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DCFPAK: Dose Coefficient Data File Package for Sandia National Laboratory

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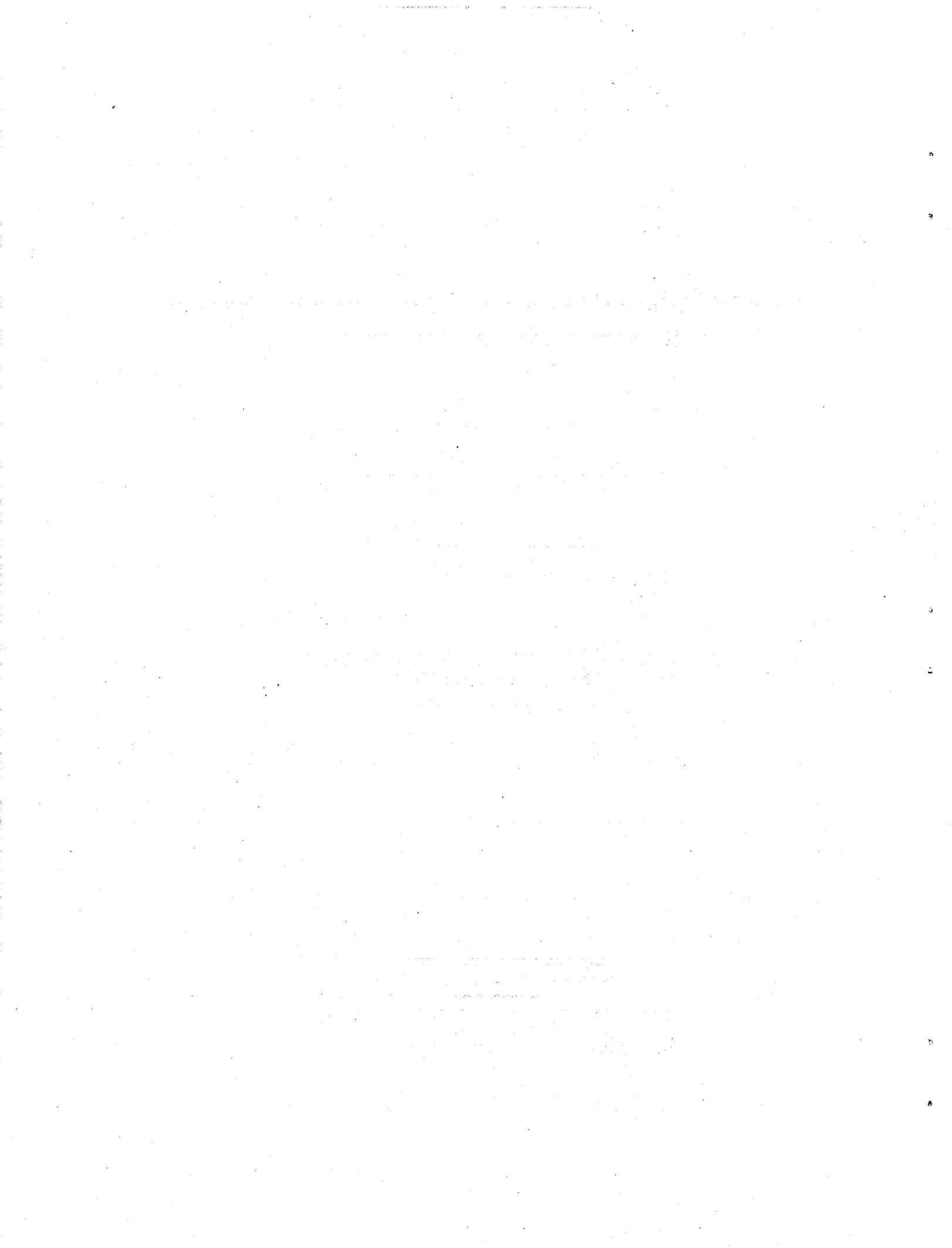
DCFPAK: Dose Coefficient Data File Package for Sandia National Laboratory

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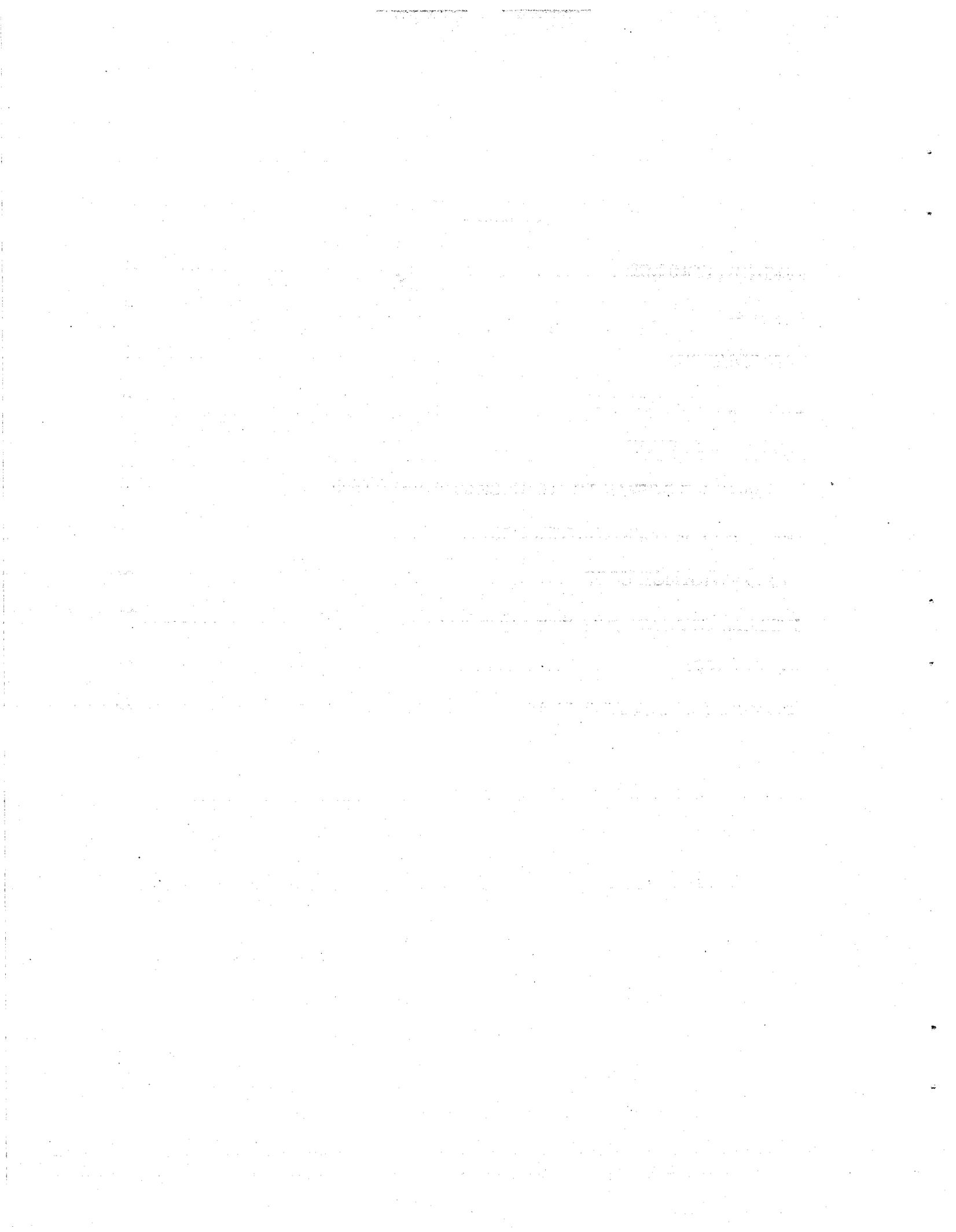
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ABSTRACT

The FORTRAN-based computer package DCFPAK (Dose Coefficient File Package) has been developed to provide electronic access to the dose coefficient data files summarized in Federal Guidance Reports 11 and 12. DCFPAK also provides access to standard information regarding decay chains and assembles dose coefficients for all dosimetrically significant radioactive progeny of a specified radionuclide. DCFPAK was designed for application on a PC but, with minor modifications, may be implemented on a UNIX workstation.

INTRODUCTION

The U.S. Environmental Protection Agency (EPA) has issued a series of "Federal Guidance" reports that provide the dosimetric information needed by government agencies to implement radiation protection programs in a consistent and adequately protective manner. This information is mainly in the form of "dose coefficients", or estimates of dose per unit exposure to individual radionuclides. These dose coefficients allow the user to relate concentrations of radionuclides in air, water, food, or soil to guidance for radiation dose to workers or members of the public.

Two Federal Guidance reports are currently in use. Federal Guidance Report No. 11 (Eckerman et al. 1988) provides dose coefficients, in the form of 50-year integrated dose equivalents, for acute ingestion or acute inhalation of radionuclides, based on the biokinetic and dosimetric models of ICRP Publication 30 (1979, 1980, 1981, 1988). Federal Guidance Report No. 12 (Eckerman and Ryman 1993) provides dose coefficients, in the form of dose per unit time-integrated exposure, for external exposure to radionuclides in air, water, or soil, based on state-of-the-art methods in external radiation dosimetry.

The tabulations in these two Federal Guidance reports include dose coefficients for the radionuclides considered in ICRP Publication 30, Limits for Intakes of Radionuclides by Workers (ICRP 1979, 1980, 1981, 1988). For each radionuclide and exposure mode, dose coefficients are provided for the seven organs or tissues assigned risk weighting factors in ICRP Publication 26 (1977): breast; lung; red marrow; bone surface; thyroid; gonads, representing the higher of the coefficients for ovaries and testes; and "remainder", representing the five remaining tissues receiving the highest doses. The tabulations include the effective dose equivalent, H_E , derived from the risk weighting factors and equivalent doses for these organs. In Federal Guidance Report No. 12, dose coefficients are also provided for skin because it is frequently the most highly irradiated organ for external exposure.

The software and data package DCFPAK (Dose Coefficient File Package) has been developed to allow electronic access to the full set of dose coefficients summarized in these two Federal Guidance reports and to facilitate consideration of dose coefficients for chains of radionuclides. In addition to the published dose coefficients, the DCFPAK libraries includes dose coefficients for 18 organs not addressed in Federal Guidance Report No. 11, and 17 organs not addressed in Federal Guidance Report No. 12 (Table 1). The additional dose coefficients were generated during the development of these two Federal Guidance reports but were excluded from the published tables to make the tables easier to use and to keep the reports at a reasonable length. For each radionuclide and exposure mode, the DCFPAK libraries include both the effective dose equivalent, H_E , based on the tissue weighting factors given in ICRP Publication 26 (1977), and the effective dose, E , based

Table 1. Tissues addressed in DCFPAK, Federal Guidance No. 11, and Federal Guidance No. 12.

| Tissue | Abbreviation in DCFPAK libraries | Listed in: | | |
|----------------------------|----------------------------------|------------|---------------------|---------------------|
| | | DCFPAK | Federal Guidance 11 | Federal Guidance 12 |
| Adrenal | Adrenal | Yes | No | No |
| Urinary Bladder Wall | Bld Wall | Yes | No | No |
| Bone Surface | B Surface | Yes | Yes | Yes |
| Brain | Brain | Yes | No | No |
| Breast | Breast | Yes | Yes | Yes |
| Esophagus | Esophagu | Yes | No | No |
| Stomach Wall | St Wall | Yes | No | No |
| Small Intestine Wall | SI Wall | Yes | No | No |
| Upper Large Intestine Wall | ULI Wall | Yes | No | No |
| Lower Large Intestine Wall | LLI Wall | Yes | No | No |
| Kidney | Kidney | Yes | No | No |
| Liver | Liver | Yes | No | No |
| Lung | Lung | Yes | Yes | Yes |
| Muscle | Muscle | Yes | No | No |
| Ovaries | Ovaries | Yes | No | No |
| Testes | Testes | Yes | No | No |
| Gonad ^a | (Not used) | No | Yes | Yes |
| Pancreas | Pancreas | Yes | No | No |
| Red Marrow | R Marrow | Yes | Yes | Yes |
| Skin | Skin | Yes | No | Yes |
| Spleen | Spleen | Yes | No | No |
| Thymus | Thymus | Yes | No | No |
| Thyroid | Thyroid | Yes | Yes | Yes |
| Uterus | Uterus | Yes | No | No |
| Remainder ^a | (Not used) | No | Yes | Yes |

^aRepresents multiple tissues considered explicitly in DCFPAK.

on the newer tissue weighting factors given in ICRP Publication 60 (1991). Tissue weighting factors recommended in ICRP Publication 26 and Publication 60 are compared in Table 2.

