. 2.2. These values are derived by subroutine INTP from graphical information in Appendix D of WASH-1400, Appendix VI (ref. 7). The same document suggests

lung clearance class D for molybdates and for compounds of technetium other than the oxides and hydroxides. The gastrointestinal absorption fractions f_1 (0.95 for molybdenum and 0.8 for technetium) were adopted from WASH-1400 and from Killough et al. respectively.^{7,14}

The matrix of dose-equivalent estimates (rem), shown for those source- and target-organ combinations prescribed in the data, is of interest primarily in judging the relative importance of cross irradiations when penetrating components (photon or neutron) are present. The entries in the "TOTAL" column, for the example at hand, represent estimates of dose equivalent to the indicated target organs from ^{99}Mo and the $^{99\text{m}}\text{Tc}$ and ^{99}Tc daughters allocated among the source organs as predicted by the models and parameters per μCi of ^{99}Mo taken into the body by inhalation. For every target, the total is the sum of all entries in the corresponding row.

The second case shown in Fig. 2.2 represents intake of ^{99}Mo by ingestion. The intake rate function $G(t)$ is the same as $H(t)$ for the previous case, and the same gastrointestinal absorption parameters (f_i) have been used. Since activity is assumed not to enter the lungs directly as a particulate (or otherwise, in this example), no respiratory parameters are used for an ingestion case. The dose matrix now excludes the columns corresponding to respiratory sources; otherwise it is interpreted as in the previous case.

The comments at the bottom of Fig. 2.2 were inserted in the input at the appropriate point and were printed on the output by the computer to aid the user in documenting the sources of information used in the calculation.

The preparation of data for input to INREM II is rather tedious, and we offer alternative descriptions. One is provided by the flow charts of Figs. 2.3 and 2.4, which diagram the logic of subroutine INPUT and show all READ and FORMAT statements (an exception is noted below, and some liberties have been taken with FORTRAN syntax in operations other than input). Subroutine INPUT reads all data for INREM II except the user's comments, which are read and printed by subroutine CMTS. For readers less familiar with FORTRAN input/output statements, the

Fig. 2.3. Flow-chart for initial segment of subroutine INPUT.

Fig. 2.4. Flow-chart for final segment of subroutine INPUT.

following outline of the input process indicates the approximate order of the data, and Fig. 2.5 is an annotated printout of the data cards used for the sample calculations with the ^{99}Mo - $^{99\text{m}}\text{Tc}$ - ^{99}Tc chain.

Outline of input data for an INREM II problem

1. Number NSPEC of radionuclides in chain, names, and radioactive half-lives;
2. Number NBR of nonzero branching ratios, followed by NBR cards, each of which contains information of the form I, J, $\text{BRANCH}(J,I) =$ fraction of nuclide I decaying to nuclide J; I and J are index numbers (1-NSPEC) corresponding to the order of nuclides in the chain, as established by the data of item 1;
3. Number NS of source organs other than lungs and GI tract, and for each, the name and mass;
4. Number NT of target organs other than lungs and GI tract, and for each, the name and mass;
5. For each radionuclide in the chain,
 - 5a. blood-to-organ transfer fraction F2PRIM and retention function parameters for each source organ other than lungs and GI tract;
 - 5b. matrix of S-factors for the indicated sources and targets;
6. Number NCASES of cases;
7. For each case,
 - 7a. exposure mode (i.e., inhalation or ingestion), length of time interval for integration, and length of subintervals;
 - 7b. data to define the intake-rate function;

inhalation	<ol style="list-style-type: none"> 7c. activity median aerodynamic diameter (AMAD) of particles; 7d. for each nuclide in the chain, <ol style="list-style-type: none"> 7d-1. literal code to signal respiratory clearance properties (D, W, Y, or special case for which user supplies additional parameters); 7d-2. GI absorption fraction for each of the four segments of the GI tract;
ingestion	<ol style="list-style-type: none"> 7c'. GI absorption fractions for each nuclide in the chain;

8. Comment cards to be printed on the output, terminated by a card with '\$' punched in column 1.

Some exceptions to items of the outline are discussed below.

Relative to item 5, we note that INREM II expects the data for the first source organ in the sequence to correspond to total body, by which we mean material that has been absorbed from the respiratory or GI tract. Uptake and retention data for this source organ are printed by subroutine OUTDAT, but they are not used in the calculation.

For some radionuclides, it is useful to include a compartment for prompt excretion, as if it were a source organ. To exercise this option, the user must modify the foregoing outline of data preparation as follows:

- a. In step 3, columns 11-23 of the card containing the number of source organs must have some nonblank character punched. A mnemonic message, such as 'PLUS EXCRET.' is suggested. The excretion compartment is not included in the count of source organs.
- b. In step 5a, the data for the excretion compartment is inserted immediately after the corresponding block of data for total body. The S-factors provided by the user for the total body source (and which must always be present) are transferred by subroutine INPUT to be used to calculate dose due to activity in the excretion compartment.

The modifications a and b shown above have been omitted from the flow charts of Figs. 2.3 and 2.4.

The outline given above describes the data preparation for a single problem (i.e., a single chain). Multiple problems may be processed in a single job, with the data for the last problem being terminated with the delimiter /* (for the IBM Operating System).

2.2 Logical Structure and COMMON Data Storage of INREM II

An effort has been made to keep INREM II well structured in the following sense:

1. The driving program and all subprograms form a hierarchy (see Fig. 2.6).
2. Each module (i.e., driving program or subprogram) is a linear sequence of structures of the following types:
 - 2a. Iteration (e.g., DO-loop)
 - 2b. Simple selection (IF-THEN-ELSE)
 - 2c. Linear sequence of fundamental operations (input/output, arithmetic statement, subprogram invocation).

These structures may, of course, be nested. For example, the scope of an iteration may be a linear sequence of structures of type 2a, 2b, and 2c. The IF-THEN-ELSE logic of a selection structure may not be implemented literally in FORTRAN IV, except in the simple case in which the THEN clause consists of a single statement and the ELSE clause is null. It is therefore desirable to position the groups of statements that comprise these clauses together and make the entry and exit point of each obvious to the reader through the use of comments.

The longer modules of INREM II (such as subroutine STEP) may be viewed as concatenated blocks of code. The beginning and end of a block are plainly marked by comments, and the block is entered only at the beginning (generally at a CONTINUE statement). There are no transfers from one block into the interior of another. Thus, revision of code within a block is less likely to have unanticipated ramifications elsewhere. Generally, backward-pointing GO TO statements have been avoided (there are perhaps two exceptions).

First let us summarize the highest level of the hierarchy shown in Fig. 2.6. As in Sect. 2.1, we consider problem to be the INREM II data for a single radionuclide chain consisting of one or more radioactive species. A problem may contain one to six cases, such as were described and illustrated in Sect. 2.1. The input deck to INREM II may then be regarded as a sequence of one or more problems.

Most of the driving program is an iterative structure. Each iteration processes a single problem: input, computation, and output. Many of the statements in the scope of the iteration are subroutine calls, although some data conversion is done at this level. Figure 2.7 is a

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Fig. 2.6. Hierarchical structure of INREM II.

Fig. 2.7. Flow-chart for INREM II driving program.

simplified flow chart of the driving program. Subroutine INPUT reads all data for the current problem (or returns an end-of-file flag if there are no more problems in the input deck). Subroutine OUTDAT prints that segment of data that is common to all cases defined by the problem (Fig. 2.1 is output from OUTDAT). An inner iteration performs computations for each case and stores the results. In the event of an inhalation case, subroutine INTP calculates the respiratory regional deposition fractions D_3 , D_4 , and D_5 that are appropriate to the AMAD value that was read. Subroutine DOSRUN manages the integration of the differential equations to estimate microcurie-days residence of activity in each compartment and combines these quantities with the S-factors to compute a dose matrix for the case. The call to DOSRUN ends the case iteration. A call to subroutine OUTPUT causes the results of all cases within the current problem to be printed (Fig. 2.2 is an example of the work of OUTPUT). Finally, subroutine CMMNTS reads and prints any comments or footnotes the user might have inserted in the input stream at the end of the problem. The comments must be followed by a card with the character '\$' punched in column 1. There is no limit to the number of comment cards that may be inserted, but if there are none, the terminating card with the '\$' punch still must be placed after the data for the problem (see Fig. 2.5 for a listing of a sample data deck which includes such comment cards).

At the first subordinate level of the hierarchy of Fig. 2.6 is subroutine DOSRUN, which manages the computations for a given case. The principal tasks of DOSRUN are

1. to compute the partition of the interval of integration $[0, T]$ into subintervals I_q , $q = 1, \dots, Q$, as described in Sect. 1.3;
2. to invoke subroutine STEP for each integration over a subinterval I_q ;
3. to determine a stage at which activity levels of all species in all donor compartments may be considered negligible, and if no further intake can occur, to combine the remaining subintervals I_q into a single final segment which can be covered by a single call to STEP;

4. to compute the entries in the source-target dose matrix for the current case and pass them to subroutine OUTPUT by way of COMMON block /DOSES/;
5. to compute, for the current case, the percent contribution of each nuclide in the chain to the total dose to each target organ and pass this information to subroutine OUTPUT through COMMON block /PERCNT/.

Task 3 adds considerable code to the subroutine and tends to obscure the general logic. But the computing time saved by its inclusion has made the additional complication worthwhile. We comment on this task in the following paragraphs.

The donor compartments considered are those associated with each of the respiratory pathways $a, \dots, i, k, l$, and each of the four segments of the GI tract, S, SI, ULI, LLI. For each compartment we calculate

$$\Lambda_v = \min_{i=1,N} (\lambda_{v,i}^B + \lambda_i^R), \quad v = a, \dots, i,$$

$$\Lambda_\sigma = \min_{i=1,N} (\lambda_\sigma + \lambda_{\sigma,i}^{ab} + \lambda_i^R), \quad \sigma = S, SI, ULI, LLI,$$

$$\Lambda_R = \min_{i=1,N} \lambda_i^R.$$

The numbers

$$\hat{T}_v = 8 \ln(2)/\Lambda_v, \quad \hat{T}_\sigma = 8 \ln(2)/\Lambda_\sigma, \quad \hat{T}_R = 8 \ln(2)/\Lambda_R$$

represent eight effective half-times of the longest-retained species in each compartment (the species achieving the maximum may vary from one compartment to another) and eight radioactive half-lives of the longest-lived species, respectively. Let $\hat{T}_{INT}$ denote the time at which intake ceases. We define

$$\hat{T}_{N-P} = \begin{cases} \hat{T}_{INT} + \max(\hat{T}_a, \hat{T}_b) & \text{for inhalation} \\ 0 & \text{for ingestion} \end{cases}$$

$$\hat{T}_{T-B_1} = \begin{cases} \hat{T}_{INT} + \max(\hat{T}_c, \hat{T}_d) & \text{for inhalation} \\ 0 & \text{for ingestion} \end{cases}$$

$$\hat{T}_P = \begin{cases} \hat{T}_{INT} + \max(\hat{T}_e, \hat{T}_f, \hat{T}_g, \hat{T}_h) & \text{for inhalation} \\ 0 & \text{for ingestion} \end{cases}$$

$$\hat{T}_{L_1} = \begin{cases} \hat{T}_{INT} + \hat{T}_h + \hat{T}_i & \text{for inhalation} \\ 0 & \text{for ingestion} \end{cases}$$

$$\hat{T}_{L_2} = \begin{cases} \hat{T}_{INT} + \hat{T}_h + \hat{T}_R & \text{for inhalation} \\ 0 & \text{for ingestion} \end{cases}$$

$$\hat{T}_{T-B_2} = \begin{cases} \hat{T}_{INT} + \hat{T}_d + \max(\hat{T}_f, \hat{T}_g) & \text{for inhalation} \\ 0 & \text{for ingestion} \end{cases}$$

$$\hat{T}_{GI} = \begin{cases} \hat{T}_S + \hat{T}_{SI} + \hat{T}_{ULI} + \hat{T}_{LLI} + \max(\hat{T}_{N-P}, \hat{T}_{T-B_1}, \hat{T}_{T-B_2}) & \text{for inhalation} \\ \hat{T}_{INT} + \hat{T}_S + \hat{T}_{SI} + \hat{T}_{ULI} + \hat{T}_{LLI} & \text{for ingestion} \end{cases}$$

As soon as DOSRUN has completed the integration for a subinterval $I_q = [t_{q-1}, t_q]$, the endpoint t_q is compared with each of the times $\hat{T}_{N-P}, \hat{T}_{T-B_1}, \hat{T}_{T-B_2}, \hat{T}_P, \hat{T}_{L_1}, \hat{T}_{L_2}, \hat{T}_{GI}$, and when t_q is larger or equal, the corresponding compartment is considered devoid of activity of all species of the chain; a flag is set and the variables which represent the levels are set equal to zero. After all donor compartments are exhausted, the integration is completed in one last call to subroutine STEP for the final receptor compartments, i.e., the organs other than respiratory or GI tract.

Some comment on task 1 of DOSRUN might be helpful. The user specifies, for each case in a problem, what he judges to be a suitable length for the subintervals of the integration interval. For a given case, let us denote this number by T_{STEP} . It is important to be aware of the following facts concerning T_{STEP} :

- i. Not all subintervals I_q will be of the same length. They will be adjusted by DOSRUN to align with the endpoints of subintervals on which the intake rate function is constant. But none will exceed T_{STEP} in length.
- ii. If all donor compartments are exhausted and intake ceases before the integration is complete, the remaining subintervals I_q are consolidated into a single final segment, the length of which may exceed T_{STEP} . But this consolidation does not represent an approximation: it is equivalent to continuing the integration individually over each of the component subintervals.

As an example, consider

$$T_{STEP} = 1825 \text{ days (5 years) ,}$$

$$\text{intake rate} = \begin{cases} 1 \text{ } \mu\text{Ci/day for } 0 \leq t < 1 \text{ day} \\ 0 \text{ } \mu\text{Ci/day for } 1 \leq t < 18,250 \text{ days (50 years) .} \end{cases}$$

If the intervals defined by the intake rate function are not considered, we calculate as a first approximation to the number of steps

$$NSTEPS = 1 + [18,250/1825] = 11,$$

where the brackets denote the largest integer which does not exceed the enclosed quotient (if the division were not exact, the remainder would be lost, and the number of steps is increased by one to compensate). For the interval $[0, 1)$ of the intake rate, we compute the number of subintervals as

$$NST = 1 + \left[\left(\frac{1 - 0}{18,250} \right) \times 11 \right] = 1$$

of length $|I_1| = 1$. For the remainder of the interval, i.e., $[1, 18250]$, we calculate

$$NST = 1 + \left[\left(\frac{18,250 - 1}{18,250} \right) \times 11 \right] = 11 \text{ intervals,}$$

each of length $|I_q| = 18,249/11 = 1659$ days, $q = 2, \dots, 12$. Therefore, the user's original specification of 10 subintervals of 1825 days each was modified to 12 subintervals, none exceeding 1659 days. Moreover, if all donor compartments are exhausted, say, in 10 years (3650 days), DOSRUN will consolidate all subintervals after the fourth:

$$1 + 1659 + 1659 = 3319 < 3650 < 1 + 3 \times 1659 = 4978$$

The result is that only five subintervals, in effect, are used. The user's specification should be made with a view of controlling the spacing of the pulse trains of activity entering the receptor compartments while the donor compartments still contain material.

Subroutine STEP, which is invoked by DOSRUN for each subinterval I_q (or the consolidated final segment), carries the integration forward for that interval. It takes the initial levels for the interval from COMMON block /LEVELS/ and returns the updated values to this block. The time-integrated activities ($\mu\text{Ci-days}$) for the subinterval are returned to COMMON block /CUMACT/. Subroutine DOSRUN keeps a cumulative total of these in the array AWIGL (ISPEC, ISOU), where the index values of ISOU have the following meanings:

ISOU	ORGAN
1	Lungs (N-P, T-B _{1,2} , P)
2	Respiratory lymph nodes (L _{1,2})
3-6	GI tract (S, SI, ULJ, LLI)
7	Total body
8-NSOU	Other source organs

The segments of STEP are clearly marked by comments in the source code and are principally devoted to organizing data for calls to subroutine MUI.COM and moving that subroutine's output to appropriate arrays.

The intake rate vector is evaluated by subroutine HAL or GES for inhalation or ingestion, respectively. While INREM II accounts for the formation of daughter nuclides in the body, intakes are limited to the first species of the chain, and accordingly, a call to HAL(T,H) or GES(T,G) returns a vector H or G whose first component is the intake rate at time T of the first species and whose other components are zero.

Transmission of information among modules of INREM II occurs primarily through COMMON storage. A list of the COMMON blocks, together with an explanation of the variables assigned to each, follows.

/RADAT/ TR(20), BRANCH(20,20)

TR(ISPEC) = radioactive half-life of nuclide species ISPEC (days).

BRANCH(ISPEC, JSPEC) = branching ratio of species JSPEC to ISPEC (JSPEC < ISPEC).

/NUMBERS/ NSPEC, NSOU, NTRG

NSPEC = number of radionuclide species in the chain.

NSOU = total number of source organs (including 2 respiratory and contents of 4 GI compartments).

NTRG = total number of target tissues (including 2 respiratory and 4 GI compartments).

/CASES/ NCASES, MODE(6), TEND(6), NINT(6), T(6,30), P(6,30),

ISOL(6,20), AMAD(6), DEFAULT(6), FLUNG(6,9,20), TBLUNG(6,9,20), F1(6,20), GIFRAC(6,20,4)

NCASES = number of cases in the current problem

MODE(ICASE) = numerical code for exposure mode of case ICASE (1 = inhalation, 2 = ingestion); first read in by subroutine INPUT as literal code ('H' = inhalation, 'G' = ingestion) and converted immediately to numeric.

TEND(ICASE) = end of integration interval (days) for case ICASE. Integration is always started at time zero.

NINT(ICASE) = number of subintervals of the integration interval needed to define the intake rate step function for case ICASE. In the present implementation, NINT(ICASE) must be ≤ 30 .

T(ICASE,K) = left endpoint (days) of the K th subinterval of the intake rate step function for case ICASE. T(ICASE,1) should equal zero.

P(ICASE,K) = intake rate ($\mu\text{Ci/day}$) in the K th subinterval for case ICASE, i.e., for times between T(ICASE,K) and T(ICASE,K+1), or if $K = \text{NINT(ICASE)}$, for times between T(ICASE,NINT(ICASE)) and TEND(ICASE).

Note. Figure 2.8 shows an example illustrating the relationship of TEND, NINT, T, and P.

ISOL(ICASE,ISPEC) = numeric code indicating respiratory clearance class (D, W, Y, or special case) of species ISPEC if case ICASE pertains to inhalation:

$$\text{ISOL} = \begin{cases} 1 & \text{for class D} \\ 2 & \text{for class W} \\ 3 & \text{for class Y} \\ 4 & \text{for special case, in which user supplies} \\ & \text{respiratory clearance parameters} \end{cases}$$

Values of ISOL are read by subroutine INPUT as literal data and converted immediately to numeric.

AMAD(ICASE) = activity median aerodynamic diameter (μm) of inhaled aerosol (applies to first nuclide species in the chain).

DEFAULT(ICASE) is not used in the present version of INREM II. FLUNG(ICASE,IPATH,ISPEC), TBLUNG(ICASE,IPATH,ISPEC) = special respiratory local deposition (FLUNG) and clearance (TBLUNG) parameters supplied by the user for case ICASE. FLUNG is a dimensionless fraction, and TBLUNG is a biological half-time (days). The index IPATH refers to one of the nine

IC = CASE INDEX
 NINT (IC) = 4
 P = INTAKE RATE (μ Ci/day)
 T, TEND = TIME (days)

Fig. 2.8. Intake rate function (μ Ci/day) for INREM II.

clearance pathways $a \rightarrow i$ (see Fig. 1.2). These special entries are read and stored by subroutine INPUT only when $ISOL(ICASE,ISPEC) = 4$.

$FI(ICASE,ISPEC)$ = GI-tract-to-blood transfer fraction for nuclide species ISPEC in case ICASE. Read and stored for both inhalation and ingestion cases.

$GIFRAC(ICASE,ISPEC,ISEG)$ = GI-tract-to-blood transfer fraction for nuclide species ISPEC in case ICASE for the segment ISEG of the GI tract.

/TGLM/ LMA(20), LMB(20), LMC(20), LMD(20), LME(20), LMF(20), LMG(20), LMH(20), LMI(20), FA(20), FB(20), FC(20), FD(20), FE(20), FF(20), FG(20), FH(20), FI(20)

$LMA(ISPEC) \rightarrow LMI(ISPEC)$ = REAL clearance rate coefficients (day^{-1}) for respiratory pathways $a \rightarrow i$, respectively;

$FA(ISPEC) \rightarrow FI(ISPEC)$ = corresponding local deposition fractions. These quantities are computed in the driving program at the beginning of each inhalation case and placed in COMMON block /TGLM/ as a means of transmitting them to subroutine DIFFUN.

/ORGDAT/ NCOMP(20,16), C(20,5,16), LMBDAB(20,5,16), F2PRIM(20,16)
 $NCOMP(ISPEC,ISOU-6)$, $C(ISPEC,IC,ISOU-6)$, $LMBDAB(ISPEC,IC,ISOU-6)$
 = parameters specifying the fractional retention function for nuclide species ISPEC in source organ ISOU (index values 1 $\rightarrow$ 6 are preempted for respiratory and GI sources). NCOMP is the number of terms in the retention function, and C and LMBDAB (REAL) are the coefficient and biological removal rate constant (day^{-1}), respectively, of term IC ($1 \leq IC \leq NCOMP$). The form is

$$\sum_{IC=1}^{NCOMP(ISPEC,ISOU-6)} C(ISPEC,IC,ISOU-6) * \exp(-LMBDAB(ISPEC,IC,ISOU-6)*T)$$

The function shown has not been corrected for radioactive decay.

F2F3IM(ISPEC,ISOU-6) = transfer fraction of nuclide species ISPEC from blood to source organ ISOU.

/DOSES/ DOSE(6,27,25)

DOSE(ICASE,ITRG,ISOU) = dose (rem) to target organ ITRG from activity of all nuclide species in source organ ISOU for case ICASE. The entries for ISOU = NSOU+1 are the target organ totals.

/MASSES/ SMASS(24), TMASS(27)

SMASS(ISOU) = mass (g) of source tissue ISOU. These are not used in the current version of INREM II.

TMASS(ITRG) = mass (g) of target tissue ITRG. These are not used in the current version of INREM II.

/NAMES/ NAMNUC(20), NAMSOU(24), NAMTRG(27)

NAMNUC(ISPEC) = DOUBLE PRECISION (IBM/360-370: 8 character) name of radionuclide species ISPEC (e.g., 'SR-90~~0000~~', where ~~0~~ = blank).

NAMSOU(ISOU) = DOUBLE PRECISION name of source organ ISOU (the first six source names are always the same and are initialized in the BLOCK DATA subroutine).

NAMTRG(ITRG) = DOUBLE PRECISION name of target organ ITRG (the first six target names are always the same and are initialized in the BLOCK DATA subroutine).

Note. Total body as a source and target must always be present and correspond to index values ISOU = ITRG = 7.

/GI/ LMGI(4), LMAB(20,4)

LMGI(ISEG) = REAL mass-clearance rate coefficient (day^{-1}) for segment ISEG of the GI tract:

$$\text{ISEG} = \begin{cases} 1 & \text{for stomach (S)} \\ 2 & \text{for small intestine (SI)} \\ 3 & \text{for upper large intestine (ULI)} \\ 4 & \text{for lower large intestine (LLI)} \end{cases}$$

LMAB(ISPEC,ISEG) = REAL absorption rate coefficient (day^{-1}) of species ISPEC from GI segment ISEG. Computed and stored by subroutine DOSRUN, LMAB is defined by Eq. (1.37).

/RESDP/ DD3, DD4, DD5

DD3, DD4, DD5 = respiratory regional deposition fractions (nasopharyngeal, tracheo-bronchial, and pulmonary regions, respectively) that are computed by subroutine INTP as functions of the activity median aerodynamic diameter (μm) and made available to subroutine STEP.

/SFACT/ S(20,27,23)

S(ISPEC,ITRG,ISOU) = dosimetric S-factor (rem/ μCi -day) to convert μCi -days residence of nuclide species ISPEC in source tissue ISOU into a dose contribution (rem) to target tissue ITRG.

/HALGES/ JCASE

JCASE = value of ICASE for the current case.

Note. This COMMON block permits communication of the case index from subroutine DOSRUN to subroutines HAL and GES.

/ALERT/ ERFLAG(6)

ERFLAG(ICASE) = LOGICAL flag to indicate input of median particle diameter [AMAD(ICASE)] that is outside the range to which the deposition model applies. The values of ERFLAG are set by subroutine INTP and transmitted to subroutine OUTPUT, which prints warnings when indicated.

/PERCNT/ PCTDOS(6,27,20)

PCTDOS(ICASE,ITRG,ISPEC) = percent contribution of species ISPEC to the total dose equivalent to target ITRG for case ICASE.

/SWITCH/ SNP, STB1, SP, SL(2), STB2(2), SGI

SNP, STB1, SP, SL(1+2), STB2(1+2), SGI = logical flags to indicate exhaustion of their respective feeder compartments: N-P, T-B₁, P, L_{1,2}, T-B₂, and GI. When all feeder compartments are exhausted (all flags set to .TRUE.) the integration is completed in one final step.

/TYME/ TSTEP(6)

TSTEP(ICASE) = user-chosen time step (days) for the integration.

/LEVELS/ YNP(20,2), Y1TB(20,2), Y2TB(20,2), YP(20,4), YL(20,2), YS(20), YSI(20), YULI(20), YLLI(20), YORG(20,5,16)

YNP(ISPEC,IPATH), ..., YORG(ISPEC,IC,ISOU-6) = microcuries in lungs (pathways α , ..., l), GI tract, and other source organs.

/CUMACT/ YNPW(20,2), Y1TBW(20,2), Y2TBW(20,2), YPW(20,4), YLW(20,2), YSW(20), YS1W(20), YULIW(20), YLLIW(20), YORGW(20,5,16)

YNPW(ISPEC,IPATH), ..., YORGW(ISPEC,IC,ISOU-6) = microcurie-days time-integrated activity in lungs (pathways α , ..., l), GI tract, and other source organs for the current integration subinterval.

2.3 Subroutines

The basic structure of the INREM II program has been described and shown schematically in Fig. 2.6. Subroutine INPUT has been described in Sect. 2.1 and outlined in Figs. 2.3 and 2.4. Descriptions of the remaining subroutines are included below.

OUTDAT: invoked by the driving program to print the physical and metabolic parameters for the given parent nuclide and its progeny. The following information is printed for each species of the chain: name, radioactive half-life, branching ratio, blood transfer fraction, retention coefficients, and biological half-times. Also a tabulation of the S-factors for the specified source and target organs is printed for each species in the decay chain. Figure 2.1 shows an example of the output produced by this subroutine. Common blocks used by OUTDAT are /RADAT/, /ORGDAT/, /NAMES/, /NUMBERS/, and /SFACT/.

PRINTS(IFIRST, LAST, ISPEC): called by OUTDAT to print a table of the S-factors for source organs with indices IFIRST through LAST for all targets for the current species, ISPEC, in the nuclide chain. Common blocks used are /NAMES/, /NUMBERS/, and /SFACT/.

INTP(AMAD, ICASE): called by the driving program to compute the lung deposition fractions D_3 , D_4 , and D_5 for a given particle size, AMAD (μm), for case ICASE, where intake is by inhalation. The fractions D_3 , D_4 , and D_5 correspond to the nasopharyngeal, tracheobronchial, and pulmonary regions, respectively. Functional relationships between particle diameter and these deposition fractions were deduced from

graphical information published in WASH-1400 (ref. 7, Fig. VI D-1). In each case the function is defined over a restricted range of AMAD: $0.1 \mu\text{m} \leq \text{AMAD} \leq 20.0 \mu\text{m}$. For particles outside this range, the boundary value of AMAD is substituted for the user's value, and a warning flag is provided to signal this condition in the output. Common blocks used are /RESDP/ and /ALERT/.

SUMMARY: called by the driving program to print a summary of the methods and assumptions employed in INREM II and a listing of the default values for lung and GI tract parameters. In the present version of the code, this subroutine is replaced by a dummy.

DOSRUN(ICASE): invoked by the driving program to manage the integration of the differential equations used to estimate the μCi -days residence in each compartment, and to calculate the dose matrix. This routine is discussed in Sect. 2.1. Common blocks used are /NAMES/, /NUMBERS/, /RADAT/, /ORGDAT/, /SFACT/, /DOSES/, /CASES/, /GI/, /HALGES/, /SOURCE/, /PERCNT/, /TGLM/, /SWITCH/, /LEVELS/, /CUMACT/, and /TYME/.

STEP(T1,T2,MODE): Invoked by DOSRUN to advance the integration of the differential equations from time T1 to T2. The variable MODE = 1 for inhalation and 2 for ingestion. Common blocks used are /SWITCH/, /LEVELS/, /CUMACT/, /ORGDAT/, /NUMBERS/, /GI/, /TGLM/, /RADAT/, /RESDP/.

HAL(T,H): invoked by step to define an array H of the inhalation intake rate at time T for each species in the decay chain. The appropriate rate is determined by selecting the element of the intake rate P which corresponds to the value of T. Common blocks used are /CASES/, /HALGES/, and /NUMBERS/.

GES(T,G): invoked by STEP to define an array G of the ingestion intake rate for each species in the decay chain at time T, in the same way as for HAL. Common blocks used are /CASES/, /HALGES/, and /NUMBERS/.

MULCOM(T,N,LMR,LMB,C,NCOMP,BRANCH,P,AO,A,AW): invoked repeatedly by subroutine STEP to compute microcuries A(I,K) and microcurie-days AW(I,K) of the Ith radionuclide species of a chain ($1 \leq I \leq N$) due to the Kth term of its fractional retention function. Species I is subject to radioactive decay rate LMR(I) (day^{-1}), and its fractional

retention kernel is assumed to have the form of Eq. (1.50), with the following notational correspondences:

t	T
λ_i^R	$LMR(I)$
λ_{ik}^E	$LMB(I,K)$
c_{ik}	$C(I,K)$
L_i	$NCOMP(I)$

The initial content of species I in the organ and associated with the K th retention term is $A0(I,K)$, the constant uptake rate is $P(I)$ ($\mu\text{Ci/day}$), and $BRANCH(I,J)$ is the fraction of species J which disintegrates to species I ($J < I$). Some details of the equations are given in Sect. 1.3. No common blocks are used.

OUTPUT: invoked by the driving program to print the case-specific information for each of the cases in the current problem. Figure 2.2 illustrates the text produced by this routine. For an ingestion case, the information includes the intake rate function and the ingestion transfer fraction f_1 (GI to blood) for each nuclide in the chain, followed by the dose matrix of all source and target organs. The dose from the respiratory source tissues is zero in this case and is not included in the dose matrix tabulation. When the intake mode for the current case is inhalation, output consists of the intake rate function, AMAD and lung deposition fractions (D_3 , D_4 , and D_5), and the respiratory clearance class (D , W , or Y) and GI uptake fraction for each species in the chain. If special lung clearance parameters are specified, these will be printed next. This is followed by a tabulation of the dose matrix over all source and target organs. When radioactive progeny are present, a table detailing the percentage of the total dose equivalent to each target organ contributed by each species of the decay chain is included. Common blocks are /NAMES/, /NUMBERS/, /CASES/, /RESDP/, and /ALERT/.

PRINTD(IFIRST, LAST): called by OUTPUT to tabulate the dose matrix for source organs with indices IFIRST through LAST for all target organs. Common blocks are /NAMES/, /NUMBERS/, /DOSES/, and /CASES/.

CMNTS: called by the driving program to print out comment cards, if any, which have been included in the input stream. Cards following the last numerical data of the input file will be printed with the program output until a card with '\$' in column 1 is encountered.

REFERENCES

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APPENDIX
LISTING OF INREM II CODE

C INREM II

```

C-----
C
C PROGRAM AUTHORS..
C
C G. G. KILLOUGH
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C EAST TENNESSEE STATE UNIVERSITY
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C-----
C
C DOUBLE PRECISION NAMNUC,NAMSOU,NAMTRG
C LOGICAL DEFAULT, LAST
C REAL LMA,LMB,LMC,LMD,LME,LMF,LMG,LMH,LMI
C COMMON /CASES/ NCASES,MODE(6),TEND(6),NINT(6),T(6,30),P(6,30),
C $ ISOL(6,20),AMAD(6),DEFAULT(6),FLUNG(6,9,20),TBLUNG(6,9,20),
C $ FI(6,20),GIFRAC(6,20,4)
C COMMON /RADAT/ TR(20),BRANCH(20,20)
C COMMON /NUMBRS/ NSPEC,NSOU,NTRG
C COMMON /TGLM/ LMA(20),LME(20),LMC(20),LMD(20),LME(20),
C $ LMF(20),LMG(20),LMH(20),LMI(20),
C $ FA(20),FB(20),FC(20),FD(20),FE(20),FF(20),FG(20),FH(20),FI(20)
C COMMON /TGLMDF/ DLMA(3),DLMB(3),DLMC(3),DLMD(3),DLME(3),DLMF(3),
C $ DLMG(3),DLMH(3),DLMI(3),
C $ DFA(3),DFB(3),DFC(3),DFD(3),DFE(3),DFF(3),DFG(3),
C $ DFH(3),DFI(3)
C COMMON /DHGDAT/ NCOMP(20,16),C(20,5,16),TS(20,5,16),
C $ F2PRIM(20,16)
C COMMON /DOSES/ DOSE(6,27,25)
C
C SET LAST CASE INDICATOR.
C LAST=.FALSE.
C
C CALL SUBROUTINE SUMMARY TO PRINT OUT A RESUME OF METHODS
C AND ASSUMPTIONS, TOGETHER WITH DEFAULT PARAMETER VALUES
C FOR THE LUNGS AND G. I. TRACT.
C CALL SUMMARY
C
C USE ASSEMBLER SUBROUTINE PGMSK TO SET PROGRAM MASK WHICH WILL
C IGNORE UNDERFLOWS AND LOSS OF SIGNIFICANCE.
C CALL PGMSK(1,1,0,0)
C
C THE FOLLOWING ITERATION (INDEX IPARNT) (1) READS DATA FOR
C A PARENT RADIONUCLIDE AND ITS DAUGHTERS AND USER SPECIFICATIONS
C FOR ONE OR MORE CASES (A CASE CONSISTS OF CALCULATING THE
C DOSES RESULTING FROM AN INTAKE HISTORY OF THE PARENT, EITHER
C BY INHALATION OR INGESTION), (2) PRINTS OUT THE PHYSICAL AND
C METABOLIC DATA, AND (3) PERFORMS THE DOSE INTEGRATION AND
C PRINTS OUT THE CASE INFORMATION AND THE RESULTS.
C
C *** EXIT FROM THE IPARNT LOOP OCCURS WHEN SUBROUTINE INPUT DETECTS
C THE END-OF-FILE AND RETURNS LAST=.TRUE.
C
C DO 100 IPARNT=1,10000
C
C CALL SUBROUTINE INPUT TO READ DATA AND CASES FOR THE NEXT CHAIN.
C CALL INPUT(LAST)
C IF(LAST) GO TO 200
C
C INVOKE SUBROUTINE OUTDAT TO PRINT PHYSICAL AND METABOLIC DATA
C FOR THE CHAIN.
C CALL OUTDAT
C
C CONVERT RADIOACTIVE HALF-LIVES TO DECAY RATE COEFFICIENTS AND
C CONVERT BIOLOGICAL HALF-TIMES TO REMOVAL COEFFICIENTS (1/DAYS)..
C DO 10 ISPEC=1,NSPEC
C IF(TR(ISPEC).GT.(.5)) TR(ISPEC)=0.6931472/TR(ISPEC)
C NS=NSOU-6
C IF(NS.EQ.0) GO TO 10
C DO 10 IS=1,NS
C AC=NCOMP(ISPEC,IS)

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      CO 10 IC=1,NC
      TEMP=TB(ISPEC,IC,IS)
      IF(TEMP.GT. 0.0) TB(ISPEC,IC,IS)=0.6931472/TEMP
10    CONTINUE
C
C THE FOLLOWING LOOP HANDLES THE SEVERAL CASES.
      DO 70 ICASE=1,NCASES
C
C DETERMINE WHETHER THIS IS AN INHALATION CASE.
      IF(MODE(ICASE) .NE. 1) GO TO 60
C
C -----
C INHALATION CASE.
C -----
C
C THE FOLLOWING LOOP INDEXED BY ISPEC MOVES TO COMMON
C BLOCK /TGLM/ THE APPROPRIATE LUNG PARAMETERS FOR
C THE CURRENT CASE, WHERE SUBROUTINE DIFFUN WILL OBTAIN
C THEM. IN THE DEFAULT CASE, ARRAY ISOL CONTAINS
C CODES FOR THE SOLUBILITIES (D.W.Y), AND THE PARAMETERS
C WILL BE TAKEN FROM COMMON BLOCK /TGLMDF/, WHERE THEY
C WERE INITIALIZED IN A BLOCK DATA SUBROUTINE. IN THE
C NON-DEFAULT CASE, THE USER HAS SUPPLIED PARAMETERS,
C AND THESE ARE IN THE ARRAYS TBLUNG (HALF-TIMES IN DAYS)
C AND FLUNG. FIRST, HALF TIMES ARE CONVERTED TO REMOVAL COEFFICIENTS.
      DO 50 ISPEC=1,NSPEC
      IF(ISOL(ICASE,ISPEC) .LT. 4) GO TO 40
      DO 20 IPATH=1,9
      IF(TBLUNG(ICASE,IPATH,ISPEC) .GT. 0.0)
        TBLUNG(ICASE,IPATH,ISPEC)=0.6931472
        /TBLUNG(ICASE,IPATH,ISPEC)
      20 CONTINUE
C MOVE LUNG PARAMETERS TO COMMON BLOCK /TGLM/..
C NON-DEFAULT CASE..
      LMA(ISPEC)=TBLUNG(ICASE,1,ISPEC)
      FA(ISPEC)=FLUNG(ICASE,1,ISPEC)
      LMB(ISPEC)=TBLUNG(ICASE,2,ISPEC)
      FB(ISPEC)=FLUNG(ICASE,2,ISPEC)
      LMC(ISPEC)=TBLUNG(ICASE,3,ISPEC)
      FC(ISPEC)=FLUNG(ICASE,3,ISPEC)
      LMD(ISPEC)=TBLUNG(ICASE,4,ISPEC)
      FD(ISPEC)=FLUNG(ICASE,4,ISPEC)
      LME(ISPEC)=TBLUNG(ICASE,5,ISPEC)
      FE(ISPEC)=FLUNG(ICASE,5,ISPEC)
      LMF(ISPEC)=TBLUNG(ICASE,6,ISPEC)
      FF(ISPEC)=FLUNG(ICASE,6,ISPEC)
      LMG(ISPEC)=TBLUNG(ICASE,7,ISPEC)
      FG(ISPEC)=FLUNG(ICASE,7,ISPEC)
      LMH(ISPEC)=TBLUNG(ICASE,8,ISPEC)
      FH(ISPEC)=FLUNG(ICASE,8,ISPEC)
      LMI(ISPEC)=TBLUNG(ICASE,9,ISPEC)
      FI(ISPEC)=FLUNG(ICASE,9,ISPEC)
C
C BRANCH AROUND DEFAULT CASE.
      GO TO 50
C
C MOVE LUNG PARAMETERS TO COMMON BLOCK /TGLM/..
C DEFAULT CASE..
      40 CONTINUE
      IS=ISOL(ICASE,ISPEC)
      LMA(ISPEC)=DLMA(IS)
      FA(ISPEC)=DFA(IS)
      LMB(ISPEC)=DLMB(IS)
      FB(ISPEC)=DFB(IS)
      LMC(ISPEC)=DLMC(IS)
      FC(ISPEC)=DFC(IS)
      LMD(ISPEC)=DLMD(IS)
      FD(ISPEC)=DFD(IS)
      LME(ISPEC)=DLME(IS)
      FE(ISPEC)=DFE(IS)
      LMF(ISPEC)=DLMF(IS)
      FF(ISPEC)=DFF(IS)
      LMG(ISPEC)=DLMG(IS)
      FG(ISPEC)=DFG(IS)
      LMH(ISPEC)=DLMH(IS)
      FH(ISPEC)=DFH(IS)
      LMI(ISPEC)=DLMI(IS)
      FI(ISPEC)=DFI(IS)
      50 CONTINUE