The DCFPAK libraries contain dose coefficients for each of nine modes of exposure to a given radionuclide: (1) ingestion; (2) inhalation; (3) submersion, meaning external exposure to (radiations emitted from) the radionuclide in air; (4) immersion, meaning external exposure to the radionuclide in water (from swimming); (5) external exposure to the radionuclide on the ground surface; and (6-9) external exposure to the radionuclide distributed to a depth of 1 cm, a depth of 5 cm, a depth of 15 cm, or an infinite depth in soil. The dose coefficients for internal exposures are 50-y integrated doses to organs following an acute intake and are given in units of Sv Bq⁻¹. The dose coefficients for external exposures are dose per unit time-integrated exposure. Dose coefficients for external exposures are in terms of Sv per Bq-s per unit volume of environmental medium (liter of air for submersion, liter of water for immersion, m² of soil for ground surface contamination, and m³ of soil for subsurface contamination of soil).

The dose coefficient for a given radionuclide and exposure scenario does not reflect ingrowth of chain members in the environment, but dose coefficients for ingestion and inhalation do reflect the contribution to dose from ingrowth of chain members in the body after intake of the parent radionuclide. For either internal or external exposure to a radionuclide, DCFPAK determines the radionuclide decay chain (if any) of that radionuclide, truncates the chain after the last potentially significant decay chain member, and assembles the dose coefficients for all potentially significant chain members. For internal exposure, DCFPAK truncates a chain if the cumulative energies for alpha, electron, and photon radiation over a 100-year period are changed less than 1% by the addition of subsequent chain members. The same procedure is followed for external exposures but with consideration restricted to electrons and photons.

The DCFPAK package, which is written in FORTRAN 77, was developed for use as a module of a radiological assessment package currently used at Sandia National Laboratory. However, DCFPAK is generic in nature and should be compatible with other FORTRAN-based radiological assessment packages. It was designed for use on a personal computer or work station and can be run interactively or in batch mode.

Table 2. Tissue weighting factors given in ICRP Publication 26 (1977) and ICRP Publication 60 (1991)*.

| Organ or tissue | Tissue weighting factor (w_T) | |
|-------------------|-----------------------------------|--------------|
| | ICRP Pub. 26 | ICRP Pub. 60 |
| Gonads | 0.25 | 0.20 |
| Bone marrow (red) | 0.12 | 0.12 |
| Colon | -- | 0.12 |
| Lung | 0.12 | 0.12 |
| Stomach | -- | 0.12 |
| Bladder | -- | 0.05 |
| Breast | 0.15 | 0.05 |
| Liver | -- | 0.05 |
| Oesophagus | -- | 0.05 |
| Thyroid | 0.03 | 0.05 |
| Skin | -- | 0.01 |
| Bone surface | 0.03 | 0.01 |
| Remainder | 0.30 | 0.05 |

*The values were developed for a reference population of equal numbers of both sexes and a wide range of ages. In the definition of effective dose they apply to workers, to the whole population, and to either sex.

For illustrative purposes DCFPAK was linked to a sample "driver" code called READDEM (source code, READDEM.FOR and executable file, READDEM.EXE). READDEM allows an interactive examination of DCFPAK's output for any of the 9 exposure modes and approximately 800 radionuclides addressed in this package.

The DCFPAK package consists of the following data libraries (data files) and software files:

1. nine libraries of dose coefficients, corresponding to the nine exposure modes listed above;
2. a library of information on the half-lives, modes of decay, branching fractions, and decay products of all 838 radionuclides considered in these two Federal Guidance reports;
3. a "data access" module that accesses the 10 data files described above and returns the relevant information;
4. an include file containing information on dimensioning of arrays in DCFPAK;
5. two include files containing common blocks;
6. an include file that provides unit designations to be reserved for IO used by DCFPAK;
7. an "initialization" file that informs DCFPAK of the location of all data files and their record lengths;
8. an illustrative driver code that serves the dual purpose of allowing an examination of available DCFPAK output and illustrating how to establish communication between the user's driver code and DCFPAK's data access module.

To access DCFPAK, the user must insert the following into his driver code: include statements that reference the files described in items 4-6 above, and a call statement, described later, that transfers the input variables describing the radionuclide, particle size, desired output, and other case-specific information to DCFPAK. The user's code and the source code DCFPAK.FOR must then be compiled and the resulting object files must be linked.

DATA FILES IN DCFPAK

Ten data files are included in DCFPAK. The data files are all "formatted direct-access files" consisting of ASCII characters, with all records in a given file of the same length and each record ending with an ASCII carriage-return (CR) and line-feed (LF) character. One of these data files contains information such as the half-time, decay modes, and branching fractions of the radionuclides and is used by DCFPAK to assemble the information on the decay chain for the parent radionuclide. The other nine data files contain dose coefficients corresponding to the nine exposure modes described earlier. A short description of each of the ten data files is given in the following.

DFEXTINT.NDX

This file is used by DCFPAK to assemble the information on the decay chain for the parent. The file contains 839 lines, including a header line with such information as the record format and one line of information for each of the 838 radionuclides addressed by DCFPAK. The line of information for a radionuclide contains the name and half-life of the radionuclide, the key (line number) of the radionuclide record in all other files, and a summary of decay properties of each radionuclide. For example, the line of information for Bi-212 gives the following information in the indicated order:

- name of radionuclide (Bi-212);
- half-life (60.55 m);
- decay modes (B-A, indicating beta-minus and alpha);
- beginning line number for Bi-212 in the inhalation dose coefficient file (2282);
- record number for Bi-212 in the ingestion dose coefficient file (699);
- record number for Bi-212 in each of the external dose coefficient files (690);
- record number in DFEXTINT.NDX of decay product Po-212 (504);
- branching fraction to Po-212 (6.4070E-01);
- record number in DFEXTINT.NDX of decay product Tl-208 (762);
- branching fraction to Tl-208 (3.5930E-01);
- total energy (MeV) of emitted alpha particles (2.1741);
- total energy (MeV) of emitted beta particles (0.4720);
- total energy (MeV) of emitted photons (0.1855);
- atomic weight (211.991271);
- date of creation of the radioactive decay data (05-May-77).

DFINHS.DAT

This file is an expanded version of Table 2.1 of Federal Guidance Report No. 11. The file contains dose coefficients for the case of acute intake of a radionuclide by inhalation. The dose coefficients represent the dose over a 50-year period following intake (Sv Bq^{-1} inhaled). Tabulated dose coefficients are for the default particle size $1 \mu\text{m}$ (activity median aerodynamic diameter, or AMAD), except for a few cases in which particle size is not relevant (e.g., for vapors). As described below, the tabulated dose coefficients are used to generate dose coefficients for any particle size specified by the user.

For each radionuclide, inhalation dose coefficients are included for each of the lung clearance classes applied to that radionuclide in ICRP Publication 30 (1977, 1980, 1981, 1988). The three main clearance classes are "D", "W", and "Y", where Class D refers to a clearance time of days, W to a clearance time of weeks, and Y to a clearance time of years from the pulmonary region of the lung. The occasionally used Class "V" refers to rapid clearance expected to occur for vapor forms of some elements. Three special clearance classes are used for carbon: "c", applied to labeled organic compounds, "m", applied to carbon monoxide, and "d", applied to carbon dioxide; differences in the three classes are associated mainly with differences in the relative amounts of deposited carbon exhaled and absorbed to blood and in the biokinetics of carbon after absorption to blood.

For each radionuclide, one or more lines of data are included for each clearance class. The first line includes the name of the radionuclide, the clearance class, the gastrointestinal absorption fraction (f_1 value) for material cleared to the gastrointestinal tract, a dose coefficient for each of the 23 tissues considered (Table 1), the effective dose equivalent, and the effective dose. For clearance class D, W, or Y (which apply to particulate matter), a second line of data provides the percentage of the dose coefficient for each organ that is attributable to deposition in the nasal-pharynx (N-P) and pulmonary (P) regions of the respiratory tract. As described below, these percentages are used by DCFPAK to calculate dose coefficients for particle sizes other than $1 \mu\text{m}$.

Dose coefficients for particle sizes other than $1 \mu\text{m}$ can be derived from the tabulated data for $1 \mu\text{m}$ as a result of the assumption in the underlying respiratory tract model (ICRP 1979) that the rate of clearance of material from the tract is independent of particle size. This assumption implies that the inhalation dose coefficient for a given radionuclide and clearance class is determined by the relative fractions of inhaled activity assigned to N-P, T-B, and P. Suppose, for example, that the user is considering inhalation of Be-10 of Class W and particle size $0.2 \mu\text{m}$. For this particle size, the deposition fractions for N-P, T-B, and P are 0.05, 0.08, and 0.5, respectively (with the missing fraction, 0.37, assumed to be promptly exhaled). For particle size $1 \mu\text{m}$, the deposition fractions for N-P, T-B, and P are 0.30, 0.08, and 0.25, respectively. According to the file DFINHS.DAT, for Be-10 of Class W and particle size $1 \mu\text{m}$, 26% of the inhalation dose coefficient (DC) for breast, for example, is attributable to activity deposited in N-P and 41% is attributable to activity deposited in P. Therefore, 33% is attributable to activity deposited in T-B. The dose coefficient for the breast for $0.2 \mu\text{m}$ would be

$$[(0.05/0.30) \times (0.26 \times DC)] + [(0.08/0.08) \times (0.33 \times DC)] + [(0.5/0.25) \times (0.41 \times DC)] = 1.1933 \times DC,$$

i.e., 1.1933 times the dose coefficient for particle size 1 μm .

For a given particle size in the range 0.1-20 μm , deposition fractions for the regions N-P, T-B, and P are based on the piecewise linear curves shown in Fig. 1 (after Fig. 5.1 of Part 1 of ICRP Publication 30 (1979)). For particle sizes less than 0.1 μm or greater than 20 μm , DCFPAK assigns fractional depositions in these regions corresponding to a particle size of 0.1 μm or 20 μm , respectively.

The esophagus was not depicted explicitly in the dosimetric human phantom used in ICRP Publication 30 and was not considered as a target organ in that document. However, the esophagus is addressed in DCFPAK because dose to the esophagus is considered in the calculation of the effective dose, E. Because internal dose calculations are not available for the esophagus, the thymus has been used as a surrogate. The esophagus was recently introduced into ORNL's human phantom and was considered explicitly in the external dose coefficients tabulated in Federal Guidance No. 12 and in DCFPAK.

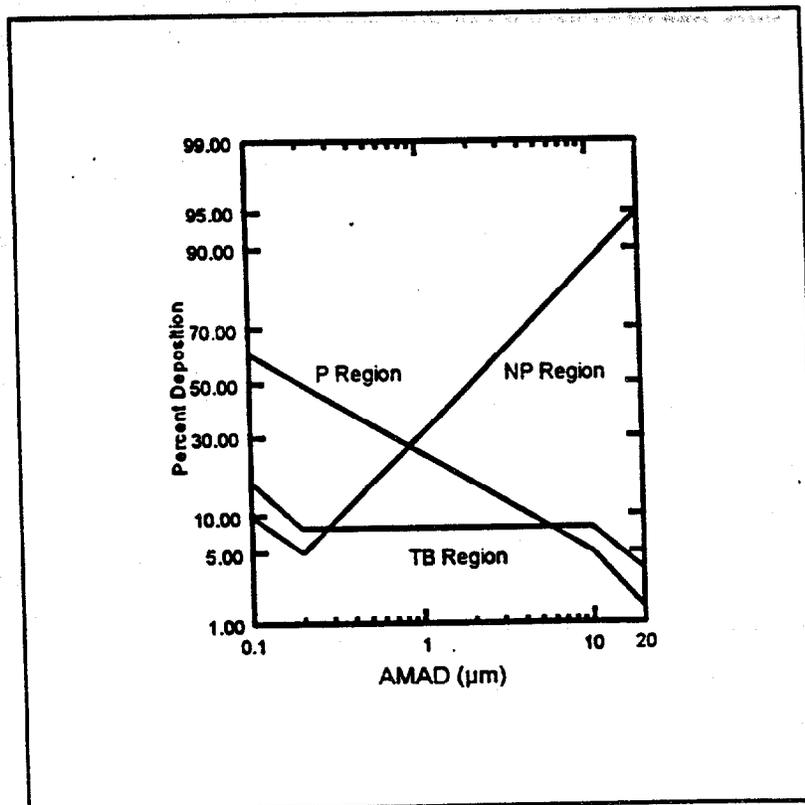


Figure 1 Deposition of particulate materials in the regions of the lung as a function of the activity median aerodynamic diameter (AMAD).