```

```

C
C CALL INTERPOLATION SUBROUTINE INTP TO COMPUTE LUNG DEPOSITION
C FRACTIONS C3,D4,D5 IN /RESDP/ FROM AMAD(ICASE).
C 55 CALL INTP(AMAD(ICASE),ICASE)

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```

C-----
C END INHALATION CASE.
C-----

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```

C 60 CONTINUE

```

```

C
C INVOKE SUBROUTINE DOSRUN TO PERFORM DOSE CALCULATIONS FOR
C THIS CASE. THE DOSE TO TARGET ORGAN ITRG FROM SOURCE ORGAN
C ISOU WILL BE STORED IN DOSE(ICASE,ITRG,ISOU) (REMS).
C FOR ISOU=NSOU+1, THE DOSES RESULT FROM THE 'REST OF BODY'
C COMPARTMENT. DOSE(ICASE,ITRG,NSOU+2) IS THE TOTAL DOSE TO
C TARGET ITRG.
C CALL DOSRUN(ICASE)

```

```

C
C END ICASE LOOP.
C 70 CONTINUE

```

```

C
C USE SUBROUTINE OUTPUT TO PRINT OUT CASE INFORMATION AND
C RESULTS.
C CALL OUTPUT

```

```

C
C LOOK FOR COMMENTS AFTER NUCLIDE DATA GROUP. IF THERE
C ARE ANY, PRINT THEM. A CARD WITH 'S' IN COLUMN 1 ENDS
C THE DATA GROUP PLUS COMMENTS.
C CALL CMMNTS

```

```

C
C END OF IPARNT LOOP.
C 100 CONTINUE

```

```

C-----
C END OF INREM II.
C-----

```

```

C 200 STOP
C END

```

BLOCK DATA

```

C
C THE FOLLOWING QUANTITIES ARE MASSES (G) OF THE

```

```

C SOURCE ORGANS.. LUNGS, RES. LYMPH, S CONT, SI CONT,
C ULI CONT, AND LLI CONT

```

```

C TARGET ORGANS.. LUNGS, RES. LYMPH, S WALL, SI WALL,
C ULI WALL, AND LLI WALL

```

```

C
C COMMON /MASSES/ SMASS(24),TMASS(27)
C DATA SMASS/1000., 15., 250., 400., 220., 135., 18*0.0/,
C $ TMASS/1000., 15., 150., 640., 210., 160., 21*0.0/

```

```

C
C THE NAMES OF THESE SPECIAL SOURCE AND TARGET TISSUES ARE
C INITIALIZED NEXT.

```

```

C
C DOUBLE PRECISION NAMNUC,NAMSOU,NAMTRG
C COMMON /NAMES/ NAMNUC(20),NAMSOU(24),NAMTRG(27)
C DATA NAMSOU/8*HLUNGS , 8*RES LYM , 8*SI CONT ,
C $ 8*SI CONT , 8*ULI CONT, 8*LLI CONT,18*8H /,
C $ NAMTRG/8*HLUNGS , 8*RES LYM , 8*SI WALL ,
C $ 8*SI WALL , 8*ULI WALL, 8*LLI WALL,21*8H /

```

```

C
C THE FOLLOWING QUANTITIES LMGI ARE TURNOVER RATES FOR THE
C G. I. TRACT SEGMENTS S, SI, ULI, LLI. THEY ARE BASED ON
C THE DOLPHIN AND EVE TRANSIT TIMES (HEALTH PHYS. 12, PP. 163-172
C (1966)). UNITS ARE RECIPROCAL DAYS.

```

```

C
C REAL LMGI,LNAB
C COMMON /GI/ LMGI(4),LNAB(20,4)
C DATA LMGI/24., 6., 1.846134, 1./

```

```

C
C NEXT ARE DEFAULT DATA FOR THE TASK GROUP LUNG MODEL.
C THE QUANTITIES LMA-LMI (RECIPROCAL DAYS) ARE CLEARANCE
C COEFFICIENTS FOR THE PATHWAYS A-I. FA-FI ARE DEPOSITION
C FRACTIONS ASSOCIATED WITH THESE PATHWAYS. THE INDEXING
C CORRESPONDS TO D=1, V=2, Y=3. THESE VALUES ARE USED WHEN
C DEFAULT IS SPECIFIED.

```

```

C
C REAL LMA,LMB,LMC,LMD,LME,LMF,LNG,LNH,LNI
C COMMON /TGLMDF/ LMA(3),LMB(3),LMC(3),LMD(3),LME(3),LMF(3),
C $ LNG(3),LNH(3),LNI(3),
C $ FA(3),FB(3),FC(3),FD(3),FE(3),FF(3),FG(3),FH(3),FI(3)

```



```

DATA LWA/3*69.21472/,
$ FA/C.5. 0.1. 0.01/,
$ LMS/69.31472. 2*1.7328EE/,
$ FH/0.5. 0.9. 0.99/,
$ LMC/3*69.31472/,
$ FC/0.95. 0.5. 0.01/,
$ LMD/2*3.465726/,
$ FJ/0.05. 0.5. 0.55/,
$ LME/1.386294. 1.386294E-2. 1.386294E-3/,
$ FE/0.8. 0.15. 0.05/,
$ LMF/0.0. 2*0.6931472/,
$ FF/0.0. 2*0.4/,
$ LMG/0.0. 1.386294E-2. 1.386294E-3/,
$ FG/0.0. 2*0.4/,
$ LMH/1.386294. 1.386294E-2. 1.386294E-3/,
$ FH/0.2. 0.05. 0.15/,
$ LMI/1.386294. 1.386294E-2. 6.931472E-4/,
$ FI/2*1.0. 0.9/
END

```

```

SUBROUTINE SUMMRY
WRITE(6,10C)
10C FORMAT('1'.*SUBROUTINE SUMMRY (DUMMY VERSION)')
RETURN
END

```

```

SUBROUTINE INPUT(LAST)
DOUBLE PRECISION NAMNUC,NAMSOU,NAMTRG,NTOTAL,NAMEXC
LOGICAL DEFALT, LAST, EXFLAG
DIMENSION DUMMY(3), F2PEX(20), CEX(20,5), TBEX(20,5), NCOEX(20)
COMMON /RADAT/ TR(20), BRANCH(20,20)
COMMON /ORGDAT/ NCOMP(20,16), C(20,5,16), TB(20,5,16),
$ F2PRIM(20,16)
COMMON /NAMES/ NAMNUC(20), NAMSOU(24), NAMTRG(27)
COMMON /MASSES/ SMASS(24), TNASS(27)
COMMON /NUMBRS/ NSPEC, NSCU, NTRG
COMMON /SFACT/ S(20,27,23)
COMMON /CASES/ NCASES, MODE(6), TEND(6), NINT(6), T(6,30), P(6,30),
$ ISOL(6,20), AMAD(6), DEFALT(6), FLUNG(6,9,20), TBLUNG(6,9,20),
$ FI(6,20), GIFRAC(6,20,4)
COMMON /TIME/ TSTEP(6)
C INPUT CHANNEL
DATA IN /5/
DATA NTOTAL/8-TOTAL /
DATA NAMEXC/8HEXCRET. /
C READ NUMBER OF NUCLIDES IN THE CHAIN, AND FOR EACH THE NAME
C AND PHYSICAL HALF-LIFE (DAYS).
READ(IN,1000,END=80) NSPEC, (NAMNUC(ISPEC), TR(ISPEC),
$ ISPEC=1, NSPEC)
C INITIALIZE MATRIX OF BRANCHING RATIOS TO ZERO.
DO 10 ISPEC=1, NSPEC
DO 10 JSPEC=1, NSPEC
BRANCH(ISPEC, JSPEC)=0.0
10 CONTINUE
IF(NSPEC.EQ. 1) GO TO 20
C READ THE NUMBER NBR OF NON-ZERO BRANCHING RATIOS TO FOLLOW.
READ(IN,1010) NBR
DO 15 K=1, NBR
READ(IN,1020) JSPEC, ISPEC, BRANCH(ISPEC, JSPEC)
15 CONTINUE
C READ NUMBER NS OF SOURCE ORGANS OTHER THAN LUNGS, RES. LYMPH.
C S CONT, SI CONT, ULI CONT, AND LLI CONT. TOTAL BODY (ABSORBED) MUST
C BE THE FIRST OF THESE AND OTHER MUST BE THE LAST.
C THEN READ THE NAMES AND MASSES (G) OF EACH.
C THE CHARACTERS IN CARD COLUMNS 11-22 ARE READ INTO THE ARRAY
C DUMMY. IF THESE ARE NON-BLANK, A PROMPT EXCRETION FUNCTION
C IS ASSUMED TO BE INCLUDED FOR EACH SPECIES BUT NOT COUNTED IN THE
C INDICATED NUMBER OF SOURCE ORGANS.
20 CONTINUE
READ(IN,1030) NS, DUMMY, (NAMSOU(ISOU+6), SMASS(ISOU+6), ISOU=1, NS)
EXFLAG=.FALSE.
IF(ICOMP(DUMMY,12H ,12) .NE. 0) EXFLAG=.TRUE.
C READ NUMBER NT OF TARGET ORGANS OTHER THAN LUNGS, RES. LYMPH.
C S WALL, SI WALL, ULI WALL, AND LLI WALL. TOTAL BODY MUST BE
C THE FIRST OF THESE. THEN READ THE NAMES AND MASSES (G).
READ(IN,1030) NT, DUMMY, (NAMTRG(ITRG+6), TNASS(ITRG+6), ITRG=1, NT)
NSOU=NS+6

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      NTRG=NT+6
      NSOU1=NSOU+1
      NAMSOU(NSOU1)=NTOTAL
C
C FOR EACH SPECIES IN THE CHAIN, READ S-FACTORS AND METABOLIC
C DATA FOR ORGANS OTHER THAN RESPIRATORY.
      DO 40 ISPEC=1,NSPEC
C
C FOR EACH SOURCE ORGAN (OTHER THAN RESPIRATORY OR G. I. TRACT)
C READ (1) FRACTIONAL TRANSFER F2-PRIME FROM BLOOD TO THE ORGAN, AND
C (2) NUMBER OF EXPONENTIAL COMPARTMENTS, AND FOR EACH A
C FRACTIONAL DEPOSITION COEFFICIENT AND A BIOLOGICAL HALF-TIME
C (DAYS).
      DO 30 ISOU=1,NS
        READ(IN,1050) F2PRIM(ISPEC,ISOU),NC,(C(ISPEC,IC,ISOU),
          & TB(ISPEC,IC,ISOU),IC=1,NC)
          NCOMP(ISPEC,ISOU)=NC
          IF(ISOU.EQ.1.AND.EXFLAG)
            & READ(IN,1050) F2PEX(ISPEC),NC,(CEX(ISPEC,IC),
              & TBEX(ISPEC,IC),IC=1,NC)
            IF(ISOU.EQ.1.AND.EXFLAG) NCOEX(ISPEC)=NC
C THE TWO PRECEDING STATEMENTS READ DATA FOR PROMPT EXCRETION FUNCTIONS
C WHEN THESE ARE PRESENT. SUCH DATA ARE INSERTED IN THE DECK
C IMMEDIATELY AFTER THE TOTAL BODY (ABSORBED) RETENTION FUNCTIONS
C IN THE SAME FORMAT.
      30 CONTINUE
C
C READ MATRIX OF S-FACTORS FOR THE CURRENT SOURCES AND TARGETS.
C REQUIRED INDEXING FOR SPECIAL ORGANS IS SHOWN BELOW..
C
C   INDEX   SOURCE      INDEX   TARGET
C   1       LUNGS       1       LUNGS
C   2       RES LYM      2       RES LYM
C   3       S CONT       3       S WALL
C   4       SI CONT      4       SI WALL
C   5       ULI CONT      5       ULI WALL
C   6       LLI CONT      6       LLI WALL
C   7       TCT BODY      7       TCT BODY
C   NSOU+1   OTHER
C
      DO 35 ITRG=1,NTRG
        READ(IN,1040)(S(ISPEC,ITRG,ISOU),ISOU=1,NSOU)
      35 CONTINUE
C
C END OF ISPEC LOOP.
      40 CONTINUE
      IF(.NOT. EXFLAG) GO TO 5200
C-----
C THE FOLLOWING BLOCK OF STATEMENTS (WITH NUMBERS IN 5000S) IS
C EXECUTED IF AND ONLY IF PROMPT EXCRETION DATA HAVE BEEN READ IN.
C THESE STATEMENTS REARRANGE THE ARRAYS SO THAT THE EXCRETION
C FUNCTIONS WILL BE DISPLAYED BEFORE THE ORGAN RETENTION FUNCTIONS
C (SOURCE INDEX 8). S-FACTORS FOR TOTAL BODY AS SOURCE ARE USED
C FOR THESE EXCRETION FUNCTIONS.
      NAMSOU(NSOU+2)=NAMSOU(NSOU+1)
      IF(NS.EQ.1) GO TO 5035
      DO 5030 IS=2,NS
        K=NS-IS+2
        NAMSOU(K+7)=NAMSOU(K+6)
        SWASS(K+7)=SWASS(K+6)
        DO 5020 ISPEC=1,NSPEC
          F2PRIM(ISPEC,K+1)=F2PRIM(ISPEC,K)
          NCOMP(ISPEC,K+1)=NCOMP(ISPEC,K)
          NC=NCOMP(ISPEC,K)
          DO 5015 IC=1,NC
            C(ISPEC,IC,K+1)=C(ISPEC,IC,K)
            TB(ISPEC,IC,K+1)=TB(ISPEC,IC,K)
          5015 CONTINUE
        5020 CONTINUE
      5030 CONTINUE
      5035 CONTINUE
      DO 5060 IS=8,NSOU
        K=NSOU-IS+8
        DO 5050 ISPEC=1,NSPEC
          DO 5040 ITRG=1,NTRG
            S(ISPEC,ITRG,K+1)=S(ISPEC,ITRG,K)
          5040 CONTINUE
        5050 CONTINUE
      5060 CONTINUE
      NAMSOU(9)=NAMESC

```

```

      DO 5100 ISPEC=1,NSPEC
        F2PRIM(ISPEC,2)=F2PEX(ISPEC)
        NCCMF(ISPEC,2)=NCCEX(ISPEC)
        NC=NC+MP(ISPEC,2)
        DO 5070 IC=1,NC
          C(ISPEC,IC,2)=CEX(ISPEC,IC)
          TB(ISPEC,IC,2)=TBEX(ISPEC,IC)
5070    CONTINUE
        DO 5080 ITRG=1,NTRG
          S(ISPEC,ITRG,3)=S(ISPEC,ITRG,7)
5080    CONTINUE
5100    CONTINUE
        NS=NS+1
        NSOU=NSOU+1
        NSOU1=NSOU1+1
C
C END OF SPECIAL SECTION FOR PROMPT EXCRETION.
-----
5200 CONTINUE
C
C READ CONTROL INFORMATION. FIRST THE NUMBER OF CASES. THEN FOR
C EACH CASE (1) THE EXPOSURE MODE (G FOR INGESTION, H FOR INHALATION),
C (2) THE TIME (DAYS) FOR ENDING INTEGRATION, (3) THE INTAKE RATE
C FUNCTION (MICROCURIES/DAY), AND (4) OTHER INFORMATION SPECIFIC TO
C THE MODE OF INTAKE.
      READ(IN,1010) NCASES
      DO 70 ICASE=1,NCASES
        READ(IN,1080) MODE(ICASE),TEND(ICASE),TSTEP(ICASE)
        IF(TSTEP(ICASE).EQ.0.0) TSTEP(ICASE)=1825.0
        IF((ICMPA(MODE(ICASE),1HH,1).EQ.0) GO TO 41
          MODE(ICASE)=2
          GO TO 42
41      MODE(ICASE)=1
42      CONTINUE
C
C READ NUMBER OF TIME INTERVALS FOR INTAKE FUNCTION. THEN FOR
C EACH INTERVAL READ THE LEFT ENDPOINT (DAYS) AND THE INTAKE
C RATE (MICROCURIES/DAY) DURING THAT INTERVAL. THE FIRST TIME
C SHOULD BE ZERO. THE ENDPOINT OF THE LAST INTERVAL IS THE
C END OF THE INTEGRATION INTERVAL.
      READ(IN,1090) NI,(T(ICASE,INT),P(ICASE,INT),INT=1,NI)
      NINT(ICASE)=NI
C
C IF EXPOSURE MODE IS INGESTION, BRANCH AROUND LUNG PARAMETER
C INPUTS.
      IF(MODE(ICASE).EQ.2) GO TO 66
C
C INPUT INHALATION PARAMETERS..
C
C READ PARTICLE SIZE (MICROMETERS).
      READ(IN,1040) AMAD(ICASE)
C
C DETERMINATION OF LUNG CLEARANCE PARAMETERS AND G. I. UPTAKE
C FRACTIONS. FOR EACH SPECIES, A LITERAL FLAG IS READ INTO
C ISOL. IF IT IS 'D', 'H', OR 'Y', THE APPROPRIATE DEFAULT
C LUNG PARAMETERS ARE USED FOR THE SPECIES. OTHERWISE, SPECIAL
C PARAMETERS FOR THE LUNG ARE READ. THE FLAG VALUES ARE STORED
C IN ARRAY ISOL AS FOLLOWS..
C
C      ISOL(ICASE,ISPEC) = 1 FOR 'D'
C                        = 2 FOR 'H'
C                        = 3 FOR 'Y'
C                        = 4 FOR 'SPECIAL CASE'
C
      DO 60 ISPEC=1,NSPEC
        READ(IN,1080) ISOL(ICASE,ISPEC)
C
C CONVERT LITERAL TO NUMERIC CODE.
      IF((ICMPA(ISOL(ICASE,ISPEC),1:D,1).EQ.0)
        GO TO 45
      IF((ICMPA(ISOL(ICASE,ISPEC),1HH,1).EQ.0)
        GO TO 46
      IF((ICMPA(ISOL(ICASE,ISPEC),1HY,1).EQ.0)
        GO TO 47
C OTHERWISE..
      GO TO 48
45      ISOL(ICASE,ISPEC)=1
      GO TO 50
46      ISOL(ICASE,ISPEC)=2
      GO TO 50
47      ISOL(ICASE,ISPEC)=3
      GO TO 50

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      48      ISOL(ICASE,ISPEC)=4
      50      CONTINUE
C
C IF SPECIAL LUNG PARAMETERS ARE TO BE READ, READ THEM.
      IF (ISOL(ICASE,ISPEC) .LT. 4) GO TO 55
      READ(IN,1040) (TBLUNG(ICASE,IPATH,ISPEC),
      $              FLUNG(ICASE,IPATH,ISPEC),IPATH=1,9)
C
C READ G. I. UPTAKE FRACTION F1.
      55      CONTINUE
      READ(IN,1040) F1(ICASE,ISPEC),(GIFRAC(ICASE,ISPEC,ISEG),
      $              ISEG=1,4)
      DO 56 ISEG=1,4
      IF (GIFRAC(ICASE,ISPEC,ISEG) .NE. 0.0) GO TO 60
      56      CONTINUE
      GIFRAC(ICASE,ISPEC,2)=F1(ICASE,ISPEC)
      60      CONTINUE
C
C END OF INPUT FOR INHALATION CASE. BRANCH AROUND
C INGESTION-CASE INPUTS, TO END OF ICASE LOOP.
      GO TO 70
C
C READ G. I. UPTAKE FRACTIONS F1 FOR INGESTION CASE.
      66      DO 69 ISPEC=1,NSPEC
      READ(IN,1040) F1(ICASE,ISPEC),(GIFRAC(ICASE,ISPEC,ISEG),
      $              ISEG=1,4)
      DO 67 ISEG=1,4
      IF (GIFRAC(ICASE,ISPEC,ISEG) .NE. 0.0) GO TO 69
      67      CONTINUE
      GIFRAC(ICASE,ISPEC,2)=F1(ICASE,ISPEC)
      69      CONTINUE
C
C END OF ICASE LOOP.
      70      CONTINUE
      RETURN
C
C SIGNAL EXIT IN CASE END-OF-FILE CARD IS DETECTED BY FIRST READ
C STATEMENT.
      80      LAST=.TRUE.
      RETURN
C
C FORMAT STATEMENTS.
      1000      FORMAT(I2/(A8,2X,E10.0))
      1010      FORMAT(I2)
      1020      FORMAT(2 I2,E10.0)
      1030      FORMAT(I2,8X,3A4/(4(A8,2X,E10.0)))
      1040      FORMAT(8E10.0)
      1050      FORMAT(E10.0,I2/(8E10.0))
      1080      FORMAT(A2,2E10.0)
      1090      FORMAT(I2/(8E10.0))
      1100      FORMAT(20A2)
      END

      SUBROUTINE OUTCAT
C PRINTS THE FOLLOWING INPUT DATA:
C (1) PHYSICAL AND METABOLIC PARAMETERS FOR DOSIMETRICALLY SIGNIFICANT
C PROGENY FOR THE GIVEN NUCLIDE
C (2) S FACTORS FOR ALL SOURCE AND TARGET ORGANS FOR EACH SPECIES IN
C THE NUCLIDE CHAIN
      INTEGER OUT
      DOUBLE PRECISION NAMNUC,NAMSOU,NAMTRG
      COMMON /RADAT/ TR(20),BRANCH(20,20)
      COMMON /ORGDAT/ NCOMP(20,16),C(20,5,16),TC(20,5,16),
      $              F2PRIM(20,16)
      COMMON /NAMES/ NAMNUC(20),NAMSOU(24),NAMTRG(27)
      COMMON /NUMBR/ NSPEC,NSOU,NTRG
      COMMON /SFACT/ S(20,27,23)
C OUTPUT CHANNEL
      DATA OUT /6/
C
C PRINT HEADING
      WRITE(OUT,2000) NAMNUC(1)
C FOR EACH NUCLIDE IN THE CHAIN, PRINT ITS NAME AND RADIOACTIVE HALF-
C LIFE
      DO 100 ISPEC=1,NSPEC
      100      WRITE (OUT,2010) NAMNUC(ISPEC),TR(ISPEC)
      IF (NSPEC.EQ.1) GO TO 110
C
C PRINT HEADING FOR BRANCHING RATIOS
      WRITE (OUT,2020)

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C
C PRINT NONZERO BRANCHING RATIOS
DO 110 JSPEC=1,NSPEC
  DO 110 ISPEC=1,NSPEC
    IF (BRANCH(ISPEC,JSPEC).NE.0.)
      $ WRITE (OUT,2030) NAMNUC(JSPEC),NAMNUC(ISPEC),
      $ BRANCH(ISPEC,JSPEC)
  110 CONTINUE
C
C PRINT HEADING FOR BLOOD TRANSFER FRACTIONS, COMPARTMENT DEPOSITION
C FRACTIONS, AND COMPARTMENT BIOLOGICAL HALF-TIMES.
  WRITE (OUT,2040)
C
C FOR EACH SOURCE ORGAN AND FOR EACH NUCLIDE IN THE CHAIN.
C PRINT BLOOD TRANSFER FRACTIONS, COMPARTMENTAL DEPOSITION FRACTIONS,
C AND COMPARTMENTAL BIOLOGICAL HALF-TIMES.
  NS=NSOU-6
  DO 120 ISOU=1,NS
    WRITE (OUT,2050) NAMSOU(ISOU+6),NAMNUC(1),F2PRIN(1,ISOU),
    $ C(1,1,ISOU),TB(1,1,ISOU)
    NCOM=NCOMP(1,ISOU)
    IF (NCOM.EQ.1) GO TO 121
    DO 122 IC=2,NCOM
      122 WRITE (OUT,2060) C(1,IC,ISOU),TB(1,IC,ISOU)
    121 IF (NSPEC.EQ.1) GO TO 120
    DO 123 ISPEC=2,NSPEC
      WRITE (OUT,2070) NAMNUC(ISPEC),F2PRIN(ISPEC,ISOU),
      $ C(ISPEC,1,ISOU), TB(ISPEC,1,ISOU)
      NCOMPA=NCOMP(ISPEC,ISOU)
      IF (NCOMPA.EQ.1) GO TO 123
      DO 124 ICOM=2,NCOMPA
        124 WRITE (OUT,2080) C(ISPEC,ICOM,ISOU),TB(ISPEC,ICOM,ISOU)
      123 CONTINUE
    120 CONTINUE
C
C PRINT S FACTORS FOR ALL SOURCES, TARGETS, AND NUCLIDES IN THE CHAIN
C
  DO 130 ISPEC=1,NSPEC
    IFIRST=1
    LAST=11
    IF (NSOU .LT. LAST) LAST=NSOU
    ISPEC1=ISPEC
    CALL PRINTS(IFIRST,LAST,ISPEC1)
    IF (LAST .EQ. NSOU) GO TO 130
    IFIRST=12
    LAST=21
    IF (NSOU .LT. LAST) LAST=NSOU
    CALL PRINTS(IFIRST,LAST,ISPEC1)
    IF (LAST .EQ. NSOU) GO TO 130
    IFIRST=22
    LAST=24
    IF (NSOU .LT. LAST) LAST=NSOU
    CALL PRINTS(IFIRST,LAST,ISPEC1)
  130 CONTINUE
C
  RETURN
C
C FORMAT STATEMENTS
C
2000 FORMAT('IRADIONUCLIDE: ',A8,' ',130(' '))' PHYSICAL AND METABOLI',
  $ 'C PARAMETERS FOR DOSIMETRICALLY SIGNIFICANT PROGENY: '///',
  $ T15,'RADIOACTIVE'/' ',T16,'HALF-LIFE'/' NUCLIDE',T17,
  $ '(DAYS)')
2010 FORMAT(' ',A8,T15,1PG10,4)
2020 FORMAT('BRANCHING RATIOS: ',T21,'FROM',T31,'TO',T41,
  $ 'FRACTION')
2030 FORMAT(' ',T21,A8,T31,A8,T40,1PG10,4)
2040 FORMAT('0',T25,'B'000',T59,'COMPARTMENT'/' ',T25,'TRANSFER',
  $ T11,'COMPARTMENT',T59,'BIOLOGICAL'/' ',T25,'FRACTION',
  $ T41,'DEPOSITION',T59,'HALF-TIME'/' ORGAN',T14,'NUCLIDE',
  $ T25,'F2-PRINE',T41,'FRACTION',T60,'(DAYS)')
2050 FORMAT(' ',A8,T14,A8,T25,1PG9,3,T41,1PG10,3,T60,1PG9,3)
2060 FORMAT(' ',T41,1PG10,3,T60,1PG9,3)
2070 FORMAT(' ',T14,A8,T25,1PG9,3,T41,1PG10,3,T60,1PG9,3)
2080 FORMAT(' ',T41,1PG10,3,T60,1PG9,3)
  END

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C
C SUBROUTINE PRINTS(IFIRST, LAST, ISPEC)
C AFTER PRINTING A HEADING AND THE NAMES OF SOURCES (IFIRST TO LAST)
C THIS SUBROUTINE PRINTS S-FACTORS FOR ALL TARGET ORGANS FOR
C THESE SOURCES.
C
C   INTEGER OUT
C   DOUBLE PRECISION NAMNUC, NAMSOU, NAMTRG
C   COMMON /NAMES/ NAMNUC(20), NAMSOU(24), NAMTRG(27)
C   COMMON /NUMBERS/ NSPEC, NSOU, NTRG
C   COMMON /SFACT/ S(20,27,23)
C OUTPUT CHANNEL
C DATA OUT /6/
C PRINT HEADING
C   WRITE (OUT,1000) NAMNUC(ISPEC)
C
C PRINT NAMES OF SOURCES
C   IF(IFIRST.EQ.1) GO TO 110
C   WRITE(OUT,1010) (NAMSOU(ISOU), ISOU=IFIRST, LAST)
C
C PRINT S-FACTORS FOR THIS SPECIES FOR SOURCE ORGANS IFIRST TO LAST
C AND FOR ALL TARGET ORGANS
C   DO 100 ITRG=1, NTRG
C     WRITE(OUT,1020) NAMTRG(ITRG), (S(ISPEC,ITRG,ISOU), ISOU=IFIRST,
C       $ LAST)
C   100 CONTINUE
C     GO TO 120
C   110 WRITE(OUT,1010) (NAMSOU(ISOU), ISOU=1,6), (NAMSOU(ISOU), ISOU=8, LAST)
C     DO 120 ITRG=1, NTRG
C       WRITE(OUT,1020) NAMTRG(ITRG), (S(ISPEC,ITRG,ISOU), ISOU=1,6),
C         $ (S(ISPEC,ITRG,ISOU), ISOU=8, LAST)
C     120 CONTINUE
C
C RETURN
C
C FORMAT STATEMENTS
C
C 1000 FORMAT(/' ', T41, 'S FACTORS (REM/MICROCURIE-DAY) FOR ', A8/
C   $ '0 TARGET', T55, 'SOURCE ORGANS'/' ORGANS')
C 1010 FORMAT('0', T14, A8, 9(3X, A8))
C 1020 FORMAT(' ', A8, T13, E10.3, 9(X, E10.3))
C
C END

C SUBROUTINE INTP(AMAD, ICASE)
C
C COMPUTES LUNG DEPOSITION FRACTIONS D3, D4, AND D5 AS A FUNCTION
C OF AMAD (ACTIVITY MEDIAN AERODYNAMIC DIAMETER)(MICRONS).
C THE FUNCTIONS EXPRESSING THE RELATIONSHIPS BETWEEN THE LUNG
C FRACTIONS AND AMAD VALUES ARE THOSE PRESENTED IN WASH-1400.
C
C LOGICAL FLAG
C COMMON /RESP/ D3, D4, D5
C COMMON /ALERT/ FLAG(6)
C P(T)=1-J-0.5*( (((0.019527*T+.00034*)*T+.115194)*T+.196854)*T
C   $ +1.0)*(-4)
C PPT(W)=- (W-((.010328*W+.802853)*W+2.515517)/(((.001308*W
C   $ +.189269)*W+1.432788)*W+1.0))
C WW(X)=SQRT(-2.0*ALCG(X))
C DO 1 J=1,6
C   1 FLAG(J)=.FALSE.
C FLAG IS A WARNING INDICATOR TO SIGNAL THAT THE GIVEN VALUE OF
C AMAD EXCEEDS THE RANGE FOR WHICH THE FUNCTIONAL RELATIONSHIP IS KNOWN.
C IN SUCH A CASE, THE BOUNDARY VALUE IS SUBSTITUTED FOR THE GIVEN
C AMAD.
C   IF(AMAD.GT. 0.0) GO TO 2
C   D3=0.02
C   D4=0.04
C   D5=0.94
C   RETURN
C 2 DO 100 I=1,3
C   IF(I.GT.1) GO TO 15
C NASAL-PHARYNX
C   IF(AMAD.LT. 0.2) GO TO 5
C   GO TO 10
C 5 U0=-0.698970
C   U1=-1.070
C   T0=PPT(WW(0.05))
C   T1=PPT(WW(0.10))
C   IF(AMAD.GE. 0.1) GO TO 50

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      AMAD=.1
      FLAG(ICASE)=.TRUE.
      GO TO 50
10  U0=-0.698970
      U1=C.301030
      T0=PPT(WW(0.05))
      T1=PPT(WW(0.50))
      IF(AMAC .LE. 20.0) GO TO 50
      AMAD=2C.0
      FLAG(ICASE)=.TRUE.
      GO TO 50
15  CONTINUE
      IF(I .GT. 2) GO TO 35
C TRACHEO-BRONCHIAL REGION
      IF(AMAD .LT. 0.2) GO TO 20
      IF(AMAD .GT. 10.0) GO TO 35
      D4=0.08
      GO TO 130
20  U0=-C.698970
      U1=-1.0
      T0=PPT(WW(0.08))
      T1=PPT(WW(0.17))
      IF(AMAC .GE. 0.1) GO TO 50
      AMAD=0.1
      FLAG(ICASE)=.TRUE.
      GO TO 50
30  U0=1.0
      U1=1.30130
      T0=PPT(WW(0.08))
      T1=PPT(WW(0.03))
      IF(AMAC .LE. 20.0) GO TO 50
      AMAD=2C.0
      FLAG(ICASE)=.TRUE.
      GO TO 50
35  CONTINUE
C PULMONARY REGION
      IF(AMAD .LT. 10.) GO TO 40
      GO TO 45
40  U0=1.0
      U1=-0.698970
      T0=PPT(WW(0.05))
      T1=PPT(WW(0.5))
      IF(AMAC .GE. 0.1) GO TO 50
      AMAD=0.1
      FLAG(ICASE)=.TRUE.
      GO TO 50
45  U0=1.0
      U1=1.301030
      T0=PPT(WW(0.05))
      T1=PPT(WW(0.02))
      IF(AMAC .LE. 20.0) GO TO 50
      AMAD=20.0
      FLAG(ICASE)=.TRUE.
50  T=(T0*(T1-T0)/(U1-U0)*(ALOG10(AMAD)-U0)
      IF(T .GE. 0.0) X=P(T)
      IF(T .LT. 0.0) X=1.0-P(-T)
      IF(I .EQ. 1) D3=X
      IF(I .EQ. 2) C4=X
      IF(I .EQ. 3) D5=X
100 CONTINUE
      RETURN
      END

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SUBROUTINE DOSRUN(ICASE)
  DOUBLE PRECISION NAMNUC,NAMSOU,NAMTRG
  REAL AMIGL(20,27),LMR
  REAL LMA,LMB,LMC,LMD,LME,LMF,LMG,LMH,LMI
  REAL LMLUNG,LNGI,LNAB,LNBDAB
C*****
  REAL AW(20,12)
C*****
  LOGICAL DEFAULT
  LOGICAL SNP,STB1,SP,SL,STB2,SG1,SEND
  COMMON /PERCNT/ PCTDOS(6,27,20)
  COMMON /YLM/ LMA(20),LMB(20),LMC(20),LMD(20),LME(20),
1  LMF(20),LMG(20),LMH(20),LMI(20),
1  FA(20),FB(20),FC(20),FD(20),FE(20),FF(20),FG(20),
1  FH(20),FI(20)
  COMMON /RADAT/ LMR(20),BRANCH(20,20)
  COMMON /SWITCH/ SNP,STB1,SP,SL(2),STB2(2),SG1

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COMMON /LEVELS/ YNP(20,2),Y1TB(20,2),Y2TB(20,2),
$ YP(20,4),YL(20,2),YS(20),YSI(20),YULI(20),
$ YLLI(20),YORG(20,5,16)
COMMON /CUMACT/ YNPW(20,2),Y1TBW(20,2),Y2TBW(20,2),
$ YPW(20,4),YLW(20,2),YSW(20),YSIW(20),YULIW(20),
$ YLLIW(20),YORGW(20,5,16)
COMMON /NUMBRS/ NSPEC,NSOU,NTRG
COMMON /NAMES/ NAMNUC(20),NAMSOU(24),NAMTRG(27)
COMMON /CASES/ NCASES,MODE(6),TEND(6),NINT(6),TI(6,30),
$ P(6,30),ISOL(6,20),AMAD(6),DEFAULT(6),FLUNG(6,9,20),
$ LMLUNG(6,9,20),FI(6,20),GIFRAC(6,20,4)
COMMON /TYPE/ TSTEP(6)
COMMON /HALGES/ JCASE
COMMON /ORGDAT/ NCOMP(20,16),C(20,5,16),LMBDAB(20,5,16),
$ F2PRIM(20,16)
COMMON /DOSES/ DOSE(6,27,25)
COMMON /SFACT/ S(20,27,23)
COMMON /GI/ LMCII(4),LHAB(20,4)

C
C NOTIFY SUBROUTINES HAL AND GES WHICH CASE IS CURRENT
C THROUGH COMMON BLOCK /HALGES/ (HAL RETURNS THE INTAKE
C RATE BY INHALATION, GES BY INGESTION).
JCASE=ICASE

C
C COMPUTE NUMBER OF TIME STEPS (NSTEPS) INTO WHICH THE INTEGRATION
C INTERVAL IS TO BE SUBDIVIDED.
NSTEPS=1+FIX(TEND(ICASE)/TSTEP(ICASE))

C
C INITIAL CONDITIONS.. SET TO ZERO ALL ARRAYS IN /LEVELS/
C BLOCK AND AWIGL.
NS=NSOU - 6
NS2=NSOU + 2
DO 30 ISPEC=1,NSPEC
  YS(ISPEC)=0.0
  YSI(ISPEC)=0.0
  YULI(ISPEC)=0.0
  YLLI(ISPEC)=0.0
DO 5 J=1,2
  YNP(ISPEC,J)=0.0
  Y1TB(ISPEC,J)=0.0
  Y2TB(ISPEC,J)=0.0
  YL(ISPEC,J)=0.0
5 CONTINUE
DO 10 J=1,4
  YP(ISPEC,J)=0.0
10 CONTINUE
DO 15 J=1,NS2
  AMIGL(ISPEC,J)=0.0
15 CONTINUE
*****
DO 16 J=1,12
  AB(ISPEC,J)=0.0
16 CONTINUE
*****
DO 25 K=1,NS
  NC=NCOMP(ISPEC,K)
DO 20 J=1,NC
  YORG(ISPEC,J,K)=0.0
20 CONTINUE
25 CONTINUE
30 CONTINUE

C
C SWITCHES SNP,....SGI INDICATE EXHAUSTION OF THEIR RESPECTIVE
C COMPARTMENTS. SEND INDICATES FINAL EXHAUSTION OF ALL FEEDER
C COMPARTMENTS AND HENCE THE INTEGRATION FOR OTHER ORGANS MAY
C BE COMPLETED IN ONE FINAL STEP. SET ALL OF THESE SWITCHES
C INITIALLY TO .FALSE..
SNP=.FALSE.
STB1=.FALSE.
SP=.FALSE.
SL(1)=.FALSE.
SL(2)=.FALSE.
STB2(1)=.FALSE.
STB2(2)=.FALSE.
IF(MODE(ICASE).EQ.1) GO TO 31
SNP=.TRUE.
STB1=.TRUE.
SP=.TRUE.
SL(1)=.TRUE.
SL(2)=.TRUE.
STB2(1)=.TRUE.
STB2(2)=.TRUE.

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31 SGI=.FALSE.
   SEND=.FALSE.
C
C SET G.I. ABSORPTION RATE PARAMETER LMAB..
DO 35 ISPEC=1,NSPEC
  DO J5 ISEG=1,4
    TEMP=AMIN1(0.95,GIFRAC(ICASE,ISPEC,ISEG))
    LMAB(ISPEC,ISEG)=LMG1(ISEG)*TEMP/(1.0-TEMP)
  35 CONTINUE
C
C COMPUTE MAXIMUM TIME TO EXHAUSTION (=8 TIMES THE LONGEST EFFECTIVE
C HALF-TIME) FOR EACH FEEDER COMPARTMENT. TA,...,TII ARE TIMES FOR
C THE RESPECTIVE RESPIRATORY PATHWAYS, AND TS,...,TLLI ARE FOR
C THE G.I. TRACT. TR IS THE TIME TO EXHAUSTION OF THE LONGEST-LIVED
C NUCLIDE IN THE CHAIN. INITIALIZE THESE TIMES WITH AN ARBITRARY,
C LARGE VALUE.
  TR=1.E10
  IF(MODE(ICASE).NE.1) GO TO 36
  TA=1.E10
  TB=1.E10
  TC=1.E10
  TD=1.E10
  TE=1.E10
  TF=1.E10
  TG=1.E10
  TH=1.E10
  TII=1.E10
36 CONTINUE
  TS=1.E10
  TSI=1.E10
  TULI=1.E10
  TLLI=1.E10
  DO 38 ISPEC=1,NSPEC
    IF(MODE(ICASE).NE.1) GO TO 37
    TA=AMIN1(TA,LMA(ISPEC)+LMR(ISPEC))
    TB=AMIN1(TB,LMB(ISPEC)+LMR(ISPEC))
    TC=AMIN1(TC,LMC(ISPEC)+LMR(ISPEC))
    TD=AMIN1(TD,LMD(ISPEC)+LMR(ISPEC))
    TE=AMIN1(TE,LME(ISPEC)+LMR(ISPEC))
    TF=AMIN1(TF,LMF(ISPEC)+LMR(ISPEC))
    TG=AMIN1(TG,LMG(ISPEC)+LMR(ISPEC))
    TH=AMIN1(TH,LMH(ISPEC)+LMR(ISPEC))
    TII=AMIN1(TII,LMI(ISPEC)+LMR(ISPEC))
    IF(LMF(ISPEC).EQ.0.0) TF=1.E10
    IF(LMG(ISPEC).EQ.0.0) TG=1.E10
  37 CONTINUE
    TS=AMIN1(TS,LNGI(1)+LMAB(ISPEC,1)+LMR(ISPEC))
    TSI=AMIN1(TSI,LNGI(2)+LMAB(ISPEC,2)+LMR(ISPEC))
    TULI=AMIN1(TULI,LNGI(3)+LMAB(ISPEC,3)+LMR(ISPEC))
    TLLI=AMIN1(TLLI,LNGI(4)+LMAB(ISPEC,4)+LMR(ISPEC))
    TR=AMIN1(TR,LMR(ISPEC))
  38 CONTINUE
  TA=8.0*0.693/TA
  TB=8.0*0.693/TB
  TC=8.0*0.693/TC
  TD=8.0*0.693/TD
  TE=8.0*0.693/TE
  TF=8.0*0.693/TF
  TG=8.0*0.693/TG
  TH=8.0*0.693/TH
  TII=8.0*0.693/TII
  NI=NINT(ICASE)
  IF(P(ICASE,NI).EQ.0.0) TINT=TI(ICASE,NI)
  IF(P(ICASE,NI).NE.0.0) TINT=TEND(ICASE)
  TNP=0.0
  IF(MODE(ICASE).EQ.1) TNP=TINT+AMAX1(TA,TB)
  TTBI=0.0
  IF(MODE(ICASE).EQ.1) TTBI=TINT+AMAX1(TC,TD)
  TP=0.0
  IF(MODE(ICASE).EQ.1) TP=TINT+AMAX1(TE,TF,TG,TH)
  TL1=0.0
  IF(MODE(ICASE).EQ.1) TL1=TINT+TH+TII
  TL2=0.0
  IF(MODE(ICASE).EQ.1) TL2=TINT+TH+TR
  TTBI2=0.0
  IF(MODE(ICASE).EQ.1) TTBI2=TINT+TC+AMAX1(TF,TG)
  TGI=TS+TSI+TULI+TLLI
  IF(MODE(ICASE).EQ.1) TGI=TGI+AMAX1(TNP,TTBI,TTBI2)
  IF(MODE(ICASE).EQ.1) TGI=TGI+TINT

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C
C OVER APPROXIMATELY NSTEPS SUBINTERVALS OF THE INTEGRATION INTERVAL.
C APPLY SUBROUTINE STEP TO ADVANCE THE CALCULATION.
  NI=NINT(ICASE)
  DO 30 II=1,NI
    IF(II.LT.NI) GO TO 40
C
C IF INTAKE HAS CEASED AND ALL FEEDER COMPARTMENTS ARE EXHAUSTED.
C SET SEND=.TRUE.
    IF(P(ICASE,NI).EQ.C.C.AND.SNP.AND.STB1.AND.
      $ SP.AND.SL(1).AND.STB2(1).AND.STB2(2).AND.SG1)
      $ SEND=.TRUE.
    TFIRST=TI(ICASE,NI)
    TLAST=TEND(ICASE)
    NST=1+FIX((TLAST-TFIRST)/TLAST*FLOAT(NSTEPS))
    GO TO 50
40  TFIRST=TI(ICASE,II)
    TLAST=TI(ICASE,II+1)
    NST=1+FIX((TLAST-TFIRST)/TEND(ICASE)*FLOAT(NSTEPS))
50  DT=(TLAST-TFIRST)/FLOAT(NST)
    DO 75 IST=1,NST
      T1=TFIRST+FLOAT(IST-1)*DT
      T2=TFIRST+FLOAT(IST)*DT
      IF(SEND) T2=TEND(ICASE)
C
C INVOKE STEP TO ADVANCE THE INTEGRATION FROM T1 TO T2.
      CALL STEP(T1,T2,MODE(ICASE))
C
C ACCUMULATE CUMULATIVE ACTIVITY AWIGL IN SOURCE TISSUES.
      DO 70 ISPEC=1,NSPEC
C
C OMIT RESPIRATORY CONTRIBUTIONS IF THIS IS AN INGESTION CASE.
      IF(MODE(ICASE).NE.1) GO TO 55
C
C MICROCURIE-DAYS IN LUNGS (NP + TB + P)..
      AWIGL(ISPEC,1)=AWIGL(ISPEC,1)+YNPW(ISPEC,1)+YNPW(ISPEC,2)
      $ +Y1TBW(ISPEC,1)+Y1TBW(ISPEC,2)
      $ +Y2TBW(ISPEC,1)+Y2TBW(ISPEC,2)
      $ +YPW(ISPEC,1)+YPW(ISPEC,2)+YPW(ISPEC,3)
      $ +YPW(ISPEC,4)
C
C MICROCURIE-DAYS IN LYMPH (L)..
      AWIGL(ISPEC,2)=AWIGL(ISPEC,2)+YLW(ISPEC,1)+YLW(ISPEC,2)
55  CONTINUE
C
C MICROCURIE-DAYS IN G.I. SEGMENTS (S,SI,ULI,LLI)..
      AWIGL(ISPEC,3)=AWIGL(ISPEC,3)+YSW(ISPEC)
      AWIGL(ISPEC,4)=AWIGL(ISPEC,4)+YSIW(ISPEC)
      AWIGL(ISPEC,5)=AWIGL(ISPEC,5)+YULIW(ISPEC)
      AWIGL(ISPEC,6)=AWIGL(ISPEC,6)+YLLIW(ISPEC)
C
C MICROCURIE-DAYS IN OTHER SOURCE ORGANS..
      DO 65 ISOU=7,NSOU
        NC=NCOMP(ISPEC,ISOU-6)
        DO 63 IC=1,NC
          AWIGL(ISPEC,ISOU)=AWIGL(ISPEC,ISOU)
          $ +YORGW(ISPEC,IC,ISOU-6)
63  CONTINUE
65  CONTINUE
C*****
C ACCUMULATED ACTIVITY FOR PATHWAYS A THROUGH L..
      IF(MODE(ICASE).NE.1) GO TO 70
      AW(ISPEC,1)=AW(ISPEC,1)+YNPW(ISPEC,1)
      AW(ISPEC,2)=AW(ISPEC,2)+YNPW(ISPEC,2)
      AW(ISPEC,3)=AW(ISPEC,3)+Y1TBW(ISPEC,1)
      AW(ISPEC,4)=AW(ISPEC,4)+Y1TBW(ISPEC,2)
      AW(ISPEC,5)=AW(ISPEC,5)+YPW(ISPEC,1)
      AW(ISPEC,6)=AW(ISPEC,6)+YPW(ISPEC,2)
      AW(ISPEC,7)=AW(ISPEC,7)+YPW(ISPEC,3)
      AW(ISPEC,8)=AW(ISPEC,8)+YPW(ISPEC,4)
      AW(ISPEC,9)=AW(ISPEC,9)+YLW(ISPEC,1)
      AW(ISPEC,10)=AW(ISPEC,10)+YLW(ISPEC,2)
      AW(ISPEC,11)=AW(ISPEC,11)+Y2TBW(ISPEC,1)
      AW(ISPEC,12)=AW(ISPEC,12)+Y2TBW(ISPEC,2)
C*****
70  CONTINUE
C
C EXIT INTEGRATION LOOP IF INTEGRATION IS DONE.
      IF(SEND) GO TO 20