For radionuclides addressed in Part 1 of ICRP Publication 30 (1979), an inhalation dose coefficient of 0.0 is given for brain. This is because the brain was not included in the human phantom used in the ICRP dosimetry until after the completion of Part 1, and because there is no suitable surrogate for brain among the organs addressed.

DFINGS.DAT

This file is an expanded version of Table 2.2 of Federal Guidance Report No. 11. The file contains dose coefficients for the case of acute intake of a radionuclide by ingestion. The dose coefficients represent the dose over a 50-year period following acute intake (Sv Bq^{-1} ingested).

With a few exceptions, one line of data is given for each radionuclide. That line includes the name of the radionuclide, the gastrointestinal absorption fraction (f_1 value) for ingested activity, a dose coefficient for each of the 23 tissues considered (Table 1), the effective dose equivalent, and the effective dose. For a few radionuclides, one or more additional lines of dose coefficients are given, corresponding to alternate f_1 values used for certain forms of the radionuclide. For example, for radioisotopes of strontium, one line of dose coefficients corresponds to the f_1 value of 0.3 used for strontium compounds other than titanate and a second line gives dose coefficients for the f_1 value of 0.01 applied to strontium titanate.

For the reasons given in the discussion of inhalation dose coefficients, an ingestion dose coefficient of 0.0 for brain is given for each of the radionuclides addressed in Part 1 of ICRP Publication 30 (1979). Also, for reasons discussed above, ingestion dose coefficients for the thymus are applied to the esophagus.

FGR12F31.DAT

This file is an expanded version of Table III.1 of Federal Guidance Report No. 12. The file contains dose coefficients for the case of external exposure to the radionuclide in air (submersion). The units are dose per time-integrated air concentration ($\text{Sv per Bq-s L}^{-1}$ air).

One line of data is given for each radionuclide. That line contains the name of the radionuclide, a dose coefficient for each of the 23 tissues considered (Table 1), the effective dose equivalent, and the effective dose.

FGR12F32.DAT

This file is an expanded version of Table III.2 of Federal Guidance Report No. 12. The file contains dose coefficients for external exposure to the radionuclide in water ("immersion"), from swimming. The units are dose per time-integrated water concentration ($\text{Sv per Bq-s L}^{-1}$ water).

One line of data is given for each radionuclide. That line contains the name of the radionuclide, a dose coefficient for each of the 23 tissues considered (Table 1), the effective dose equivalent, and the effective dose.

FGR12F33.DAT

This file is an expanded version of Table III.3 of Federal Guidance Report No. 12. The file contains dose coefficients for external exposure to the radionuclide on the ground surface. The units are dose per time-integrated surface concentration (Sv per Bq-s m⁻²).

One line of data is given for each radionuclide. That line contains the name of the radionuclide, a dose coefficient for each of the 23 tissues considered (Table 1), the effective dose equivalent, and the effective dose.

FGR12F34.DAT

This file is an expanded version of Table III.4 of Federal Guidance Report No. 12. The file contains dose coefficients for external exposure to the radionuclide distributed to a depth of 1 cm in the soil. The units are dose per time-integrated concentration (Sv per Bq-s m⁻³).

One line of data is given for each radionuclide. That line contains the name of the radionuclide, a dose coefficient for each of the 23 tissues considered (Table 1), the effective dose equivalent, and the effective dose.

FGR12F35.DAT

This file is an expanded version of Table III.5 of Federal Guidance Report No. 12. The file contains dose coefficients for external exposure to the radionuclide distributed to a depth of 5 cm in the soil. The units are dose per time-integrated concentration (Sv per Bq-s m⁻³).

One line of data is given for each radionuclide. That line contains the name of the radionuclide, a dose coefficient for each of the 23 tissues considered (Table 1), the effective dose equivalent, and the effective dose.

FGR12F36.DAT

This file is an expanded version of Table III.6 of Federal Guidance Report No. 12. The file contains dose coefficients for external exposure to the radionuclide distributed to a depth of 15 cm in the soil. The units are dose per time-integrated concentration (Sv per Bq-s m⁻³).

One line of data is given for each radionuclide. That line contains the name of the radionuclide, a dose coefficient for each of the 23 tissues considered (Table 1), the effective dose equivalent, and the effective dose.

FGR12F37.DAT

This file is an expanded version of Table III.7 of Federal Guidance Report No. 12. This file contains dose coefficients for external exposure to the radionuclide distributed to an infinite depth in the soil. The units are dose per time-integrated concentration (Sv per Bq-s m⁻³).

One line of data is given for each radionuclide. That line contains the name of the radionuclide, a dose coefficient for each of the 23 tissues considered (Table 1), the effective dose equivalent, and the effective dose.

DCFPAK SOFTWARE

The DCFPAK software files, written in FORTRAN 77, are described below. In the following descriptions, the code that calls DCFPAK's data access module will be referred to as the "user's driver code".

DCFPAK.FOR

This is the FORTRAN source code for the data access module that accesses the data files and returns the relevant information. It should be compiled on the user's system.

PAKPARAM.FOR

This "include" file should be referenced by the user's driver code, along with the include file DCFPAK.CMN described below. The file contains the following two lines of FORTRAN code that determine the dimensioning of arrays in DCFPAK:

```
integer mspec, morg, mfact
parameter(mspec = 25, morg = 25, mfact = 9)
```

Here, MSPEC is the maximum length of the decay chain, MFACT is the maximum number of dose factors types, and MORG is the maximum number of organs in the dose factor file.

DCFPAK.CMN

This include file should be referenced by the user's driver code in any routines that access dosimetric information for the chain members. As noted above, PAKPARAM.FOR should also be included in these routines. The file contains the common blocks that will contain the information extracted from the data files by DCFPAK:

```
common /dfacts/ organ(morg), df(mspec, mfact, morg), flinh(mspec),
:               florl(mspec), classo(mspec), iflag(mspec, mfact),
:               nint, next

common /radat/ thalf(mspec), iu(mspec), nucnam(mspec),
:             branch(mspec, mspec), lmr(mspec),
:             ibr(mspec, mspec), nbr(mspec), nspec
```

The common block DFACTS contains the dose coefficients. The variables in the dimension statements are defined in the include file PAKPARAM.FOR. The definitions of the variables in this block are as follows:

ORGAN: A character(*9) array of organ names of maximum length MORG. The 23 organs addressed by DCFPAK are listed in Table 1.

DF: A real variable array of dose coefficients by chain member, exposure pathway, and organ.

F1INH: Real variable array of gastrointestinal uptake (f_i) values for inhalation, by chain member.

F1ORL: Real variable array of gastrointestinal uptake (f_i) values for ingestion, by chain member.

CLASSO: A character(*1) array of clearance class notation for the inhalation coefficients of the chain members.

IFLAG: An array of logical flags, by chain member and pathway, set to true in each case for which DCFPAK returns a coefficient in DF array.

NINT: Integer variable for the number of chain members that are used in the evaluation of inhalation and ingestion intakes (i.e., the length of the chain, or truncated chain, used in the calculation).

NEXT: Integer variable for the number of chain members that must be considered for external exposures.

The common block RADAT, shown above, contains information on the decay chain under consideration. The definitions of the variables in this block are as follows:

THALF: A character(*8) array of the half-life of each chain member.

IU: A character(*2) array of the units of the half-life of each chain member.

NUCNAM: A character(*7) array of the names of the chain members.

BRANCH: A two-dimensional real array (upper triangular matrix) of branching fractions, with an entry representing the fraction of the decays of the i th chain member forming the j th chain member.

LMR: A double precision array of decay constants (d^{-1}) for the chain members.

NBR: An integer array containing the number of chain members that decay directly to the specific chain member.

IBR: An integer array containing the indices of the chain members which form the specific chain member. For example, ($ibr(I, ispec), I=1, nbr(ispec)$) are the indices of the precursor of member $ispec$.

NSPEC: The length of the decay chain.

BATCH.CMN

This include file should be referenced by the user's driver code. The file contains two lines of code, including a common block with a logical flag that determines whether DCFPAK is operated in an interactive or a non-interactive mode:

```
logical dbatch
common/dcalbat/dbatch
```

The DBATCH logical variable inserted into the user's code should be set to "false" for the interactive mode and "true" for the non-interactive mode. Setting the DBATCH logical variable to "true" eliminates output to the screen that occurs in the interactive mode.

IOLIST.CMN

This include file should reside in the same directory as the file DCFPAK.FOR when the latter is compiled. This four-line file contains the unit designations for the IO used by DCFPAK:

```
integer idex, ingx, inhx, i31, i32, i33, i34, i35, i36,
:      i37, olog
parameter (idex = 10, ingx=11, inhx=12, i31=13, i32=14,
:          i33=15, i34=16, i35=17, i36=18, i37=19, olog=20)
```

The unit designations in IOLIST.CMN must be reserved for DCFPAK input and output; that is, they must differ from unit designations in the user's driver code. In addition to these units, DCFPAK uses unit 40.

DCFPAK.INI

This "initialization" file should be placed in the directory where the software is run. The file informs DCFPAK of the location of all data files and their record lengths. This file enables the user to place DCFPAK's data files in a directory distinct from that used for code output. The following is a sample version of DCFPAK.INI. The real version should show the actual path to each file indicated in the second field:

```
'snlindex.ndx', 'c:\snl\dcf\dfextint.ndx', 125
'ingestsf.dfs', 'c:\snl\dcf\dfings.dat', 240
'inhalesf.dfs', 'c:\snl\dcf\dfinhs.dat', 232
'submrsin.dfs', 'c:\snl\dcf\fgr12f31.dat', 232
'imersion.dfs', 'c:\snl\dcf\fgr12f32.dat', 232
'grsurf00.dfs', 'c:\snl\dcf\fgr12f33.dat', 232
'grvol_01.dfs', 'c:\snl\dcf\fgr12f34.dat', 232
```

```
'grvol_05.dfs', 'c:\snl\dcf\fgr12f35.dat', 232
'grvol_15.dfs', 'c:\snl\dcf\fgr12f36.dat', 232
'grvolinf.dfs', 'c:\snl\dcf\fgr12f37.dat', 232
'EOF', ' ' <- end of file marker
```

The first field is the file name within DCFPAK, and the second field is the full name of the file, including its path. For example, the record

```
'snlindex.ndx', 'snl\dcf\dfextint.ndx'
```

indicates that the file 'snlindex.ndx' is to be read as snl\dcf\dfextint.ndx, where "snl\dcf" is the path to the directory containing the file. The user should not edit the first field and should limit the path in the second field so that the field length does not exceed 64. The third field is the integer value for the record length for the file to be used in the FORTRAN open statement.

Not all FORTRAN compilers define the record length in the same manner when opening direct access files. DCFPAK was developed using the Microsoft FORTRAN compiler, which uses the physical length of the record less 2 bytes corresponding to the carriage return (CR)- line feed (LF) that separate formatted direct records. The integer values in the third field above specify the RECL parameter for the Microsoft compiler. Some other compilers (e.g, Lahey) specify RECL as the length of the physical record, which includes the 2 bytes associated with the CR-LF. For such compilers, DCFPAK.INI should be edited to increase the integer values indicated above by 2. For additional information, see the comments included in the files after the EOF marker.

READEM.FOR

This is the source code for a sample driver code that accesses DCFPAK and returns to the screen the decay chain and dose coefficients for the chain members, based on the user's input. This code is included for illustrative purposes.