```

C TEST FEEDER COMPARTMENTS FOR EXHAUSTION.
 IF(MODE(ICASE).EQ. 2) GO TO 920

```

    IF(SNP) GO TO 810
    IF(T2.LT.TNP) GO TO 810
    SNP=.TRUE.
    DO 800 ISPEC=1,NSPEC
      YNPW(ISPEC,1)=0.0
      YNPW(ISPEC,2)=0.0
800  CONTINUE
810  CONTINUE
    IF(STB1) GO TO 830
    IF(T2.LT.TT81) GO TO 830
    STB1=.TRUE.
    DO 820 ISPEC=1,NSPEC
      YITBW(ISPEC,1)=0.0
      YITBW(ISPEC,2)=0.0
820  CONTINUE
830  CONTINUE
    IF(SP) GO TO 850
    IF(T2.LT.TP) GO TO 850
    SP=.TRUE.
    DO 840 ISPEC=1,NSPEC
      YPW(ISPEC,1)=0.0
      YPW(ISPEC,2)=0.0
      YPW(ISPEC,3)=0.0
      YPW(ISPEC,4)=0.0
840  CONTINUE
850  CONTINUE
    IF(SL(1)) GO TO 870
    IF(T2.LT.TL1) GO TO 870
    SL(1)=.TRUE.
    DO 860 ISPEC=1,NSPEC
      YLW(ISPEC,1)=0.0
      YLW(ISPEC,2)=0.0
860  CONTINUE
870  CONTINUE
    IF(SL(2)) GO TO 872
    IF(T2.LT.TL2) GO TO 872
    SL(2)=.TRUE.
    DO 871 ISPEC=1,NSPEC
      YLW(ISPEC,2)=0.0
871  CONTINUE
872  CONTINUE
    IF(STB2(1)) GO TO 890
    IF(T2.LT.TINT+TF+TD) GO TO 890
    STB2(1)=.TRUE.
    DO 880 ISPEC=1,NSPEC
      Y2TBW(ISPEC,1)=0.0
880  CONTINUE
890  CONTINUE
    IF(STB2(2)) GO TO 910
    IF(T2.LT.TINT+TG+TD) GO TO 910
    STB2(2)=.TRUE.
    DO 900 ISPEC=1,NSPEC
      Y2TBW(ISPEC,2)=0.0
900  CONTINUE
910  CONTINUE

```

```

C
920  CONTINUE
    IF(SGI) GO TO 940
    IF(T2.LT.TGI) GO TO 940
    SGI=.TRUE.
    DO 930 ISPEC=1,NSPEC
      YSW(ISPEC)=0.0
      YSIW(ISPEC)=0.0
      YULIW(ISPEC)=0.0
      YLLIW(ISPEC)=0.0
930  CONTINUE
940  CONTINUE
75  CONTINUE
80  CONTINUE

```

 C COMPUTE THE TARGET-SOURCE DOSE MATRIX FOR THE CURRENT CASE.

```

    DO 100 ISOU=1,NSOU
      DO 95 ITRG=1,NTRG
        DOSE(ICASE,ITRG,ISOU)=0.0
        DO 90 ISPEC=1,NSPEC
          DOSE(ICASE,ITRG,ISOU)=DOSE(ICASE,ITRG,ISOU)
            +S(ISPEC,ITRG,ISOU)*AWIGL(ISPEC,ISOU)
90  CONTINUE

```

```

95  CONTINUE
100 CONTINUE
C-----
C
C COMPUTE TOTAL DOSE TO EACH TARGET ORGAN.
  NSOU1=NSOU+1
  DO 380 ITRG=1,NTRG
    DOSE(ICASE,ITRG,NSOU1)=0.0
    DO 375 ISOU=1,NSOU
      IF(ISOU.EQ. 7) GO TO 375
      DOSE(ICASE,ITRG,NSOU1)=DOSE(ICASE,ITRG,NSOU1)
      +DOSE(ICASE,ITRG,ISOU)
    375 CONTINUE
  380 CONTINUE
C*****
C IF NSPEC IS GREATER THAN 1, COMPUTE PERCENT OF TOTAL DOSE TO EACH
C TARGET ORGAN DUE TO EACH SPECIES OF THE CHAIN.
  IF(NSPEC.EQ. 1) GO TO 210
  DO 205 ITRG=1,NTRG
    DO 200 ISPEC=1,NSPEC
      PCTDOS(ICASE,ITRG,ISPEC)=0.0
      DO 201 ISOU=1,NSOU
        IF(ISOU.EQ. 7) GO TO 201
        PCTDOS(ICASE,ITRG,ISPEC)=PCTDOS(ICASE,ITRG,ISPEC)+
          S(ISPEC,ITRG,ISOU)*AWIGL(ISPEC,ISOU)
      201 CONTINUE
      PCTDOS(ICASE,ITRG,ISPEC)=PCTDOS(ICASE,ITRG,ISPEC)*100./
        DOSE(ICASE,ITRG,NSOU1)
    205 CONTINUE
C*****
  210 WRITE(16,9991) NAMNUC(1),ICASE, TSTEP/ICASE)
    IF(NSOU.GT. 12) GO TO 9002
    WRITE(16,9992) (NAMSOU(I),I=1,NSOU)
    DO 9001 ISPEC=1,NSPEC
      9001 WRITE(16,9993) NAMNUC(ISPEC),(AWIGL(ISPEC,I),I=1,NSOU)
      GO TO 9005
    9002 WRITE(16,9992) (NAMSOU(I),I=1,12)
      DO 9003 ISPEC=1,NSPEC
        9003 WRITE(16,9993) NAMNUC(ISPEC),(AWIGL(ISPEC,I),I=1,12)
        WRITE(16,9992) (NAMSOU(I),I=13,NSOU)
        DO 9004 ISPEC=1,NSPEC
          9004 WRITE(16,9993) NAMNUC(ISPEC),(AWIGL(ISPEC,I),I=13,NSOU)
          9005 WRITE(16,9994)
            DO 9006 ISPEC=1,NSPEC
              9006 WRITE(16,9993) NAMNUC(ISPEC),(AWIGL(ISPEC,I),I=1,12)
            9991 FORMAT(1H0,/,60X,A8,/,50X,'MICROCURIE-DAYS FOR CASE ',12,/,45X,
              $ '(TIME STEP FOR INTEGRATION =',F6.0,' DAYS)')
            9992 FORMAT(1H0,'NUCLIDE ',12(A8,2X))
            9993 FORMAT(1H ,A8,1X,1P12E10,3)
            9994 FORMAT(1H0,39X,'ACCUMULATED ACTIVITY FOR TGLM PATHWAYS A ',
              $ 'THROUGH L',/,12X,'A',9X,'B',9X,'C',9X,'D',9X,'E',9X,'F',9X,'G',
              $ '9X,'H',9X,'I',9X,'J',9X,'K',9X,'L')
C*****
  410 RETURN
C-----
C END OF DOSRUM
C-----
END

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      SUPROUTINE STEP(T1,T2,MODE)
C
C ADVANCES THE RESIDENCE TIME INTEGRATION FROM TIME T1 TO T2 (DAYS).
C MODE = 1 FOR INHALATION, = 2 FOR INGESTION.
  INTEGER NCTEMP(20)
  REAL LNGI(4),LMAB(20,4),LMR(20),BRANCH(20,20)
  REAL G(20),H(20)
  REAL LMBDAB
  LOGICAL SNP,STB1,SP,SL,STB2,SGI
  COMMON /SWITCH/ SNP,STB1,SP,SL(2),STB2(2),SGI
  COMMON /LEVELS/ YNP(20,2),Y1TP(20,2),Y2TB(20,2),
    $ YP(20,4),YL(20,2),YS(20),YI(20),YULI(20),
    $ YLLI(20),YORG(20,5,16)
  COMMON /CUMACT/ YNPW(20,2),Y1TBW(20,2),Y2TBW(20,2),
    $ YPW(20,4),YLW(20,2),YSW(20),YSIW(20),YULIW(20),
    $ YLLIW(20),YORGW(20,5,16)
  COMMON /ORGOAT/ NCOMP(20,16),C(20,5,16),LMBDAB(20,5,16),
    $ F2PRDM(20,16)
  REAL LB(20,5),CTEMP(20,5),PTEMP(20),YTEMP0(20,5),YTEMP(20,5),
    $ YTEMPW(20,5)
  REAL LMA,LMB,LMC,LMD,LME,LNF,LNG,LNH,LNI

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      DOUBLE PRECISION T
      COMMON /NUMBRS/ NSPEC,NSCU,NTRG
      COMMON /GI/ LMG1,LMB1
      COMMON /RADAT/ LMR,ERANCH
      COMMON /TGLM/ LMA(20),LMB(20),LMC(20),LMD(20),LME(20),LMF(20),
      & LMG(20),LMH(20),LMI(20),
      & FA(20),FB(20),FC(20),FD(20),FE(20),FF(20),FG(20),FH(20),
      & FI(20)
      COMMON /RESOP/ D3,D4,D5
      DELT=T2-T1
      T=D3LE(0.5*(T1+T2))

C
C IF THIS CASE IS NOT INHALATION, BRANCH TO INGESTION.
C   IF(MODE.NE. 1) GO TO 13C
C
C -----
C RESPIRATORY TRACT (TASK GROUP LUNG MODEL FOR AEROSOLS)
C -----
      CALL HAL(T,H)
      IF(SNP) GO TO 21

C NASOPHARYNGEAL REGION (A,B)
C -----
      IPATH=1 FOR A
      &=2 FOR B
      DO 10 ISPEC=1,NSPEC
C INFLOW-RATE VECTOR PTEMP.. INITIALIZE TO ZERO.
      PTEMP(ISPEC)=0.0
C NUMBER OF SUBCOMPARTMENTS..
      NCTEMP(ISPEC)=2
C SUBCOMPARTMENT FRACTIONS..
      CTEMP(ISPEC,1)=FA(ISPEC)
      CTEMP(ISPEC,2)=FB(ISPEC)
C BIOLOGICAL CLEARANCE COEFFICIENTS..
      LB(ISPEC,1)=LMA(ISPEC)
      LB(ISPEC,2)=LMB(ISPEC)
C INITIAL CONDITIONS..
      DO 5 IPATH=1,2
        YTEMP0(ISPEC,IPATH)=YNF(ISPEC,IPATH)
      5 CONTINUE
      10 CONTINUE
C FIRST COMPONENT OF INTAKE VECTOR..
      PTEMP(1)=D3*H(1)
C (ALL OTHER COMPONENTS OF H ARE ZERO).
      CALL MULCOM(DELT,NSPEC,LMR,LB,CTEMP,NCTEMP,BRANCH,
      & PTEMP,YTEMP0,YTEMP,YTEMPW)
C MOVE OUTPUTS FOR A,B PATHWAYS..
      DO 20 ISPEC=1,NSPEC
        DO 15 IPATH=1,2
          YNP(ISPEC,IPATH)=YTEMP(ISPEC,IPATH)
          YNPW(ISPEC,IPATH)=YTEMPW(ISPEC,IPATH)
        15 CONTINUE
      20 CONTINUE
      21 CONTINUE
      IF(STB1) GO TO 41

C TRACHEOBRONCHIAL REGION (C,D)
C -----
      IPATH=1 FOR C
      &=2 FOR D
      DO 30 ISPEC=1,NSPEC
C INFLOW RATE VECTOR..
      PTEMP(ISPEC)=0.0
C COMPARTMENT FRACTIONS..
      CTEMP(ISPEC,1)=FC(ISPEC)
      CTEMP(ISPEC,2)=FD(ISPEC)
C BIOLOGICAL CLEARANCE COEFFICIENTS..
      LB(ISPEC,1)=LMC(ISPEC)
      LB(ISPEC,2)=LMD(ISPEC)

```

```

C
C INITIAL CONDITIONS..
  DO 25 IPATH=1,2
    YTEMP0(ISPEC,IPATH)=YIT0(ISPEC,IPATH)
  25 CONTINUE
  30 CONTINUE
C
C FIRST COMPONENT OF INTAKE VECTOR..
  PTEMP(1)=D4*H(1)
  CALL MULCOM(DELT,NSPEC,LMR,LB,CTEMP,NCTEMP,BRANCH,
    1 PTEMP,YTEMP0,YTEMP,YTEMP0)
C
C MOVE OUTPUTS FOR C,D PATHWAYS..
  DO 40 ISPEC=1,NSPEC
    DO 35 IPATH=1,2
      YIT0(ISPEC,IPATH)=YTEMP(ISPEC,IPATH)
      YIT00(ISPEC,IPATH)=YTEMP0(ISPEC,IPATH)
    35 CONTINUE
  40 CONTINUE
  41 CONTINUE
  IF(SF) GO TO 61
C
C PULMONARY REGION (E,F,G,H)
C -----
C   IPATH=1 FOR E
C   =2 FOR F
C   =3 FOR G
C   =4 FOR H
C   DO 50 ISPEC=1,NSPEC
C
C INFLOW RATE VECTOR..
  PTEMP(ISPEC)=0.0
C
C NUMBER OF SUBCOMPARTMENTS..
  NCTEMP(ISPEC)=4
C
C SUBCOMPARTMENT FRACTIONS..
  CTEMP(1,ISPEC)=FE(ISPEC)
  CTEMP(2,ISPEC)=FF(ISPEC)
  CTEMP(3,ISPEC)=FG(ISPEC)
  CTEMP(4,ISPEC)=FH(ISPEC)
C
C BIOLOGICAL CLEARANCE COEFFICIENTS..
  LB(1,ISPEC)=LME(ISPEC)
  LB(2,ISPEC)=LMF(ISPEC)
  LB(3,ISPEC)=LMG(ISPEC)
  LB(4,ISPEC)=LMH(ISPEC)
C
C INITIAL CONDITIONS..
  DO 45 IPATH=1,4
    YTEMP0(ISPEC,IPATH)=YP(ISPEC,IPATH)
  45 CONTINUE
  50 CONTINUE
C
C FIRST COMPONENT OF INFLOW VECTOR..
  PTEMP(1)=D5*H(1)
  CALL MULCOM(DELT,NSPEC,LMR,L2,CTEMP,NCTEMP,BRANCH,
    1 PTEMP,YTEMP0,YTEMP,YTEMP0)
C
C MOVE OUTPUTS FOR E,F,G,H PATHWAYS..
  DO 60 ISPEC=1,NSPEC
    DO 55 IPATH=1,4
      YP(ISPEC,IPATH)=YTEMPF(ISPEC,IPATH)
      YPW(ISPEC,IPATH)=YTEMPW(ISPEC,IPATH)
    55 CONTINUE
  60 CONTINUE
  61 CONTINUE
  IF(SL(1).AND.SL(2)) GO TO 81
C
C LYMPHATIC TISSUE (I,J)
C -----
C   IPATH=1 FOR I
C   =2 FOR J
C   DO 70 ISPEC=1,NSPEC
C
C INFLOW RATE..
  PTEMP(ISPEC)=0.0
C
C NUMBER OF SUBCOMPARTMENTS..
  NCTEMP(ISPEC)=2

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```

C
C SUBCOMPARTMENT FRACTIONS..
  CTEMP( ISPEC,1)=F1( ISPEC)
  CTEMP( ISPEC,2)=1.0-F1( ISPEC)
C
C BIOLOGICAL CLEARANCE COEFFICIENTS..
  LB( ISPEC,1)=LMI( ISPEC)
  LB( ISPEC,2)=0.0
C (THE J SUBCOMPARTMENT IS SUBJECT ONLY TO RADIOACTIVE DECAY).
C
C INITIAL CONDITIONS.. ADD TOTAL OUTFLOW OF PATHWAY H.
  DO 65 IPATH=1,2
    YTEMP( ISPEC, IPATH)=YL( ISPEC, IPATH)
    1  *LMH( ISPEC)*YPH( ISPEC,4)*CTEMP( ISPEC, IPATH)
  65 CONTINUE
  70 CONTINUE
  CALL MULCOM( DELT, NSPEC, LMR, LB, CTEMP, NCTEMP, BRANCH,
    1  PTEMP, YTEMP0, YTEMP, YTEMP0)
C
C MOVE OUTPUTS FOR (I,J) PATHWAYS..
  DO 80 ISPEC=1, NSPEC
    DO 75 IPATH=1,2
      YL( ISPEC, IPATH)=YTEMP( ISPEC, IPATH)
      YLM( ISPEC, IPATH)=YTEMP0( ISPEC, IPATH)
    75 CONTINUE
  80 CONTINUE
  81 CONTINUE
  IF( STB2(1)) GO TO 101
C
C TRACHEOBRONCHIAL FEEDBACK (K,L)
C -----
C THIS WILL REQUIRE TWO CALLS TO MULCOM..
C (1) INPUT FROM F, OUTPUT K
C (2) INPUT FROM G, OUTPUT L
C PATHWAYS K AND L ARE INDEPENDENT SUBCOMPARTMENTS.
C
C PATHWAY K
C -----
  DO 90 ISPEC=1, NSPEC
C
C INFLW VECTOR..
  PTEMP( ISPEC)=0.0
C
C NUMBER OF SUBCOMPARTMENTS..
  NCTEMP( ISPEC)=1
C
C SUBCOMPARTMENT FRACTIONS (=UNITY)..
  CTEMP( ISPEC,1)=1.0
C
C BIOLOGICAL CLEARANCE COEFFICIENTS..
  LB( ISPEC,1)=LMD( ISPEC)
C (REMOVAL IS REGULATED BY TRACHEOBRONCHIAL CLEARANCE TO G.I.).
C
C INITIAL CONDITIONS.. ADD OUTFLOW OF PATHWAY F.
  YTEMP0( ISPEC,1)=Y2TB( ISPEC,1)+LMF( ISPEC)*YPH( ISPEC,2)
  90 CONTINUE
  CALL MULCOM( DELT, NSPEC, LMR, LB, CTEMP, NCTEMP, BRANCH,
    1  PTEMP, YTEMP0, YTEMP, YTEMP0)
C
C MOVE OUTPUT FOR K PATHWAY..
  DO 100 ISPEC=1, NSPEC
    Y2TB( ISPEC,1)=YTEMP( ISPEC,1)
    Y2TB0( ISPEC,1)=YTEMP0( ISPEC,1)
  100 CONTINUE
  101 CONTINUE
  IF( STB2(2)) GO TO 130
C
C PATHWAY L
C -----
  DO 110 ISPEC=1, NSPEC
C
C INFLW VECTOR.. ZERO AS BEFORE.
  PTEMP( ISPEC)=0.0
C
C NCTEMP, CTEMP, AND LB..
  NCTEMP( ISPEC)=1
  CTEMP( ISPEC,1)=1.0
  LB( ISPEC,1)=LMD( ISPEC)
C
C INITIAL CONDITIONS.. ADD TOTAL OUTFLOW FROM PATHWAY G.
  YTEMP0( ISPEC,1)=Y2TB( ISPEC,2)+LMG( ISPEC)*YPH( ISPEC,3)
  110 CONTINUE

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      CALL MULCOM(DELT,NSPEC,LMR,LB,CTEMP,NCTEMP,BRANCH,
      $ PTEMP,YTEMP,YTEMPN)
C
C  MOVE OUTPUT FOR L PATHWAY..
      DO 120 ISPEC=1,NSPEC
        Y2TB(ISPEC,2)=YTEMP(ISPEC,1)
        Y2TBN(ISPEC,2)=YTEMPN(ISPEC,1)
      120 CONTINUE
C-----
C  END OF RESPIRATORY SEGMENT
C-----
      130 CONTINUE
        IF(SGI) GO TO 220
C-----
C  G. I. TRACT
C-----
C
C  STOMACH (S)
C-----
      IF(MODE.EQ. 2) CALL GES(T,G)
      DO 140 ISPEC=1,NSPEC
C
C  INFLOW RATE VECTOR..
      IF(MODE.EQ. 2) PTEMP(ISPEC)=G(ISPEC)
C
C  NUMBER OF SUBCOMPARTMENTS, COEFFICIENTS, AND BIOLOGICAL REMOVAL
C  COEFFICIENTS.
      NCTEMP(ISPEC)=1
      CTEMP(ISPEC,1)=1.0
      LB(ISPEC,1)=LMGI(1)+LMAB(ISPEC,1)
C
C  INITIAL CONDITIONS..
      YTEMPO(ISPEC,1)=YS(ISPEC)
      IF(MODE.EQ. 1) YTEMPO(ISPEC,1)=YTEMPO(ISPEC,1)
      $ +LMB(ISPEC)*YNPW(ISPEC,2)+LMD(ISPEC)*(Y1TBW(ISPEC,2)
      $ +Y2TBW(ISPEC,1)+Y2TBW(ISPEC,2))
      140 CONTINUE
      CALL MULCOM(DELT,NSPEC,LMR,LB,CTEMP,NCTEMP,BRANCH,
      $ PTEMP,YTEMPO,YTEMP,YTEMPN)
C
C  MOVE OUTPUTS FOR S..
      DO 150 ISPEC=1,NSPEC
        YS(ISPEC)=YTEMP(ISPEC,1)
        YSW(ISPEC)=YTEMPN(ISPEC,1)
      150 CONTINUE
C
C  SMALL INTESTINE (SI)
C-----
      DO 160 ISPEC=1,NSPEC
C
C  INFLOW RATE VECTOR..
      PTEMPF(ISPEC)=0.0
C
C  NCTEMP AND CTEMP ARE AS FOR THE STOMACH.
C
C  BIOLOGICAL REMOVAL RATES (ABSORPTION PLUS EMPTYING)..
      LB(ISPEC,1)=LMAB(ISPEC,2)+LMGI(2)
C
C  INITIAL CONDITIONS..
      YTEMPO(ISPEC,1)=YSI(ISPEC)+LMGI(1)*YSW(ISPEC)
      160 CONTINUE
      CALL MULCOM(DELT,NSPEC,LMR,LB,CTEMP,NCTEMP,BRANCH,
      $ PTEMP,YTEMPO,YTEMP,YTEMPN)
C
C  MOVE OUTPUTS FOR SI..
      DO 170 ISPEC=1,NSPEC
        YSI(ISPEC)=YTEMP(ISPEC,1)
        YSIW(ISPEC)=YTEMPN(ISPEC,1)
      170 CONTINUE
C
C  UPPER LARGE INTESTINE (ULI)
C-----
      DO 180 ISPEC=1,NSPEC
C
C  INFLOW VECTOR.. ZERO AS BEFORE.
C
C  NCTEMP AND CTEMP ARE AS FOR SI, EMPTYING RATES..
      LB(ISPEC,1)=LMGI(3)+LMAB(ISPEC,3)
C
C  INITIAL CONDITIONS..
      YTEMPO(ISPEC,1)=YULI(ISPEC)+LMGI(2)*YSIW(ISPEC)
      180 CONTINUE

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      CALL MULCOM(DELTA,NSPEC,LWR,LB,CTEMP,NCTEMP,BRANCH,
1      PTEMP,YTEMPO,YTEMP,YTEMPW)
C
C MOVE ULI OUTPUTS..
DO 190 ISPEC=1,NSPEC
  YULI(ISPEC)=YTEMP(ISPEC,1)
  YULIW(ISPEC)=YTEMPW(ISPEC,1)
190 CONTINUE
C
C LOWER LARGE INTESTINE (LLI)
C -----
DO 200 ISPEC=1,ISPEC
C
C INFLOW VECTOR.. ZERO AS BEFORE.
C
C NCTEMP AND CTEMP ARE AS FOR ULI. EMPTYING RATE..
  LJ(ISPEC,1)=LMGI(4)+LMAB(ISPEC,4)
C
C INITIAL CONDITIONS..
  YTEMPO(ISPEC,1)=YLLI(ISPEC)+LMGI(3)*YULIW(ISPEC)
200 CONTINUE
  CALL MULCOM(DELTA,NSPEC,LWR,LB,CTEMP,NCTEMP,BRANCH,
1      PTEMP,YTEMPO,YTEMP,YTEMPW)
C
C MOVE OUTPUTS FOR LLI..
DO 210 ISPEC=1,NSPEC
  YLLI(ISPEC)=YTEMP(ISPEC,1)
  YLLIW(ISPEC)=YTEMPW(ISPEC,1)
210 CONTINUE
C-----
C END OF G.I. TRACT CALCULATION.
C-----
220 CONTINUE
C-----
C OTHER ORGANS
C-----
  NORG=NSOU-6
  DO 250 IORG=1,NORG
    DO 230 ISPEC=1,NSPEC
C
C INFLOW RATE VECTOR = ZERO..
  PTEMP(ISPEC)=0.0
C
C NUMBER OF SUBCOMPARTMENTS, COEFFICIENTS, REMOVAL RATES, AND
C INITIAL CONDITIONS..
  NCTEMP(ISPEC)=NCOMP(ISPEC,IORG)
  NC=NCOMP(ISPEC,IORG)
  DO 225 IC=1,NC
    CTEMP(ISPEC,IC)=C(ISPEC,IC,IORG)
    LB(ISPEC,IC)=LMEDAB(ISPEC,IC,IORG)
    YTEMPO(ISPEC,IC)=YCRG(ISPEC,IC,IORG)
    IF(MODE.EQ.1) YTEMPO(ISPEC,IC)=YTEMPO(ISPEC,IC)
    + (LMA(ISPEC)*YNPW(ISPEC,1)+LMC(ISPEC)*YITBW(ISPEC,1)
    + LNE(ISPEC)*YPW(ISPEC,1)+LMI(ISPEC)*YLIW(ISPEC,1))
    *CTEMP(ISPEC,IC)*F2PRIM(ISPEC,IORG)
    YTEMPO(ISPEC,IC)=YTEMPO(ISPEC,IC)+(LMAB(ISPEC,1)
    *YSW(ISPEC)+LMAB(ISPEC,2)*YSIW(ISPEC)
    +LMAB(ISPEC,3)*YULIW(ISPEC)
    +LMAB(ISPEC,4)*YLLIW(ISPEC))
    *CTEMP(ISPEC,IC)*F2PRIM(ISPEC,IORG)
  225 CONTINUE
  230 CONTINUE
  CALL MULCOM(DELTA,NSPEC,LWR,LB,CTEMP,NCTEMP,BRANCH,
1      PTEMP,YTEMPO,YTEMP,YTEMPW)
C
C MOVE OUTPUTS FROM ORGAN IORG..
DO 240 ISPEC=1,NSPEC
  NC=NCOMP(ISPEC,IORG)
  DO 235 IC=1,NC
    YORG(ISPEC,IC,IORG)=YTEMP(ISPEC,IC)
    YORGW(ISPEC,IC,IORG)=YTEMPW(ISPEC,IC)
  235 CONTINUE
  240 CONTINUE
C
C END OF IORG LOOP..
250 CONTINUE
C-----
C END OF OTHER ORGANS
C-----
  RETURN
  END