READEM.EXE

This is the executable file for READEM.FOR.

CONNECTING DCFPAK TO THE USER'S DRIVER CODE

The DCFPAK data files and software are distributed in a self-extracting ZIP file named SNL.EXE. After extraction, the DCFPAK package can be connected to the user's driver code as follows:

Step 1: Copy the file snl.exe into a directory, preferably the directory that contains the user's driver code.

Step 2: Type "snl" and hit the "Enter" key. This extracts all data and software files. The data files may be moved to another directory. The new address of the data files must be specified in the file DCFPAK.INI.

Step 3: In the user's driver code, insert include statements referencing the include files PAKPARAM.FOR, DCFPAK.CMN, BATCH.CMN, and IOLIST.CMN as illustrated in the sample driver source code, READEM.FOR.

Step 4: Insert the following "call" into the user's drive code, as illustrated in READEM.FOR:

```
CALL DOSECOF (NUKE, F1ORAL, CLASS, F1INHI, AMAD, IPATH)
```

to obtain the information for radionuclide NUKE. The dose conversion factor information is returned in the common blocks discussed above. The variables NUKE and IPATH must be specified. If the other variables are not specified, default values are supplied by DCFPAK. If the library has multiple sets of dose coefficients (e.g., corresponding to different f1 values for a radionuclide), then DCFPAK will assign the most conservative set of coefficients. To obtain a particular set of coefficients one can specify the f1 values for inhalation and ingestion as well as the clearance class for inhalation. These variables are described in the following section. Illustrative read statements are given in the sample driver source code, READEM.FOR.

Step 5: As discussed in the following section and illustrated in READEM.FOR, insert data input statements into the user's driver code to define the radionuclide (NUKE), the operative exposure pathway (IPATH), and optional input if used.

Step 6: Insert the calls "CALL OPENEM" and "CALL CLOSEM" into the user's driver code in appropriate places for opening and closing the data files, respectively, as illustrated in READEM.FOR.

Step 7: Compile DCFPAK.FOR and the user's driver code, and link the resulting object files.

INPUT TO THE USER'S DRIVER CODE

Prior to calling the routine DOSECOF, a call should be made to the routine NUKEOK to determine if the nuclide of interest is contained in DCFPAK's data files. Thus, the user's code should include the following call:

```
CALL NUKEOK(NUKE, OK)
```

The variables are defined as:

NUKE: This character*7 variable represents the name of the radionuclide of interest. The naming convention for radionuclides follows standard practice (e.g., Co-60, Cs-137, Tc-99m). DCFPAK includes a character*7 function CHECK, which is called to place the nuclide name in the proper format.

OK: This is a logical variable which is set to true if the nuclide is present in the data files and is otherwise returned as false.

If the nuclide is present in the data files, then the user's driver code should access the data files through the call to DOSECOF described above:

```
CALL DOSECOF (NUKE, F1ORAL, CLASS, F1INH1, AMAD, IPATH)
```

The user's driver code should be set up so that the variables in this call are input variables, even though default values are supplied by DCFPAK for most of these variables. The variables are defined in the following.

NUKE: This variable was defined above.

F1ORAL: This is a real variable representing the value of the f_1 parameter (gastrointestinal uptake factor) associated with the ingested chemical form of the radionuclide. f_1 represents the fraction of the ingested material reaching blood in the absence of radioactive decay. For most radionuclides, a single f_1 value is applied to all chemical forms. However, for uranium, plutonium, and a few other elements, separate f_1 values are applied to relatively soluble and relatively insoluble compounds. If F1ORAL is set to zero, DCFPAK will return the ingestion coefficients for the chemical form that has the highest effective dose.

F1INH1: This is a real variable representing the gastrointestinal uptake factor for inhaled material that moves from the respiratory tract to the gastrointestinal tract. If F1INH1 is set to zero, DCFPAK will assign the default value to F1INH1 associated with the radionuclide and the CLASS variable.

CLASS: This is a character*1 variable that specifies the clearance class for inhaled forms of the radionuclide. The dose coefficients are based on the lung model of ICRP Publication 30, and the variable has values of "D", "W", "Y", and "V". Class D refers to a clearance time of days, W to a clearance time of weeks, and Y to a clearance time of years. The less frequently used Class "V" refers to rapid clearance such as occurs for vapor forms of some elements. If CLASS is not supplied, DCFPAK will select the classification of the chemical form giving the highest effective dose.

AMAD: This is a real variable representing the activity median aerodynamic diameter of the aerosol. If unspecified, a default AMAD of 1 μm is applied. If specified, DCFPAK calculates coefficients for the user's supplied AMAD. DCFPAK applies the value of AMAD to all chain members.

IPATH: This is a logical array (size 9) used to flag the type of dose coefficients that are of interest to the user. IPATH should be set to "true" to return tables of dose coefficients for all nine exposure models addressed by DCFPAK.

In addition to assembling the decay chain and the corresponding dose coefficients, DCFPAK can be used to compute the activities of the chain members as a function of time. The calculations assume a unit activity of the chain parent at time zero and no initial activity of other chain members. To make use of this capability, the following call should be inserted into the user's driver code after a call to DOSECOF:

CALL BIRCH(ISPEC, T, A, AINT)

The variables are defined as follows:

ISPEC: This input variable is the index number of the chain member of interest. ISPEC ranges from 1, the chain parent, to NSPEC, the last radioactive member of the chain.

T: This input variable is the time (d) for which the activity of chain member ISPEC is to be computed.

A: This output variable of the routine BIRCH is the activity of ISPEC at time T assuming that one unit of activity was present at T=0 for the parent and all daughter activities at that time were zero.

AINT: The output variable is the time integrated activity of ISPEC during the period of length T, assuming that one unit of activity was present at T=0 for the parent and all daughter activities were zero at T=0. The unit is days. The number of nuclear transformations of ISPEC per Bq of the parent during this period would be $8.64\text{E}04 \times \text{AINT}$.

To produce activities for multiple chain members and/or multiple times, the call may be looped over ISPEC and/or T. For long decay chains and short times the computed values A and AINT may exhibit numerical noise for some chain members due to loss of significance in the computations. Although these artifacts can be seen when tabulating values as a function of time, they are typically of no dosimetric consequence. An extended precision version of this routine is available from the authors but was not used in DFCPAK because its computations are considerably slower than those of the present version.

Before any calls to BIRCH, the routine DOSECOF must be called to assemble the decay chain. The user should see READEM.FOR for an illustrative implementation.

The user should examine the source code READEM.FOR for an example of how the routines of DCFPAK should be called.

DEMONSTRATION CODE

The READEM code included with this software package is an interactive code that can be used to examine available DCFPAK output. To run the code, type "readem" and press <Enter>. You will be prompted for the name of the radionuclide, the inhalation clearance class (a default is provided, as explained earlier), and the particle size (a default value of 1 μm is provided). In this demonstration code, default values are used for the other variables in the call DOSECOF. After responding to the three prompts described above, you will be shown the half-lives, branching fractions, and cumulative alpha, beta, and gamma energies of each member of the (non-truncated) decay chain for that radionuclide. Press <Enter> to see inhalation dose coefficients for the parent radionuclide, press <Enter> again to see inhalation dose coefficients for the next decay chain member in the truncated chain, and so forth. Repeatedly pressing <Enter> will take you through the dose coefficients for all members of the truncated chain, for all nine exposure modes addressed in DCFPAK.

Following the listing of the dose coefficients assembled for the chain, you will be asked to provide a time at which the activities of the chain members should be computed. If this computation is not desired, enter a time of zero; you will then be prompted to enter the next radionuclide. Entering the time (in days) will produce a tabulation of the activity and time-integrated activity for the chain members, as derived by the routine BIRCH. This computation is carried out only for the chain members that have been judged by DCFPAK to be significant in the dosimetry.

To exit READEM, press <Enter> when prompted for the next radionuclide.

INSTALLATION ON UNIX WORKSTATION

The following additional steps allow a user to run READEM on a UNIX (SUN) workstation:

1. Convert all files extracted from SNL.EXE (with the exception of convert2unix, wdaf, and wdaf.f) from DOS format to UNIX format. A batch file named convert2unix is included as an example of the necessary unix commands to convert the files.
2. Rewrite the data files as direct access files since the direct access attribute is lost in conversion from DOS to UNIX. A short FORTRAN program named wdaf (write direct access files) is included as an example of how to rewrite the files to restore the direct access attribute.
3. Replace the extension "for" on the files readem.for, dcfpak.for, and pakparm.for with extension "f".
4. Replace the variable "nargs" in readem.f with "iargc".
5. Replace "len_trim" with "lnblnk" in readem.f and dcfpak.f.
6. Compile the package as

```
f77 -03 -native -libmil -o readem readem.f dcfpak.f $LIB
```

REFERENCES

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- International Commission on Radiological Protection. Annals of the ICRP 1. ICRP Publication 26. Oxford: Pergamon Press; 1977.
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- International Commission on Radiological Protection. Limits for intakes by workers. ICRP Publication 30. Oxford: Pergamon Press; Part 3: 1981.
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APPENDIX A: Source Code Listings

A1. INCLUDE FILES

INCLUDE FILE PAKPARAM.FOR

* The following parameter values give the maximum dimensions of the
* arrays in the dose factor package. To increase the problem size edit
* this file and recompile all routines.

* mspec is the maximum number of nuclides in a chain
* mfact is the maximum number of dose factors types
* morg is the maximum number of organs in the dose factor file.

integer mspec, morg, mfact
parameter(mspec = 25, morg = 25, mfact = 9)

INCLUDE FILE DCFPAK.CMN

```
character*9 organ
character*8 thalf
character*7 nucnam
character*2 iu
character*1 classo
real branch
double precision lmr
c integer*4 ibr, nbr, nint, next
logical iflag
common /dfacts/ organ(morg), df(mspec, mfact, morg), flinh(mspec),
:          florl(mspec), classo(mspec), iflag(mspec, mfact),
:          nint, next
*
common /radat/ thalf(mspec), iu(mspec), nucnam(mspec),
:          branch(mspec, mspec), lmr(mspec), ibr(mspec,mspec),
:          nbr(mspec), nspec
```

INCLUDE FILE BATCH.CMN

```
* SNL batch flag
logical dbatch
common/dcalbat/dbatch
```

INCLUDE FILE IOLIST.CMN

```
integer idex, ingx, inhx, i31, i32, i33, i34, i35, i36,
:          i37, olog
parameter (idex = 10, ingx=11, inhx=12, i31=13, i32=14,
:          i33=15, i34=16, i35=17, i36=18, i37=19, olog=20)
```

A2. PROGRAM DCFPAK.FOR

* DCFPAK: Dose Coefficient File Package ORNL/TM-13347

* K.F. Eckerman and R.W. Leggett

* Oak Ridge National Laboratory

* The following is DCFPAK's source code. The routines are presented
* in alphabetical order by function; the order is:

- * 1. computational subroutines,
- * 2. screen routines,
- * 3. functions routines.

* The code was written in FORTRAN 77 using the Microsoft FORTRAN

* Compiler 5.1. Microsoft's LEN_TRIM function has been used,

* however at the end of the listing is a replacement function that

* can be activated by uncommenting the statements.

* K.F. Eckerman July 1, 1996.