```

```

SUBROUTINE MULCOM(T,N,LMH,LMB,C,NCOMP,BRANCH,P,A0,A,AW)
REAL T,LMH(20),LMB(20,5),C(20,5),BRANCH(20,20),P(20),
$ A0(20,5),A(20,5),AW(20,5)
DOUBLE PRECISION TA1,TA2,TAW1,TAW2,TERM
INTEGER NCOMP(20)
DOUBLE PRECISION E(550),H(20,5),D(20,5),G
DOUBLE PRECISION LM(20,5),LX(100)
DOUBLE PRECISION EXPFUN,EXPF1,ELXI,EXLI,
$ TEMP,TEM2
C THE FOLLOWING INTEGER-VALUED STATEMENT FUNCTION COMPUTES THE INDEX
C OF THE (I,J,M)-TH ENTRY IN THE ARRAY E.
INDEX(I,J,M)=J*(I-1)*(I-2)/2+(M-1)*NN2
NN2=N*(N-1)/2
IF(T.GT. 0.0) GO TO 20
DO 10 I=1,N
  NCI=NCOMP(I)
  DO 5 M=1,NCI
    A(I,M)=A0(I,M)
    AW(I,M)=0.0
  5 CONTINUE
  10 CONTINUE
  GO TO 300
20 CONTINUE
C
C COMPUTE TOTAL LAMBCAS AND STORE IN LINEAR ARRAY LX FOR SEPARATION.
KOUNT=0
DO 40 I=1,N
  NCI=NCOMP(I)
  DO 30 M=1,NCI
    KOUNT=KOUNT+1
    LX(KOUNT)=LMH(I)+LMB(I,M)
  30 CONTINUE
  40 CONTINUE
C
C IF TWO LX(I) ARE NEARLY EQUAL, SEPARATE THEM.
C
C SKIP SEPARATION ROUTINE IF N=1.
IF(N.EQ. 1) GO TO 65
C
C BEGINNING OF SEPARATION ROUTINE. KOUNT=NO. ELEMENTS IN LX.
KOUNT1=KOUNT-1
C CODE IS A SWITCH FOR WHICH THE VALUE 1 MEANS ANOTHER
C PASS SHOULD BE MADE.
KODE=1
45 IF(KODE.NE. 1) GO TO 65
KODE=0
C BEGIN PASS.
DO 60 K=1,KOUNT1
  K1=K+1
  DO 55 L=K1,KOUNT
    C IF LX(L) AND LX(K) ARE NEARLY EQUAL, SEPARATE THEM.
    IF(DABS(LX(L)/LX(K)-1.000).GE. 1.0D-6) GO TO 55
    LX(L)=LX(K)*1.0000100
    KODE=1
  55 CONTINUE
  60 CONTINUE
C RETURN FOR (POSSIBLY) ANOTHER PASS BY MEANS OF BACKWARD-POINTING
C GO TO STATEMENT.
GO TO 45
C END OF SEPARATION ROUTINE.
65 CONTINUE
C
C MOVE SEPARATED RATE COEFFICIENTS FROM LX TO LM.
KOUNT=0
DO 80 I=1,N
  NCI=NCOMP(I)
  DO 70 M=1,NCI
    KOUNT=KOUNT+1
    LM(I,M)=LX(KOUNT)
  70 CONTINUE
  80 CONTINUE
C
C BEGIN MAIN CALCULATION. I=1 IS HANDLED AS A SPECIAL CASE.
I=1
NCI=NCOMP(I)
DO 90 K=1,NCI
  D(I,K)=DBLE(C(I,K)*P(I))/LM(I,K)
  H(I,K)=DBLE(A0(I,K))-D(I,K)
  A(I,K)=SNGL(D(I,K)+H(I,K)*EXPFUN(-DBLE(T)*LM(I,K)))
  AW(I,K)=SNGL(D(I,K)*DBLE(T)+H(I,K)*EXPF1(LM(I,K),
$ DBLE(T)))
  90 CONTINUE
IF(I.EQ. N) GO TO 300

```

```

DO 200 I=2,N
  I1=I-1
  NCI=NCOMP(I)
  DO 110 K=1,NCI
    TEMP=0.000
    DO 93 J=1,I1
      TEMP1=0.000
      NCJ=NCOMP(J)
      DO 91 M=1,NCJ
        TEMP1=TEMP1+D(J,M)
      91 CONTINUE
      TEMP=TEMP+DBLE(BRANCH(I,J))*TEMP1
    93 CONTINUE
    C(I,K)=DBLE(C(I,K))/LM(I,K)*(DBLE(LMR(I))*TEMP+P(I))
    TEMP=0.000
  110 CONTINUE
  DO 150 J=1,I1
    NCJ=NCOMP(J)
    DO 140 M=1,NCJ
      IJM=INDEXE(I,J,M)
      E(IJM)=0.000
      IF(J.GT. I-2) GO TO 140
      J1=J+1
      DO 130 IR=J1,I1
        TEMP1=0.000
        NCIR=NCOMP(IR)
        DO 120 MU=1,NCIR
          IRJM=INDEXE(IR,J,M)
          TEMP1=TEMP1+DBLE(C(IR,MU)*LMR(IR))/(LM(IR,MU)-LM(J,M))
          * (E(IRJM)+DBLE(BRANCH(IR,J))*H(J,M))
        120 CONTINUE
        E(IJM)=E(IJM)+DBLE(BRANCH(I,IR))*TEMP1
      130 CONTINUE
    140 CONTINUE
  150 CONTINUE
C
C COMPUTE H(I,K), K=1,....,NCOMP(I).
DO 180 K=1,NCI
  TEMP=0.000
  DO 175 J=1,I1
    NCJ=NCOMP(J)
    DO 170 M=1,NCJ
      IJM=INDEXE(I,J,M)
      TEMP=TEMP+DBLE(LMR(I))/(LM(I,K)-LM(J,M))
      * (E(IJM)+DBLE(BRANCH(I,J))*H(J,M))
    170 CONTINUE
  175 CONTINUE
  H(I,K)=DBLE(A0(I,K))-D(I,K)-DBLE(C(I,K))*TEMP
  180 CONTINUE
  200 CONTINUE
C END OF CALCULATION OF D(I,K), H(I,K), E(I,J,M).
C
C BEGIN COMPUTATION OF A(I,K), AB(I,K)
DO 250 I=2,N
  I1=I-1
  NCI=NCOMP(I)
  DO 245 K=1,NCI
    EXLI=EXPFUN(-LM(I,K)*DBLE(T))
    EXLI1=EXPFI(LM(I,K),DBLE(T))
    TA1=0.000
    TA2=0.000
    TAW1=0.000
    TAW2=0.000
    DO 240 J=1,I1
      NCJ=NCOMP(J)
      DO 235 M=1,NCJ
        IJM=INDEXE(I,J,M)
        G=DBLE(C(I,K))*DBLE(LMR(I))/(LM(I,K)-LM(J,M))
        * (E(IJM)+DBLE(BRANCH(I,J))*H(J,M))
        TERM=G*(EXPFUN(-LM(J,M)*DBLE(T))-EXLI)
        IF(TERM .GE. 0.000) TA1=TA1+TERM
        IF(TERM .LT. 0.000) TA2=TA2+TERM
        TERM=G*(EXPFI(LM(J,M),DBLE(T))-EXLI1)
        IF(TERM .GE. 0.000) TAW1=TAW1+TERM
        IF(TERM .LT. 0.000) TAW2=TAW2+TERM
      235 CONTINUE
    240 CONTINUE
    TERM=LM(I,K)*D(I,K)*EXLI1+DBLE(A0(I,K))*EXLI
    IF(TERM .GE. 0.000) TA1=TA1+TERM
    IF(TERM .LT. 0.000) TA2=TA2+TERM
    A(I,K)=SNGL(TA1+TA2)
    IF(ABS(A(I,K)) .LE. 1.E-15*SNGL(TA1-TA2)) A(I,K)=0.0
  245 CONTINUE
  250 CONTINUE

```

```

      TERM=D(I,K)*(DBLE(T)-EXILI)+DBLE(AO(I,K))*EXILI
      IF (TERM .GE. 0.000) TAW1=TAW1+TERM
      IF (TERM .LT. 0.000) TAW2=TAW2+TERM
      AW(I,K)=SNGL(TAW1+TAW2)
      IF (ABS(AW(I,K)) .LE. 1.E-15*SNGL(TAW1-TAW2)) AW(I,K)=0.7
245    CONTINUE
250    CONTINUE
300    RETURN
      END

```

```

C
C
      DOUBLE PRECISION FUNCTION EXPFUN(T)
      DOUBLE PRECISION T
      EXPFUN=1.000
      IF (T.LT.-100.000) GO TO 10
      EXPFUN=DEXP(T)
10    RETURN
      END

```

```

C
C
      DOUBLE PRECISION FUNCTION EXPFI(LM,T)
      DOUBLE PRECISION LM,T,LMT,EXPFUN
      LMT=LM*T
      IF (LMT.LT.0.0300) GO TO 10
      GO TO 20
10    EXPFI=T*(((LMT/7.000-1.000)*LMT/6.000+1.000)
      $ *LMT/5.000-1.000)*LMT/4.000+1.000)*LMT/3.000-1.000)
      $ *LMT/2.000+1.000)
      GO TO 30
20    EXPFI=(1.000-EXPFUN(-LMT))/LM
30    RETURN
      END

```

```

      SUBROUTINE HAL(TIME,H)
C
C CALCULATES THE INTAKE RATE BY INHALATION
C
      DOUBLE PRECISION TIME
      LOGICAL DEFAULT
      DIMENSION H(20)
      COMMON /CASES/ NCASES,MODE(6),TEND(6),NINT(6),T(6,30),P(6,30),
      $ ISOL(6,20),ANAD(6),DEFAULT(6),FLUNG(6,9,20),TBLUNG(6,9,20),
      $ FI(6,20),GIFRAC(6,20,4)
      COMMON /HALGES/ ICASE
      COMMON /NUMBRS/ NSPEC,NSOU,NTRG
      DO 10 ISPEC=1,NSPEC
        H(ISPEC)=0.0
10    CONTINUE
      IF (MODE(ICASE).NE.1) GO TO 40
      N11=NINT(ICASE)-1
      IF (N11.EQ.0) GO TO 30
      DO 20 I=1,N11
        IF (SNGL(TIME).GE.T(ICASE,I+1)) GO TO 20
        H(I)=P(ICASE,I)
        GO TO 40
20    CONTINUE
30    H(1)=P(ICASE,N11+1)
40    RETURN
      END

```

```

      SUBROUTINE GES(TIME,G)
C
C CALCULATES THE INTAKE RATE BY INGESTION
C
      DOUBLE PRECISION TIME
      LOGICAL DEFAULT
      DIMENSION G(20)
      COMMON /CASES/ NCASES,MODE(6),TEND(6),NINT(6),T(6,30),P(6,30),
      $ ISOL(6,20),ANAD(6),DEFAULT(6),FLUNG(6,9,20),TBLUNG(6,9,20),
      $ FI(6,20),GIFRAC(6,20,4)
      COMMON /HALGES/ ICASE
      COMMON /NUMBRS/ NSPEC,NSOU,NTRG
      DO 10 ISPEC=1,NSPEC
        G(ISPEC)=0.0
10    CONTINUE

```

```

      IF (MODE(ICASE).NE.2) GO TO 40
      NI=NINT(ICASE)-1
      IF (NI.EQ.0) GO TO 30
      DO 20 I=1,NI
        IF (SNGL(TIME).GE.T(ICASE,I+1)) GO TO 20
        G(I)=P(ICASE,I)
      GO TO 40
20  CONTINUE
30  G(1)=P(ICASE,NI+1)
40  RETURN
      END

```

SUBROUTINE OUTPUT

```

C
C PRINTS SPECIFICATION INFORMATION AND OUTPUT FOR EACH
C OF THE CASES.
      DOUBLE PRECISION NAMNUC,NAMSCU,NAMTRG,NAMTOT,GISEG
      LOGICAL DEFAULT,ERFLAG
      INTEGER OUT
      DIMENSION FOUT(5),TCUT(9),GISEG(4)
      COMMON /PERCENT/ PCTDOS(6,27,20)
      COMMON /NAMES/ NAMNUC(20),NAMSCU(24),NAMTRG(27)
      COMMON /NUMBERS/ NSPEC,NSCU,NTRG
      COMMON /DOSES/ DOSE(6,27,25)
      COMMON /CASES/ NCASES,MODE(6),TEND(6),NINT(6),T(6,30),
1    P(6,30),ISOL(6,20),AMAD(6),DEFAULT(6),FLUNG(6,9,20),
2    TBLUNG(6,9,20),F1(5,20),GIFRAC(6,20,4)
      COMMON /RESP/ D3,D4,DE
      COMMON /ALERT/ ERFLAG(6)
      DATA GISEG/8HSTOMACH ,8HS INT ,8MU L INT ,8ML L INT /
      DATA OUT/6/
      DATA NAMTOT/8HTOTAL /
      DATA CLIT,YLIT,YLIT,STAR/4HD ,4HW ,4HY ,4H* /
C STORE HEADING FOR 'TOTAL' COLUMN OF DOSE MATRIX.
      NAMSCU(NSCU+1)=NAMTOT
C
C FOR EACH OF THE SEVERAL CASES, PRINT OUTPUT.
      DO 75 ICASE=1,NCASES
C
C DETERMINE EXPOSURE MODE FOR THE CURRENT CASE.
      IF (MODE(ICASE).EQ.1) GO TO 30
C -----
C INGESTION CASE
C -----
      NI=NINT(ICASE)
      WRITE(OUT,1000) ICASE
      INT=NI+1
      T(ICASE,INT)=TEND(ICASE)
      WRITE(OUT,1010)(T(ICASE,INT),T(ICASE,INT+1),P(ICASE,INT),
1    INT=1,NI)
      NS=NSPEC
      IF(NSPEC.GT.12) NS=12
      WRITE(OUT,1020)
      WRITE(OUT,1030) (NAMNUC(ISPEC),ISPEC=1,NS)
      DO 5 ISEG=1,4
6    WRITE(OUT,1040) GISEG(ISEG),(GIFRAC(ICASE,ISPEC,ISEG),
1    ISPEC=1,NS)
      IF(NS.EQ.NSPEC) GO TO 10
      NS1=NS+1
      WRITE(OUT,1030) (NAMNUC(ISPEC),ISPEC=NS1,NSPEC)
      DO 6 ISEG=1,4
6    WRITE(OUT,1040) GISEG(ISEG),(GIFRAC(ICASE,ISPEC,ISEG),
1    ISPEC=1,NS)
10  CONTINUE
C
C BRANCH TO SEGMENT WHICH PRINTS DOSE MATRIX.
      GO TO 64
C -----
C END OF CASE INFORMATION FOR INGESTION.
C -----
30  CONTINUE
C -----
C INHALATION CASE.
C -----
      NI=NINT(ICASE)
      WRITE(OUT,1050) ICASE
      INT=NI+1
      T(ICASE,INT)=TEND(ICASE)
      WRITE(OUT,1060)(T(ICASE,INT),T(ICASE,INT+1),P(ICASE,INT),
1    INT=1,NI)

```

```

C CHECK FOR WARNING CONDITION FROM SUBROUTINE INTP.
  IF (ERFLAG(ICASE)) WRITE(OUT,1100)
  WRITE(OUT,1070) AMAD(ICASE),C3,C4,C5
C
C NSC COUNTS SPECIES FOR WHICH SPECIAL LUNG PARAMETERS
C HAVE BEEN ENTERED FOR THE CURRENT CASE.
  NSC=0
C
C PRINT A TABLE OF SOLUBILITY CLASSES AND G. I. UPTAKE
C FRACTIONS FI. IF THE USER HAS PROVIDED SPECIAL LUNG
C PARAMETERS, THIS IS INDICATED BY AN ASTERISK.
  WRITE(OUT,1075)
  DO 40 ISPEC=1,NSPEC
    IF (ISOL(ICASE,ISPEC) .EQ. 1) GO TO 31
    IF (ISOL(ICASE,ISPEC) .EQ. 2) GO TO 32
    IF (ISOL(ICASE,ISPEC) .EQ. 3) GO TO 33
    GO TO 34
  31 FLAG=DLIT
    GO TO 35
  32 FLAG=WLIT
    GO TO 35
  33 FLAG=YLIT
    GO TO 35
  34 FLAG=STAM
    NSC=NSC+1
  35 WRITE(OUT,1080) NAMNUC(ISPEC),FLAG,(GIFRAC(ICASE,ISPEC,ISEG),
    * ISEG=1,4)
  40 CONTINUE
C
C IF THERE ARE NO SPECIAL LUNG PARAMETERS, PROCEED TO SEGMENT
C WHICH PRINTS DOSE MATRIX.
  IF(NSC .EQ. 0) GO TO 64
C
C OTHERWISE, WRITE OUT SPECIAL LUNG PARAMETERS.
  WRITE(OUT,1085)
  DO 50 ISPEC=1,NSPEC
    IF (ISOL(ICASE,ISPEC) .LT. 4) GO TO 50
    DO 45 IPATH=1,9
      FOUT(IPATH)=FLUNG(ICASE,IPATH,ISPEC)
      TOUT(IPATH)=TBLUNG(ICASE,IPATH,ISPEC)
      IF(TOUT(IPATH) .GT. 0.0) TOUT(IPATH)=0.6931472
    45 CONTINUE
    WRITE(OUT,1090) NAMNLC(ISPEC),FOUT,TOUT
  50 CONTINUE
C-----
C PRINT DOSE MATRIX
C-----
  64 CONTINUE
C IF INGESTION CASE, DOSE FROM LLNGS AND RES. LYMPH IS ZERO AND IS
C NOT PRINTED.
C BRANCH TO INGESTION CASE IN THIS EVENT.
  IF (MODE(ICASE).EQ.2) GO TO 65
C-----
C INHALATION CASE
C-----
  IFIRST=1
  NSOU2=NSOU+1
  ILAST=NSOU+1
  IF (NSOU2.GT.12) ILAST=12
  CALL PRINTD(IFIRST,ILAST,ICASE)
  IF (ILAST.EQ.NSOU2) GO TO 70
  IFIRST=13
  ILAST=NSOU2
  IF (NSOU2.GT.23) ILAST=23
  CALL PRINTD(IFIRST,ILAST,ICASE)
  IF (ILAST.EQ.NSOU2) GO TO 70
  IFIRST=24
  ILAST=NSOU2
  CALL PRINTD(IFIRST,ILAST,ICASE)
  GO TO 70
C-----
C INGESTION CASE
C-----
  65 IFIRST=3
  NSOU2=NSOU+1
  ILAST=NSOU+1
  IF (NSOU2.GT.14) ILAST=14
  CALL PRINTD(IFIRST,ILAST,ICASE)
  IF (ILAST.EQ.NSOU2) GO TO 71
  IFIRST=15

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      ILAST=NSOU2
      IF (NSOU2.GT.24) ILAST=24
      CALL PRINTD(IFIRST,ILAST,ICASE)
C-----
C PUNCH DOSES ON CARDS FOR LATER TABULATIONS.
C-----
      71 WRITE(7,2002) NAMNUC(1),ICASE,MODE(ICASE),F1(ICASE,1),
        $ (DOSE(ICASE,JTARG,NSOU2),JTARG=1,NTRG)
      2002 FORMAT(A8,14,14,14X,SE10.3/ 7E10.3,9X,'2'/ 7E10.3,9X,'3'/ 4E10.3,
        $ 39X,'4')
      GO TO 72
      70 WRITE(7,2000) NAMNUC(1),ICASE,MODE(ICASE),ISOL(ICASE,1),
        $ AMAD(ICASE),
        $ F1(ICASE,1),(DOSE(ICASE,JTARG,NSOU2),JTARG=1,NTRG)
      2000 FORMAT(A8,14,14,14,6E10.3/ 7E10.3,9X,'2'/ 7E10.3,9X,'3'/ 4E10.3,
        $ 39X,'4')
      72 CONTINUE
C-----
C IF NSPEC IS GREATER THAN 1, PRINT TABLE CONTAINING PERCENT OF TOTAL
C DOSE TO EACH TARGET ORGAN DUE TO EACH SPECIES OF THE CHAIN.
C-----
      IF(NSPEC.EQ.1) GO TO 80
      WRITE(OUT,100)
      WRITE(OUT,101) (NAMNUC(ISPEC),ISPEC=1,NSPEC)
      WRITE(OUT,102)
      DO 30 ITRG=1,NTRG
      WRITE(OUT,103) NAMTRG(ITRG),(PCTDOS(ICASE,ITRG,ISPEC),
        $ ISPEC=1,NSPEC)
      30 CONTINUE
      75 CONTINUE
      RETURN
C
C FORMAT STATEMENTS
      100 FORMAT('PERCENT DOSE EQUIVALENT..')
      101 FORMAT('NUCLIDE',T13,14A8,A7)
      102 FORMAT('TARGET')
      103 FORMAT(' ',A8,T12,14(F5.1,3X),F5.1)
      1000 FORMAT(' ',CASE',12,'.. INGESTION',T19,'-')
      1010 FORMAT(' ',INGESTION INTAKE RATE FUNCTION (MICROCURIES/DAY)'/
        $ ' ',T6,' FROM (DAYS)',T20,' TO (DAYS)',T33,'RATE'/
        $ (' ',1P3G13.3))
      1020 FORMAT(' ',INGESTION TRANSFER FRACTIONS (G. 1. TRACT TO BLCOD)
        $ ' ')
      1030 FORMAT(' ',T9,12(2X,A8))
      1040 FORMAT(' ',A8,T10,1P12G10.3)
      1050 FORMAT(' ',CASE',12,'.. INHALATION',T20,'-')
      1060 FORMAT(' ',INHALATION INTAKE RATE FUNCTION (MICROCURIES/DAY)'/
        $ ' ',T6,' FROM (DAYS)',T20,' TO (DAYS)',T33,'RATE'/
        $ (' ',1P3G13.3))
      1070 FORMAT(' ',AMAD (MICRON).. ',1PG9.3,5X,'D3 ='',G9.3,
        $ 5X,'D4 ='',G9.3,5X,'D5 ='',G9.3)
      1075 FORMAT(' ',T34,'G.1. UPTAKE FRACTIONS',T13,'SOLUBILITY',T26,
        $ 37(' ')/',T15,'CLASS',T26,'STOMACH',T36,'S INT',
        $ T46,'U L INT',T56,'L L INT')
      1080 FORMAT(' ',A8,T17,A1,T25,1F4G10.3)
      1085 FORMAT(' ',SPECIAL LUNG CLEARANCE PARAMETERS. T=HALF-TIME (DAYS).
        $ F=DEPOSITION FRACTION,'/' CLEARANCE,'/' PATHWAY..',
        $ T16,'A',T26,'B',T36,'C',T46,'D',T56,'E',T66,'F',T76,'G',
        $ T86,'H',T96,'I')
      1090 FORMAT(' ',A8,2X,'F',9(1X,1PG9.2)/',T12,'T',9(1X,1PG9.2))
      1100 FORMAT('WARNING: AMAD EXCEEDS THE RANGE OF AVAILABLE DATA ',
        $ 'FOR D3,D4 AND D5 FUNCTIONS')
      END
C
      SUBROUTINE PRINTD(IFIRST,ILAST,ICASE)
C
C PRINTS A HEADING AND THEN PRINTS COLUMNS IFIRST THROUGH ILAST OF THE DOSE
C MATRIX WHEN CALLED BY THE OUTPUT SUBROUTINE
      DOUBLE PRECISION NAMNUC, NAMSOU, NAMTRG
      INTEGER OUT
      COMMON /NAMES/ NAMNUC(20),NAMSOU(24),NAMTRG(27)
      COMMON /NUMBRS/ NSPEC,NSOU,NTRG
      COMMON /DOSES/ DOSE(6,27,25)
      COMMON /CASES/ NCASES,MODE(6),TEND(6),NINT(6),T(5,30),P(6,30),
        $ ISOL(6,20),AMAD(6),DEFAULT(6),FLUNG(6,9,20),TBLUNG(6,9,20),
        $ F1(6,20),GIFRAC(6,20,4)
      DATA OUT/6/
C PRINT HEADING
      WRITE(OUT,100)
C PRINT NAMES OF SOURCES
      IF(IFIRST.LT.7) GO TO 20

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      WRITE(OUT,110) (NAMSOU(ISO),ISO=IFIRST,ILAST)
C PRINT LABEL
      WRITE(OUT,120)
C PRINT NAMES OF TARGETS AND DCSES
      DO 10 ITRG=1,NTRG
        WRITE(OUT,130) NAMTRG(ITRG),(DOSE(JCASE,ITRG,ISO),ISO=
          $ IFIRST,ILAST)
      10 CONTINUE
      GO TO 30
      20 WRITE(OUT,110) (NAMSOU(ISO),ISO=IFIRST,6),(NAMSOU(ISO),ISO=8,
        $ ILAST)
        WRITE(OUT,120)
        DO 30 ITRG=1,NTRG
          WRITE(OUT,130) NAMTRG(ITRG),(DOSE(JCASE,ITRG,ISO),ISO=IFIRST,6),
            $ (DOSE(JCASE,ITRG,ISO),ISO=8,ILAST)
        30 CONTINUE
C
      RETURN
C
C FORMAT STATEMENTS
      100 FORMAT('DOSE EQUIVALENT (REM)')
      110 FORMAT('SOURCE',T13,11(A8,3X))
      120 FORMAT('TARGET')
      130 FORMAT(' ',A8,T12,11(1PG10,3,1X))
      END

      SUBROUTINE CMNNTS
      INTEGER*4 LINE(20),IN,OUT,COLLAR
      DATA OUT/6/, IN/5/
      DATA COLLAR/'$'/
C READ THE NEXT CARD. IF THE FIRST CHARACTER IS '$', RETURN.
C OTHERWISE PRINT THE CARD AND REPEAT.
      10 READ(IN,4010,END=20) LINE
      4010 FORMAT(20A4)
      IF(ICOMPARE(LINE,COLLAR,1).EQ.0) RETURN
      WRITE(OUT,4020) LINE
      4020 FORMAT(' ',20A4)
      GO TO 10
      20 STOP
      END

```



```

PGMM TITLE 'SUBROUTINE PGMMASK (I,J,K,L) -- TO SET PROGRAM MASK'
PROGRAM MASK SETTING ROUTINE
*
* ACCEPTS CALLING SEQUENCE
*
* CALL PGMMASK (IFXPTO,IDECD,IEXP,ISIG)
*
* A ZERO VALUE FOR ANY ARGUMENT DISABLES THE CORRESPONDING
* INTERUPT.
* NON-ZERO VALUES ALLOW THE INTERUPT TO OCCUR.
*
* IFXPTO -- FIXED-POINT OVERFLOW.
* IDECD -- DECIMAL OVERFLOW.
* IEXP -- EXPONENT UNDERFLOW.
* ISIG -- LOSS OF SIGNIFICANCE. (ZERO FRACTION IN A FLOATING
* POINT NUMBER)
*
* FOR EXAMPLE,
* CALL PGMMASK (1,1,0,0)
* CAUSES UNDERFLOWS AND LOSS OF SIGNIFICANCE TO BE IGNORED
* AND FIXED AND DECIMAL OVERFLOW TO BE HANDLED AS USUAL.
*
* PROGRAM AUTHOR -- R. K. GRIDER
* COMPUTING TECHNOLOGY CENTER
* OAK RIDGE, TENNESSEE
*
PGMMASKRG CSECT
ENTRY PGMMASK
USING 4,15
PGMMASK SAVE (14,12),,*
SR 0,0
LM 5,8,C(1)
L 3,=X'C800C000'
SR 4,4
CL 0,0(0,5)
BE 11
LR 4,3
I1 SRA 3,1
CL 0,0(0,6)
BE 12
OR 4,3
I2 SRA 3,1
CL 0,0(0,7)
BE 13
OR 4,3
I3 SRA 3,1
CL 0,0(0,8)
BE 14
OR 4,3
I4 SPM 4
RETURN (14,12),T
END

```

```

PGMM0C10
PGMM0C20
PGMM0C30
PGMM0C40
PGMM0C50
PGMM0C60
PGMM0C70
PGMM0C80
PGMM0C90
PGMM0100
PGMM0110
PGMM0120
PGMM0130
PGMM0140
PGMM0150
PGMM0160
PGMM0170
PGMM0180
PGMM0190
PGMM0200
PGMM0210
PGMM0220
PGMM0230
PGMM0240
PGMM0250
PGMM0260
PGMM0270
PGMM0280
PGMM0290
PGMM0300
PGMM0310
PGMM0320
PGMM0330
PGMM0340
PGMM0350
PGMM0360
PGMM0370
PGMM0380
PGMM0390
PGMM0400
PGMM0410
PGMM0420
PGMM0430
PGMM0440
PGMM0450
PGMM0460
PGMM0470
PGMM0480
PGMM0490
PGMM0500
PGMM0510
PGMM0520

```

ICOMPARE	START	0	ICOMPARE(STRA,STRB,N) =0 IF N.LE.0	ICOMP	10
	ENTRY	ICOMPA	THIS AN ENTRY FOR FTM IV	ICOMP	20
ICOMPA	EQU	*	THIS AN ENTRY FOR FTM IV	ICOMP	30
	USING	*.15	((N-1) MODULO 256) + 1 FOR N.GT.256	ICOMP	40
* BY RPR,	JULY	18, 1966.		ICOMP	50
	ST	2,SAVE		ICOMP	60
	L	2,9(0.1)	X2 = A(N)	ICOMP	70
	L	2,0(0.2)	X2=A	ICOMP	80
	LA	0,1	X0=+1	ICOMP	90
	SR	2,0	X2=N-1	ICOMP	100
	BZ	N1	BRANCH TO N1 IF N=1	ICOMP	110
	BM	DONE1	RETURN 0 IN A.LE.0	ICOMP	120
	STC	2,COM+1	STORE N-1 IN COM+1 (COMPARE N CHAR.)	ICOMP	130
	L	2,4(0.1)	X2=A(STRB)	ICOMP	140
	L	1,0(0.1)	X1=A(STRA)	ICOMP	150
COM	CLC	0(0.1),0(2)	COMPARE N CHAR. OF STRA WITH STRB	ICOMP	160
	L	2,SAVE	THIS LOAD DOES NOT EFFECT THE CONDITION CODE	ICOMP	170
	BL	NONE		ICOMP	180
	BE	DONE		ICOMP	190
* PREVIOUS LA	SET	X0=+1	X0=+1 STRA.GT.STRB	ICOMP	200
	BR	14		ICOMP	210
NONE	LNR	0,0	X0=-1 STRA.LT.STRB	ICOMP	220
	BR	14		ICOMP	230
DONE1	L	2,SAVE		ICOMP	240
DONE	SR	0,0	X0=0 STRA.EQ.STRB	ICOMP	250
	BR	14		ICOMP	260
* THIS SECTION	IS FOR N=1			ICOMP	270
N1	L	2,4(0.1)	X2=A(STRB)	ICOMP	280
	L	1,0(0.1)	X1=A(STRA)	ICOMP	290
	IC	2,0(0.2)	X2=FIRST CHAR OF STRB	ICOMP	300
	STC	2,COM1+1	STORE FIRST CHAR OF STRB IN COM1	ICOMP	310
COM1	CLI	0(1),X'00'	COMPARE 1 CHAR	ICOMP	320
	L	2,SAVE		ICOMP	330
	BL	NONE		ICOMP	340
	BE	DONE		ICOMP	350
*			X0=+1 STRA.GT.STRB	ICOMP	360
	BR	14		ICOMP	370
SAVE	DS	F		ICOMP	380
	END			ICOMP	390