* Routine call tree for DCFPAK

* DOSECOF <----- Entry point to DCFPAK

* CHAIN

* BIRCH <----- Can call after DOSECOF

* BATMAN

* EXPF1

* EXPFUN

* EXPFUN

* CLS

* FORWARD

* IBINRY

```

*
* ICUTOFF
*
* LEN_TRIM
*
* ORDER
*
* PATH
*
* PAUSEIT
*
* PRINTM
*
* CLS
*
* RECVR
*
* TIMEST
*
* CLS
*
* DEFRAC
*
* IBINRY
*
* LEN_TRIM
*
* NEWDFS
*
* SORTM
*
* ZEROM

```

Call cross-reference

```

*
* BATMAN called by: BIRCH
*
* BIRCH called by: CHAIN
*
* CHAIN called by: DOSECOF
*
* CHECK called by: CHEKAB NUKEOK
*
* CHEKAB called by: NUKEOK
*
* CHEKMN called by: NUKEOK
*
* CLS called by: CHAIN DOSECOF PRINTM
*
* DEFRAC called by: DOSECOF
*
* EXPF1 called by: BATMAN
*
* EXPFUN called by: BATMAN EXPF1

```

```

*
* FILEINI called by: OPENEM
*
* FORWARD called by: CHAIN
*
* IBINRY called by: DOSECOF FORWARD READEM NUKEOK
*
* ICUTOFF called by: CHAIN
*
* LCASE called by: FILEINI
*
* LEN_TRIM called by: CHAIN CHEKAB DOSECOF FILEINI
*
* LCASE LTRIM CASE
*
* LTRIM called by: CHECK TABLEM
*
* NEWDFS called by: DOSECOF
*
* ORDER called by: CHAIN
*
* PATH called by: CHAIN
*
* PAUSEIT called by: CHAIN
*
* PRINTM called by: CHAIN
*
* RECVR called by: CHAIN
*
* SORTM called by: NEWDFS
*
* TIMEST called by: CHAIN
*
* ZEROM called by: DOSECOF

```

The user's code should call the following routines

```

*
* OPENEM <-- to open the data files
*
* NUKEOK <-- to check the the nuclide name is valid.
*
* DOSECOF <-- to assemble the decay chain
*
* CLOSEM <-- to close the data files

```

1. Computational Routines

block data

```

include 'pakparm.for'
include 'dcfpak.cmn'

```

```

data organ /'Adrenals ', 'Bld Wall ', 'B Surface', 'Brain ',
:          'Breasts ', 'Esophagus', 'St Wall ', 'SI Wall ',
:          'ULI Wall ', 'LLI Wall ', 'Kidneys ', 'Liver ',
:          'Lungs ', 'Muscle ', 'Ovaries ', 'Pancreas ',
:          'R Marrow ', 'Skin ', 'Spleen ', 'Testes ',
:          'Thymus ', 'Thyroid ', 'Uterus ', 'H sub E ',
:          ' E ',
end
-----
*
subroutine batman(b0, zk, zkt, an1, an2, t, n)
-----
*
include 'pakparm.for'
*
call variables.
double precision b0, zk, zkt, an1, an2, zero
integer n
dimension b0(mspec), zkt(mspec), zk(mspec)
*
local variables.
double precision s1, s2, ss1, ss2, prod, expfun, expf1
integer i, j, k
parameter (zero=0.0d0)
include 'iolist.cmn'
an1 = zero
an2 = zero
do 50 i = 1, n
  if (b0(i) .ne. zero) then
    s1 = zero
    s2 = zero
    ss1 = zero
    ss2 = zero
    do 40 j = i, n
      prod = zkt(n) / zk(n) * zk(j) / zkt(i)
      do 30 k = 1, n
        if (k .ne. j) prod = prod * zk(k) / (zkt(k) - zkt(j))
30      continue
        if (prod .lt. zero) then
          s1 = s1 + dabs(prod) * expfun(-zkt(j)) * dble(t)
          ss1 = ss1 + dabs(prod) * expf1(zkt(j), dble(t))
        else
          s2 = s2 + prod * expfun(-zkt(j)) * dble(t)
          ss2 = ss2 + prod * expf1(zkt(j), dble(t))
40      continue
*
*      only positive values are retained; negatives are zero
*
        if (s2 .gt. s1) an1 = an1 + b0(i) * (s2 - s1)
        if (ss2 .gt. ss1) an2 = an2 + b0(i) * (ss2 - ss1)
      end if
50    continue
*
return

```

```

end
-----
*
subroutine birch(imem, t, rx1, rx2)
-----
*
include 'pakparm.for'
include 'dcfpak.cmn'
integer mpath, max
common/calcul/ max(mspec), mpath(mspec, mspec)
*
call variables.
integer imem
*
local variables.
integer i, j, mark, jpath, ipath, nmem, m
double precision zkt, zk, b, b0, an1, an2, x1, x2, zerod
dimension b(mspec), b0(mspec), zkt(mspec), zk(mspec), mark(mspec),
:          jpath(mspec), ipath(mspec)
parameter(zero = 0.0, zerod = 0.0d0)
*
* Trace the pathway backwards from Imem to decide which elements
* of the Mpath matrix to choose.
*
rx1 = zero
rx2 = zero
x1 = zerod
x2 = zerod
do 30 i = 1, nspec
  mark(i) = 1
  b(i) = dble(branch(i, i))
30 continue
31 nmem = 1
  jpath(1) = imem
*
  if (max(imem) .eq. 0) goto 35
33  imem = mpath(mark(imem), imem)
  nmem = nmem + 1
  jpath(nmem) = imem
  if (max(imem) .gt. 0) goto 33
35 do 40 i = 1, nmem
  ipath(i) = jpath(nmem - i + 1)
40 continue
  imem = ipath(nmem)
  do 50 i = 1, nmem
    b0(i) = b(ipath(i))
    zkt(i) = lmr(ipath(i))
    if (i .lt. nmem) then
      zkt(i) = dble(branch(ipath(i), ipath(i + 1))) * zkt(i)
    else
      zkt(i) = zkt(i)
    end if
50 continue
  call batman(b0, zk, zkt, an1, an2, t, nmem)
  x1 = x1 + an1
  x2 = x2 + an2
60 do 80 i = 1, nmem
  b(ipath(i)) = zerod

```

```

if (i .gt. 1) then
  if (mark(ipath(i)) .ne. max(ipath(i))) then
    m = ipath(i)
    mark(m) = mark(m) + 1
    do 70 j = 1, m - 1
      mark(j) = 1
      b(j) = dble(branch(j, j))
70    continue
      goto 31
    end if
  end if
80 continue
imem = ipath(nmem)
rx1 = snl(x1)
rx2 = snl(x2)
return
end
-----
*
*      subroutine chain(nuke)
*
*-----
* routine: chain
* author:  k. f. eckerman
* date:    04/06/89 : 09/25/91 : 08/06/92: 02/28/95 :06/04/96
* purpose: assemble decay chain. the name of the parent nuclide should
*           be passed to the routine as namen(1) in the common block
*           /chains/. upon return the chain members will be contained
*           in namen, and ndau is the length of the chain.
*
*           include 'pakparm.for'
*           include 'defpak.cmn'
*           include 'batch.cmn'
* common block /chaind/.
* character*7 named, nuke
* real fhold
* integer iptb, iparb, ibrch, ipar, ipt, n
* logical eob, pob
* common/chaind/named(mspec), fhold(mspec), iptb(mspec),
*           iparb(mspec), ipt, ibrch, ipar, eob, pob
* common/energy/ealpha(mspec), ebeta(mspec), egamma(mspec)
* dimension eat(mspec), ebt(mspec), egt(mspec)
* local variables.
* character*78 text
* character*8 t12
* character*2 t12u
* double precision zln2, timest
* parameter(zln2=0.693147181d0, zero=0.0)
* include 'iolist.cmn'
*
* initialize chain parameters
*
* ibrch = 0
* ipar = 1
* nspec = 1
* eob = .true.
* pob = .false.

```

```

nucnam(1) = nuke
do 11 i = 1, mspec
  do 10 j = 1, mspec
    branch(i, j) = zero
10  continue
11 continue
*
* assign one unit of activity to the parent, rest are zero
*
branch(1, 1) = 1.0
lmr(1) = 0.0d0
*
20 call forward
if (nspec .le. 0) then
  i = len_trim(nucnam(1))
  write(*, '(1x, a), ' is not in data base!') nucnam(1):(i)
  return
endif
call recver
if (.not. eob) goto 20
nspec = nspec - 1
if (pob) call order
do 100 i = 1, nspec
  if (nucnam(i):(2) .eq. 'Sf') then
    lmr(i) = 0.0D0
  else
    lmr(i) = zln2 / timest(thalf(i), iu(i))
  end if
100 continue
t12 = thalf(1)
t12u = iu(1)
text = nucnam(1):(len_trim(nucnam(1))) // ' Decay Chain:'
text = text:(len_trim(text)) // ' Half-lives and Branching'
text = text:(len_trim(text)) // ' Fractions'
if(.not. dbatch) then
  write(*,*) text:(len_trim(text))
  write(olog, '(/a)') text:(len_trim(text))
  call printm
  if (nspec .gt. 5) call cls
end if
call path
times = 36525.0
*
if(.not. dbatch) then
text = ': Activity, Transformations, & Cumulative Energies (MeV) a
:t 100y'
write(*,*) nucnam(1):(len_trim(nucnam(1))), text:(len_trim(text))
write(olog,*)nucnam(1):(len_trim(nucnam(1))),text:(len_trim(text))
write(*, '( ' Nuclide T1/2 A(t)/Ao intA/Ao(d) Ealph
.a Ebeta Egamma'))
write(olog, '( ' Nuclide T1/2 A(t)/Ao intA/Ao(d) Ea
.lpha Ebeta Egamma'))
end if
*
ea = zero
eb = zero
eg = zero

```

```

do 50 ispec = 1, nspec
  if (nucnam(ispec)(:2) .eq. 'Sf') goto 50
  call birch(ispec, times, rx1, rx2)
  ea = ea + rx2 * ealpha(ispec)
  eb = eb + rx2 * ebeta(ispec)
  eg = eg + rx2 * egamma(ispec)
*
  if (.not. dbatch) then
:   write(*,'(i4, 1x, a7, 1x, a8, a2, 1p2d12.5,3e9.2)') ispec,
:   nucnam(ispec), thalf(ispec), iu(ispec), rx1, rx2, ea, eb, eg
:   write(olog,'(i4, 1x, a7, 1x, a8, a2, 1p2d12.5,3e9.2)') ispec,
:   nucnam(ispec), thalf(ispec), iu(ispec), rx1, rx2, ea, eb, eg
  end if
*
  eat(ispec) = ea
  ebt(ispec) = eb
  egt(ispec) = eg
50 continue
  if (nucnam(nspec)(:2) .eq. 'Sf') then
    nint = icutoff(eat, ebt, egt, 0, nspec-1)
    next = icutoff(eat, ebt, egt, 1, nspec-1)
  else
    nint = icutoff(eat, ebt, egt, 0, nspec)
    next = icutoff(eat, ebt, egt, 1, nspec)
  end if
  if (nspec .eq. 1) then
    nint = 1
    next = 1
  end if
  if (.not. dbatch) call pauseit
  do 70 jspec = 2, nspec
    n = 0
    do 60 ispec = 1, nspec
      if (nucnam(ispec)(:2) .eq. 'Sf') goto 60
      if (branch(ispec, jspec) .gt. 1.0E-6) then
        n = n + 1
        lbr(n, jspec) = ispec
      end if
    60 continue
    nbr(jspec) = n
  70 continue
*
  return
end
*-----*
*
  subroutine chekab( nuke )
*-----*
*
  routine: chekab
*
  author: M. Cristy
*
  date: 05/05/93
*
  purpose: if nuclide not found, checks whether "a" & "b" isomers
*
  exist
*
  character*7 nuke, nukeab, nukea, nukeb, check
  character*6 thalf1, thalf2

```

```

parameter (nnuke = 9)
dimension nukeab(nnuke), nukea(nnuke), nukeb(nnuke),
:   thalf1(nnuke), thalf2(nnuke)
data nukeab /'Eu-150 ', 'In-110 ', 'Ir-186 ', 'Nb-89 ',
.'Np-236 ', 'Re-182 ', 'Sb-120 ', 'Sb-128 ', 'Ta-178 '/
data nukea /'Eu-150a', 'In-110a', 'Ir-186a', 'Nb-89a ',
.'Np-236a', 'Re-182a', 'Sb-120a', 'Sb-128a', 'Ta-178a'/
data nukeb /'Eu-150b', 'In-110b', 'Ir-186b', 'Nb-89b ',
.'Np-236b', 'Re-182b', 'Sb-120b', 'Sb-128b', 'Ta-178b'/
data thalf1/'12.62h', '69.1m', '15.8h', '66m', '115E3y',
.'12.7h', '15.89m', '10.4m', '9.31m'/
data thalf2/'34.2y', '4.9h', '1.75h', '122m', '22.5h',
.'64.0h', '5.76d', '9.01h', '2.2h'/
do 10 i = 1, nnuke
  if (nuke .eq. nukeab(i)) then
    if (nuke .eq. nukea(i)) then
      write(*,9110) nuke, nukea(i), thalf1(i),nukeb(i),thalf2(i)
100  write(*,'(a)') ' Input nuclide or <Enter> to quit-> '
      read(*,'(bn, a7)') nuke
      nuke = check( nuke )
      if (len_trim(nuke) .eq. 0) stop
      return
    endif
  10 continue
  return
9110 format( 4x,'Nuclide ',a,'has 2 isomers:'/20x,a,' with half-life ',a
./16x,'and ',a,' with half-life ',a/4x,
.'Re-input entire name with appropriate "a" or "b" designation',/)
end
*-----*
*
  subroutine chekmn( nuke )
*-----*
*
  routine: chekmn
*
  author: M. Cristy
*
  date: 05/05/93, revised 8/16/93
*
  purpose: if "m" isomer is requested, checks whether "n" isomer
*
  also exists.
*
  character*7 nuke, nukem, nuken
  character*6 thalfm, thalfn
  character*1 meta
  dimension nukem(3), nuken(3), thalfm(3), thalfn(3)
data nukem /'Ir-190m', 'Sb-124m', 'Tb-156m'/
data nuken /'Ir-190n', 'Sb-124n', 'Tb-156n'/
data thalfm/'1.2h', '93s', '24.4h'/
data thalfn/'3.1h', '20.2m', '5.0h'/
data nnuke /3/
do 20 i = 1, nnuke
  if (nuke .eq. nukem(i)) then
    if (nuke .eq. nuken(i)) then
      write(*, 9110) nuke, nukem(i), thalfm(i), nuken(i), thalfn(i)
10  write(*, 9120) nukem(i), nuken(i)
      read(*,'(a1)') meta
      if (meta.eq.' ' .or. meta.eq.'m' .or. meta.eq.'M') then
        return
      elseif (meta.eq.'n' .or. meta.eq.'N') then
        nuke = nuke(1:6) // 'n'

```

```

        return
    else
        goto 10
    endif
endif
20 continue
return
9110 format(4x,'Nuclide ',a,' has 2 metastable isomers:'/20x,
:a,' with halflife ',a/16x,'and ', a,' with halflife ',a)
9120 format(4x,'Input <Enter> to accept ',a,', or input "n" for ',a,
:': ',/)
end

```

```
-----
*
```

```
*      subroutine closen
*
```

```
-----
*
```

```

include 'iolist.cmn'
close(idex)
close(ingx)
close(inhx)
close(i31)
close(i32)
close(i33)
close(i34)
close(i35)
close(i36)
close(i37)
close(olog)
return
end

```

```
-----
*
```

```
*      subroutine depfrac (amad, d3, d4, d5)
*
```

```
-----
*
```

```

author:  k. f. eckerman
date:    08/20/93
purpose: routine computes the deposition fractions in the three
regions of the lung: nasal-pharynx (d3), tracheo-bronchial
(d4) and pulmonary (d5).

```

```

p(t) = 1.0 - 0.5*(((0.019527*t + 0.000344)*t + 0.115194)*t +
:          0.196854)*t + 1.0)**(-4)
ppt(w) = -(w - ((0.010328*w + 0.802853)*w + 2.515517) /
:          ((0.001308*w + 0.189269)*w + 1.432788)*w + 1.0))
ww(x) = sqrt(-2.0*log(x))

```

```

*      Nasal-pharynx region
*      if (amad .eq. 0.0) then

```

```

d3 = 0.30
elseif (amad .le. 0.1) then
d3 = 0.1
elseif (amad .ge. 20) then
d3 = 0.95
elseif (amad .gt. 0.1 .and. amad .lt. 0.2) then

```

```

u0 = -0.698970
u1 = -1.00
t0 = ppt(ww(0.05))
t1 = ppt(ww(0.10))
t = t0 + (t1 - t0) / (u1 - u0) * (alog10(amad) - u0)
if (t .ge. 0.0) then
d3 = p(t)
else
d3 = 1.0 - p(-t)
end if
elseif (amad .ge. 0.2 .and. amad .le. 10.0) then
u0 = -0.698970
u1 = 0.301030
t0 = ppt(ww(0.05))
t1 = ppt(ww(0.5))
t = t0 + (t1 - t0) / (u1 - u0) * (alog10(amad) - u0)
if (t .ge. 0.0) then
d3 = p(t)
else
d3 = 1.0 - p(-t)
end if
elseif (amad .gt. 10.0 .and. amad .lt. 20.0) then
u0 = 1.0
u1 = 1.301030
t0 = ppt(ww(0.875))
t1 = ppt(ww(0.95))
t = t0 + (t1 - t0) / (u1 - u0) * (alog10(amad) - u0)
if (t .ge. 0.0) then
d3 = p(t)
else
d3 = 1.0 - p(-t)
end if
end if
*      TB region
*      if (amad .eq. 0.0) then
d4 = 0.08
elseif (amad .le. 0.1) then
d4 = 0.17
elseif (amad .ge. 20) then
d4 = 0.035
elseif (amad .gt. 0.1 .and. amad .lt. 0.2) then
u0 = -0.698970
u1 = -1.0
t0 = ppt(ww(0.08))
t1 = ppt(ww(0.17))
t = t0 + (t1 - t0) / (u1 - u0) * (alog10(amad) - u0)
if (t .ge. 0.0) then
d4 = p(t)
else
d4 = 1.0 - p(-t)
end if
elseif (amad .ge. 0.2 .and. amad .le. 10.0) then
d4 = 0.08
elseif (amad .gt. 10.0 .and. amad .lt. 20.0) then
u0 = 1.0
u1 = 1.30130
t0 = ppt(ww(0.08))

```

```

t1 = ppt(ww(0.035))
t = t0 + (t1 - t0) / (u1 - u0) * (alog10(amad) - u0)
if (t .ge. 0.0) then
  d4 = p(t)
else
  d4 = 1.0 - p(-t)
end if
end if
Pulmonary region
if (amad .eq. 0.0) then
  d5 = 0.25
elseif (amad .le. 0.1) then
  d5 = 0.6150
elseif (amad .ge. 20.0) then
  d5 = 0.015
elseif (amad .gt. 0.1 .and. amad .lt. 0.2) then
  u0 = -0.698970
  u1 = -1.00
  t0 = ppt(ww(0.5))
  t1 = ppt(ww(0.615))
  t = t0 + (t1 - t0) / (u1 - u0) * (alog10(amad) - u0)
  if (t .ge. 0.0) then
    d5 = p(t)
  else
    d5 = 1.0 - p(-t)
  end if
elseif (amad .ge. 0.2 .and. amad .le. 10.0) then
  u0 = -0.698970
  u1 = 1.0
  t0 = ppt(ww(0.5))
  t1 = ppt(ww(0.05))
  t = t0 + (t1 - t0) / (u1 - u0) * (alog10(amad) - u0)
  if (t .ge. 0.0) then
    d5 = p(t)
  else
    d5 = 1.0 - p(-t)
  end if
elseif (amad .gt. 10.0 .and. amad .lt. 20.0) then
  u0 = 1.0
  u1 = 1.301030
  t0 = ppt(ww(0.05))
  t1 = ppt(ww(0.015))
  t = t0 + (t1 - t0) / (u1 - u0) * (alog10(amad) - u0)
  if (t .ge. 0.0) then
    d5 = p(t)
  else
    d5 = 1.0 - p(-t)
  end if
end if
end if
50 continue
return
end

```

```

-----
*
*      subroutine dosecof(nuke, flo, class, fli, amad, ipath)
*
*-----
*      routine: dosecof
*      author:  k.f. eckerman
*      data:    05/20/96
*      purpose: assemble the decay chain and extract the dose coefficients
*                for the chain members.
*-----
*      input variables
*      nuke      parent of the chain in standard notation; e.g., Cs-137
*      flo       f_1 value for oral intakes (defaults to highest effective
*                dose
*      class     inhalation clearance class for parent.  decay products
*                will be of this class if possible or class with highest
*                effective dose.
*      fli       f_1 value for inhalation.  coefficients are actually
*                picked by class.
*      amad      amad for the aerosol in  $\mu\text{m}$ .
*      ipath(i)  pathway logical flag of size 9.  1 inhalation,
*                2 ingestion, 3 submersion, 4 immersion, 5 ground surface,
*                6 1 cm thick soil sample, 7 5 cm, 8 15 cm, 9 infinite.
*
*      output
*      output is through the common blocks in the include file dcfpak.cmn
*      as shown below.
*      common /dfacts/ organ(morg), df(mspec, mfact, morg), flinh(mspec),
*      :          flori(mspec), classo(mspec), iflag(mspec, mfact),
*      :          nint, next
*      organ     character*9 array of organ names.
*      df        dose factors array by chain member, pathway, and organ
*      flinh     array of f_1 values for inhalation by chain member
*      flori     array of f_1 values for ingestion by chain member
*      classo    array of class notation for inhalation by chain member
*      iflag     logical flags for dose factor by chain member and pathway
*      nint      length of chain for internal factors
*      next      length of chain for external factors
*
*      common /radat/ thalf(mspec), iu(mspec), nucnam(mspec),
*      :          branch(mspec, mspec), lmr(mspec),
*      :          ibr(mspec,mspec), nbr(mspec), nspec
*      thalf     half-life of chain members
*      iu        units of the half-lives
*      nucnam    names of the chain members
*      branch    branching fraction
*      lmr       decay constant in 1/d
*      ibr       branch pointer
*      nbr       number of branches for chain members
*      nspec     length of chain
*
*      include 'pakparm.for'
*      include 'dcfpak.cmn'
*      include 'batch.cmn'
*      character*7 nuke, nuclide
*      character*1 cishld, class, cx

```

```

integer ipt, ibinry, idep
logical ipath(9)
dimension dx(4, 25), fhld(4), clshld(4), idep(4, 25, 2), ifi(7)
include 'iolist.cmn'
data ifi /131, 132, 133, 134, 135, 136, 137/
if (.not. dbatch) call cls
*
* zero out the dose factor array
*
call zerom
*
* assemble the decay chain
*
call chain (nuke)
*
* first do the external coefficients for the next chain members
*
do 20 ispec = 1, next
  nuke = nucnam(ispec)
  ipt = ibinry( nuke )
  if (ipt .ne. 0) then
    read(idex,'(a7,a8,a2,a6,3i5)', rec=ipt) nuke, t, ix, mode,
:    inh, ing, iex
    if (lex .ne. 0) then
      do 10 ip = 3, 9
        if (ipath(ip)) then
          iflag(ispec,ip) = .true.
          read(ifi(ip-2),'(a7, 1p25e9.0)', rec = iex)
:          nuclide, (df(ispec,ip, j), j = 1, 25)
        end if
      10 continue
    end if
  20 continue
*
* now do the inhalation and ingestion coefficients
*
if (amad .ne. 1.0) call depfrac (amad, d3, d4, d5)
do 200 ispec = 1, nint
  nuke = nucnam(ispec)
  ipt = ibinry( nuke )
  read(idex,'(a7,a8,a2,a6,3i5)', rec=ipt) nuke, t, ix, mode, inh,
:    ing, iex
c
c inhalation
c
if (ipath(1).and. inh .ne. 0) then
  imax = 0
  dmax = 0.0
  irec = inh - 1
  iflag(ispec, 1) = .true.
  do 50 itry = 1, 4
    irec = irec + 1
    read(inhx,'(a7, 1x, a1, e8.0, 25e9.0)', rec=irec, end=60)
:    nuclide, cx, fhld(itry),
:    (dx(itry, j), j = 1, 25)
*

```

```

* if we have a particulate factor then read the next record
* to get the contribution of the deposition in the NP and P
* region to the organ dose.
*
if (cx .eq. 'D' .or. cx .eq. 'W' .or. cx .eq. 'Y') then
  irec = irec + 1
  read(inhx, '(17x, 25(i5, 14))', rec = irec)
:    (idep(itry, j, 1), idep(itry, j, 2), j = 1, 25)
end if
clshld(itry) = cx
if (len_trim(nuclide) .gt. 0 .and. nuclide .ne. nuke) then
  goto 60
elseif (len_trim(nuclide).eq.0 .or. nuclide.eq.nuke) then
  if (class .eq. clshld(itry) .and.
:    fli .eq. fhld(itry)) then
*
* calculate the factors for this amad if <> 1 µm
*
if (amad.ne.1.0) call newdfs (itry,d3,d4,d5,dx,idep)
*
do 30 j = 1, 25
  df(ispec, 1, j) = dx(itry, j)
30 continue
  flinh(ispec) = fhld(itry)
  classo(ispec) = clshld(itry)
  goto 80
elseif (class .eq. clshld(itry)) then
*
* calculate the factors for this amad if <> 1 µm
*
if (amad.ne.1.0) call newdfs (itry,d3,d4,d5,dx,idep)
*
do 40 j = 1, 25
  df(ispec, 1, j) = dx(itry, j)
40 continue
  flinh(ispec) = fhld(itry)
  classo(ispec) = clshld(itry)
  goto 80
else
  if (dx(itry, 25) .gt. dmax) then
    dmax = dx(itry, 25)
    imax = itry
  end if
end if
else
  goto 60
end if
50 continue
*
* calculate the factors for this amad if <> 1 µm
*
60 if (amad.ne.1.0) call newdfs (imax, d3, d4, d5, dx, idep)
*
do 70 j = 1, 25
  df(ispec, 1, j) = dx(imax, j)
70 continue
  flinh(ispec) = fhld(imax)

```

```

        classo(ispec) = clshld(imax)
    end if
80    continue
c
c    ingestion
c
    if (ipath(2) .and. ing .ne. 0) then
        imax = 0
        dmax = 0.0
        irec = ing - 1
        iflag(ispec, 2) = .true.
        do 100 itry = 1, 4
            irec = irec + 1
            read(ingx, '(a7, e8.0, 25e9.0)', rec = irec, end = 110)
            nuclide, fihld(itry), (dx(itry, j), j = 1, 25)
:            if (len_trim(nuclide) .gt. 0 .and. nuclide .ne. nuke) then
                goto 110
            elseif (len_trim(nuclide).eq.0 .or. nuclide.eq.nuke) then
                if (fio .eq. fihld(itry)) then
                    do 90 j = 1, 25
                        df(ispec, 2, j) = dx(itry, j)
90                    continue
                        florl(ispec) = fio
                        goto 130
                    else
                        if (dx(itry, 25) .ge. dmax) then
                            dmax = dx(itry, 25)
                            imax = itry
                        end if
                    end if
                    else
                        goto 110
                    end if
                continue
100            do 120 j = 1, 25
110                df(ispec, 2, j) = dx(imax, j)
120            continue
                florl(ispec) = fihld(imax)
            end if
130        continue
200    continue
        return
    end
*-----*
*
*    subroutine fileini(fnpath, target, nlen, nulog, nuini, program)
*-----*
*
*    Author: K. F. Eckerman
*    Opens file 'program'.ini and finds the full file name, including path,
*    for the file target and its record length nlen. See the ini file for
*    additional comments.
*    target = file name passed to this subprogram
*    fnstd = standard file name read from file 'program'.INI
*    fnpath = file name including path
*

```

```

character*(*) fnpath, target, program
character*12 fnini, fnstd, lcase
integer nulog
logical test
parameter (maxfil = 40)
fnini = program(1:len_trim(program)) // '.ini'
inquire (file = fnini, exist = test)
if (.not. test) goto 20
open(nuini, file=fnini, status='old')
target = lcase(target)
do 10 i = 1, maxfil
    read(nuini, *, end=15) fnstd, fnpath, nlen
    if (fnstd(:3) .eq. 'EOF') goto 15
    if (lcase(fnstd) .eq. target) goto 20
10 continue

15 write(nulog, 9110) target(:len_trim(target)), fnini(:len_trim(fnini))
write(*, 9110) target(:len_trim(target)), fnini(:len_trim(fnini))
close(nuini)
stop 1
20 close(nuini)
return
9110 format(' **** FATAL ERROR in function FileIni: Unable to find the
:file ', a, ' ;'/6x, 'check ', a, ' for proper assignments ****')
end
*-----*
*
*    subroutine forward
*-----*
*
*    routine: forward
*    author: k. f. eckerman
*    date: 01/14/92
*    purpose: read down a branch of a decay chain.
*
    include 'pakparm.for'
    include 'dcfpak.cmn'
    character*7 named
    real fhold
    integer iptb, iparb, ibrch, ipar, ipt
    logical eob, pob
    common/chaind/named(mspec), fhold(mspec), iptb(mspec),
:    iparb(mspec), ipt, ibrch, ipar, eob, pob
    common/energy/ealpha(mspec), ebeta(mspec), egamma(mspec)
*
*    functions referenced.
*
    integer ibinry
    character*8 t, mode
    character*7 nuke, d1
    character*2 ix
    integer j
    include 'iolist.cmn'
*
*    get parent record.
*

```

```

if (ipar .eq. 1) then
  nuke = nucnam(ipar)
  ipt = ibinry(nuke)
  if (ipt .eq. 0) then
    nspec = 0
    return
  endif
endif
10 if (ipt .lt. 999) then
  read(idex, 'a7,a8,a2,a6,315,3(i4,e11.0),3f7.0,e11.0,ix,a9)',
:   rec=ipt) nuke, t, ix, mode, inh, ing, lex, id1, f1,
:   id2, f2, id3, f3, ea, eb, eg, amu, endsf
else
  id1 = 0
  f1 = 0.0
  id2 = 0
  f2 = 0.0
  id3 = 0
  f3 = 0.0
  nuke = 'sf'
  ea = 0.
  eb = 0.
  eg = 0.
  t = ' '
  ix = ' '
end if
*
* ids = 999 denotes "sf" which is not a daughter product, thus set
* the ids to zero if "sf".
*
if (id1 .eq. 999 .and. id2 .ne. 0) then
  if (id3 .eq. 0) then
    fhld = f1
    ihld = id1
    f1 = f2
    id1 = id2
    f2 = fhld
    id2 = ihld
  else
    fhld = f1
    ihld = id1
    f1 = f2
    id1 = id2
    f2 = f3
    id2 = id3
    f3 = fhld
    id3 = ihld
  end if
end if
if (id2 .eq. 999 .and. id3 .ne. 0) then
  fhld = f2
  id2 = id3
  f2 = f3
  id3 = ihld
  f3 = fhld
end if

```

```

*
* if processing a branch then check to see if d1 has already
* been included in nucnam, if so only fix up branch(ipar,past) and
* terminate chain, i.e., chain has converged.
*
if (pob) then
  if (id1 .gt. 0 .and. id1 .lt. 999) then
    read(idex, 50, rec = id1) d1
  elseif (id1 .eq. 999) then
    d1 = 'sf'
  end if
  do 15 j = 1, nspec - 1
    if (d1 .eq. nucnam(j)) goto 16
15  continue
    goto 17
*
* have already handled this daughter; chain has converged.
* set end of chain and return.
*
16  branch(ipar, j) = f1
    nucnam(ipar) = nuke
    thalf(ipar) = t
    ealpha(ipar) = ea
    ebeta(ipar) = eb
    egamma(ipar) = eg
    iu(ipar) = ix
    nspec = nspec + 1
    return
  end if
*
* need to treat this chain member.
*
17  nucnam(ipar) = nuke
    thalf(ipar) = t
    ealpha(ipar) = ea
    ebeta(ipar) = eb
    egamma(ipar) = eg
    iu(ipar) = ix
    nspec = nspec + 1
    branch(ipar, nspec) = f1
*
* no further daughters in chain - set end of chain
*
if (id1 .ne. 0) then
  further daughters, treat id1 and check for possible branches.
  ipt = id1
*
* if (id2 .ne. 0) then
*
* set end of branch to false, increment branch counter, store
* pointer of parent, and record number of second or third daughter
* while following current chain. routine recver will direct
* recovery of branches.
*
  eob = .false.
  ibrch = ibrch + 1
  iptb(ibrch) = id2

```

```

fhold(ibrch) = f2
iparb(ibrch) = ipar
if (id2 .ne. 999) then
  read(idex, 50, rec = id2) named(ibrch)
else
  named(ibrch) = 'Sf'
end if
endif
* third daughter, branch info held as above.
if (id3 .ne. 0) then
  eob = .false.
  ibrch = ibrch + 1
  iptb(ibrch) = id3
  fhold(ibrch) = f3
  iparb(ibrch) = ipar
  if (id3 .ne. 999) then
    read(idex, 50, rec = id3) named(ibrch)
  else
    named(ibrch) = 'Sf'
  end if
endif
ipar = nspec
if (ipt .ne. 999) goto 10
endif
return
*
50 format (a7,a8,a2,a8,i7,i5,i6,i4,3(i4,e11.0),f7.0,2f8.0,a10)
end
-----
*
subroutine newdfs (i, d3, d4, d5, dx, idep)
*
-----
*
routine: newdfs
*
author: k.f. eckerman
*
date: 10/23/93
*
purpose: compute h_e and e for d3, d4, d5 depositions
*
dimension dx(4, 25), idep(4, 25, 2), dsort(12), isort(12)
data isort / 1, 4, 7, 8, 9, 10, 11, 12, 16, 19, 21, 23/
*
calculate the inhalation coefficient for this new depositions
*
do 10 j = 1, 23
  f = d3 * float(idep(i, j, 1)) / 0.30 +
:   d5 * float(idep(i, j, 2)) / 0.25 +
:   d4 * (float(100 - idep(i,j,1) - idep(i,j,2))) / 0.08
  dx(i, j) = 0.01 * f * dx(i, j)
10 continue
*
compute the effective dose equivalent (weighting factors of icrp-26)
*
and the effective dose (weighting factors of icrp-60) for the new
*
depositions.
*
he = 0.25 * max(dx(i, 15), dx(i, 20)) + 0.15 * dx(i, 5) +
:   0.12 * dx(i, 13) + 0.12 * dx(i, 17) + 0.03 * dx(i, 22) +
:   0.03 * dx(i, 3)

```

```

do 20 j = 1, 12
  dsort(j) = dx(i, isort(j))
20 continue
call sortem (dsort, 12)
he = he + 0.06 * (dsort(12) + dsort(11) + dsort(10) + dsort(9) +
:   dsort(8))
e = 0.20 * max(dx(i,15), dx(i,20)) + 0.05 * dx(i,5) +
:   0.12 * dx(i,10) + 0.12 * dx(i,17) + 0.12 * dx(i, 13) +
:   0.12 * dx(i,7) + 0.05 * dx(i,2) + 0.05 * dx(i, 12) +
:   0.05 * dx(i,6) + 0.05 * dx(i,22) + 0.01 * dx(i, 3) +
:   0.01 * dx(i,18)
hr = (14. * dx(i,1) + 1400. * dx(i, 4) + 640. * dx(i, 8) +
:   310. * dx(i,11) + 28000. * dx(i, 14) + 100. * dx(i,16) +
:   180. * dx(i,19) + 20. * dx(i, 21) + 80. * dx(i,23)) /
:   30744.
e = e + 0.05 * hr
dx(i, 24) = he
dx(i, 25) = e
return
end

```

```

-----
*
subroutine openem
*

```

```

-----
*
routine: openem
*
author: k.f. eckerman
*
date: 10/23/93
*
purpose: open index and dose coefficient files.
*

```

```

character*64 fpath
character*12 target
character*8 prog
include 'iolist.cmn'
open(olog, file = 'df_read.log')
prog = 'dcfpak'
target = 'snlindex.ndx'
call fileini(fpath, target, nlen, olog, 41, prog)
open(idex, file=fpath, access='direct', recl=nlen, form=
:   'formatted', status='old')
target = 'ingestsf.dfs'
call fileini(fpath, target, nlen, olog, 41, prog)
open(ingx, file=fpath, access='direct', recl=nlen, form=
:   'formatted', status='old')
target = 'inhalesf.dfs'
call fileini(fpath, target, nlen, olog, 41, prog)
open(inhx, file=fpath, access='direct', recl=nlen, form=
:   'formatted', status='old')
target = 'submrsin.dfs'
call fileini(fpath, target, nlen, olog, 41, prog)
open(i31, file=fpath, access='direct', recl=nlen, form=
:   'formatted', status='old')
target = 'imersion.dfs'
call fileini(fpath, target, nlen, olog, 41, prog)
open(i32, file=fpath, access='direct', recl=nlen, form=
:   'formatted', status='old')

```

```

target='grsurf00.dfs'
call fileini(fpath, target, nlen, olog, 41, prog)
open(i33, file=fpath, access='direct', recl=nlen, form=
: 'formatted', status='old')
target = 'grvol_01.dfs'
call fileini(fpath, target, nlen, olog, 41, prog)
open(i34, file=fpath, access='direct', recl=nlen, form=
: 'formatted', status='old')
target = 'grvol_05.dfs'
call fileini(fpath, target, nlen, olog, 41, prog)
open(i35, file=fpath, access='direct', recl=nlen, form=
: 'formatted', status='old')
target = 'grvol_15.dfs'
call fileini(fpath, target, nlen, olog, 41, prog)
open(i36, file=fpath, access='direct', recl=nlen, form=
: 'formatted', status='old')
target = 'grvolinf.dfs'
call fileini(fpath, target, nlen, olog, 41, prog)
open(i37, file=fpath, access='direct', recl=nlen, form=
: 'formatted', status='old')
return
end
-----
*
*      subroutine order
*
*-----
*
* routine:  order
* author:   k. f. eckerman
* date:    04/06/89
* purpose:  order the chain so daughter index > parents.
*
include 'pakparm.for'
include 'dcfpak.cmn'
common/energy/ealpha(mspec), ebeta(mspec), egamma(mspec)
character*8 thold
character*7 nuke
character*2 ix
real rsave, csave
integer i, j, ip, jp, ipass, move
dimension rsave(mspec), csave(mspec)
include 'iolist.cmn'
*
* move # of elements to move
*
ipass = 0
100 move = 0
ipass = ipass + 1
if (ipass .gt. 4*nspec) then
write(olog,('' Failure in routine order: greater than'',i3,
: '' passes for '', a7, ''.'')) ipass, nucnam(1)
write(*,('' Failure in routine order: greater than'',i3,
: '' passes for '', a7, ''.'')) ipass, nucnam(1)
stop 1
endif
*

```

```

do 10 i = 1, nspec
do 10 j = 1, i-1
if (branch(i, j) .ne. 0.) then
ip = i
jp = j
move = 1
go to 15
endif
10 continue
*
* if no elements to move then return
*
15 if (move .eq. 0) return
nuke = nucnam(ip)
thold = thalf(ip)
ea = ealpha(ip)
eb = ebeta(ip)
eg = egamma(ip)
ix = iu(ip)
do 20 j = 1, nspec
rsave(j) = branch(ip, j)
20 continue
do 30 i = ip - 1, jp, -1
nucnam(i + 1) = nucnam(i)
thalf(i + 1) = thalf(i)
ealpha(i + 1) = ealpha(i)
ebeta(i + 1) = ebeta(i)
egamma(i + 1) = egamma(i)
iu(i + 1) = iu(i)
do 30 j = 1, nspec
branch(i + 1, j) = branch(i, j)
30 continue
nucnam(jp) = nuke
thalf(jp) = thold
iu(jp) = ix
ealpha(jp) = ea
ebeta(jp) = eb
egamma(jp) = eg
do 40 j = 1, nspec
branch(jp, j) = rsave(j)
40 continue
do 50 i = 1, nspec
csave(i) = branch(i, ip)
50 continue
do 60 j = ip - 1, jp, -1
do 60 i = 1, nspec
branch(i, j + 1) = branch(i, j)
60 continue
do 70 i = 1, nspec
branch(i, jp) = csave(i)
70 continue
*
* Yes we do have backward point gotos in FORTRAN, sorry!
*
goto 100
*
end

```

```

*-----*
*
*      subroutine path
*-----*
*
*      author:  K.F. Eckerman
*      date:    04/06/89
*      purpose: initialize mpath and max matrices
*              Adopted from A. Birchall, Health Phys. 50, 3, 389-397, 1986.
*
*      include 'pakparm.for'
*      include 'dcfpak.cmn'
*      integer max, mpath
*      common/calcul/ max(mspec), mpath(mspec, mspec)
*      initializes mpath and max matrices.
*      do 10 i = 1, nspec
*          max(i) = 0
*          do 10 j = 1, nspec
*              mpath(i,j) = 0
10 continue
*      do 20 j = 2, nspec
*          do 20 i = 1, j - 1
*              if (branch(i, j) .ne. 0.) then
*                  max(j) = max(j) + 1
*                  mpath(max(j), j) = i
*              end if
20 continue
*      return
*      end
*-----*
*
*      subroutine pauseit
*-----*
*
*      routine: pause
*      author:  K.F. Eckerman
*      date:    10/23/93
*      purpose: pause w/o line feed
*
*      character*1 dummy
*      write(*, '(a\)' ) ' Hit <Enter> to continue.'
*      read(*, '(bn, a1)' ) dummy
*      return
*      end

```

```

*-----*
*
*      subroutine printm
*-----*
*
*      routine: printm
*      author:  k. f. eckerman with modifications by j. c. ryman
*      date:    01/15/92
*      purpose: print the decay chain
*
*      include 'pakparm.for'
*      include 'dcfpak.cmn'
*
*      local variables.
*      character*7 nuke, rlist
*      integer i, j, k, nlist, jlist
*      dimension jlist(mspec), nuke(mspec), rlist(mspec)
*      include 'iolist.cmn'
*      write(*, 8001)
*      write(olog, 8001)
*      if (nspec .eq. 1) then
*          write(*, 8002) nspec, nucnam(1), thalf(1), iu(1)
*          write(olog, 8002) nspec, nucnam(1), thalf(1), iu(1)
*      else
*          do 20 i = 1, nspec
*              if(nucnam(i)(:2) .eq. 'SF') goto 20
*              nlist = 0
*              do 10 j = 1, nspec
*                  if (i .ne. j .and. branch(i,j) .ne. 0.0) then
*                      nlist = nlist + 1
*                      jlist(nlist) = j
*                      nuke(nlist) = nucnam(j)
*                      write (rlist(nlist), '(1pe7.1)' ) branch(i,j)
*                      do 5 k = 4, 6
*                          rlist(nlist)(k:k) = rlist(nlist)(k+1:k+1)
5                          continue
*                      rlist(nlist)(7:7) = ' '
*                      endif
10                     continue
*                   write(*, 8002) i, nucnam(i), thalf(i), iu(i),
*                      (rlist(j), jlist(j), nuke(j), j = 1, nlist)
*                   write(olog, 8002) i, nucnam(i), thalf(i), iu(i),
*                      (rlist(j), jlist(j), nuke(j), j = 1, nlist)
20                     continue
*                   if (nspec .gt. 5) pause
*                   endif
*
*                  clear screen and return
*
*                  if (nspec .gt. 5) call cls
*                  return
*
*                  formats
*
*                  8001 format(' ',3x,'Nuclide Halflife   f1',7x,'Nuclide   f2',7x,
*                      : 'Nuclide   f3',7x,'Nuclide')

```

```
8002 format(' ',i2,1x,a7,1x,a8,a2,:,3(1x,a6,'->',i2,1x,a7))
end
```

```
-----
*
*   subroutine recver
*-----
* routine: recver
* author: k. f. eckerman
* date: 04/06/89
* purpose: recover info on branches in the chain that were detected
* by frward and direct the reading of the new branch.
*
* include 'pakparm.for'
* include 'dcfpak.cmn'
* character*7 named
* real fhold
* integer iptb, iparb, ibrch, ipar, ipt
* logical eob, pob
* common/chaind/named(mspec), fhold(mspec), iptb(mspec),
* : iparb(mspec), ipt, ibrch, ipar, eob, pob
* local variables.
* character*7 nuke
* integer i
* include 'iolist.cmn'
*
* no branches to treat, set end of branch to true and return.
*
* 1 if (ibrch .eq. 0) then
*   eob = .true.
*   elseif (iptb(ibrch) .eq. 999) then
*   eob = .true.
* else
*
*   consider remaining branches. recover parent's
*   index at branch (ipar) and daughter's record number (ipt).
*   decrement branch counter and return.
*
*   pob = .true.
*   ipar = iparb(ibrch)
*   ipt = iptb(ibrch)
*   nuke = named(ibrch)
*
*   need to check to see of the daughter of the branch has already
*   a member of the chain.
*
*   do 10 i = 1, nspec - 1
*     if (nuke .eq. nucnam(i)) goto 15
* 10 continue
*   nucnam(nspec) = nuke
*   branch(ipar, nspec) = fhold(ibrch)
*   ibrch = ibrch - 1
*   ipar = nspec
*   return
*
*   if already a chain member set r, decrement the branch counter
*   and look for another branch to process.
```

```
*
* 15 branch(ipar,i) = fhold(ibrch)
*
*   ibrch = ibrch - 1
*   go to 1
*
* endif
*
* return
* end
*-----
*
* subroutine sortem (ar, n)
*-----
* routine: sortem
* author: k.f. eckerman
* date: 10/23/93
* purpose: sort array a into descending numerical order
*
* dimension ar(*)
* do 20 j = 2, n
*   a = ar(j)
*   do 11 i = j-1, 1, -1
*     if(ar(i) .le. a) goto 12
*     ar(i+1) = ar(i)
* 11 continue
*   i = 0
* 12 ar(i+1) = a
* 20 continue
* return
* end
*-----
*
* subroutine nukeok (nuke, ok)
*-----
* character*7 nuke, check
* logical ok
*
* function check ensure proper format of user input
*
* nuke = check( nuke )
* call chekmn( nuke )
*
* find the nuclide in the index file
*
* ipt = ibinry( nuke )
* if (ipt .eq. 0) then
*   call chekab( nuke )
*   ipt = ibinry( nuke )
* end if
*
* if pointer ipt is zero, the nuclide is not in the index file
* else we have a valid nuclide to process
*
* if (ipt .eq. 0) then
```

```

    ok = .false.
else
    ok = .true.
end if
return
end

-----
*
*
*   subroutine zerom
*
-----
*   routine: zerom
*   author: k.f. eckerman
*   date: 10/23/93
*   purpose: set the dose coefficient arrays to zero
*
include 'pakparm.for'
include 'dcfpak.cmn'
logical ifalse
dimension dzero(morg*mspec*mfact), ifalse(mspec*mfact)
equivalence (df(1,1,1), dzero(1)), (iflag(1,1), ifalse(1))
parameter(zero = 0.0)
do 10 i= 1, morg * mspec * mfact
    dzero(i) = zero
10 continue
do 20 i = 1, mspec * mfact
    ifalse(i) = .false.
20 continue
return
end

-----
*
*
*   2. Screen Routines
*
-----
*
*   subroutine cls
*
-----
*
*   author: k. f. eckerman
*   date: 12/08/93
*   routine to clear screen
*   write(*,*) char(27),'[2J'
*   return
*   end
*
-----
*
*   subroutine curright(icol)
*
-----
*
*   author: k. f. eckerman
*   date: 12/08/93
*   move the cursor icol columns right on the display.
*

```

```

character*2 col
write(col, '(i2.2)') icol
write(*, '(a\)' ) ' ' // char(27) // '[' // col // 'C'
return
end

-----
*
*   subroutine curpos(irow, icol)
*
-----
*
*   author: k. f. eckerman
*   date: 12/08/93
*   move cursor to the indicated row and column.
*
character*2 row, col
write(row, '(i2.2)') irow
if (icol .ne. 0) then
    write(col, '(i2.2)') icol
else
    col = '01'
end if
write(*, '(a\)' ) ' ' // char(27) // '[' // row // ';' // col // 'H'
return
end

-----
*
*   3. Function Routines
*
-----
*
*   character*(*) function check(nuke)
*
-----
*
*   function: check
*   author: r.j. westfall
*   date: 07/20/89
*   purpose: convert chemical symbol in nuclide name to proper
*            notation, e.g.; Kr-85m, etc.
*
character*(*) nuke
character*7 ltrim

remove any leading blanks from nuke

nuke = ltrim( nuke )

ensure first character is upper case.

if (nuke(:1) .ge. 'a' .and. nuke(:1) .le. 'z')
:   nuke = char(ichar(nuke(:1)) - 32) // nuke(2:7)

ensure second character, if present, is lower case.

if (nuke(2:2) .ge. 'A' .and. nuke(2:2) .le. 'Z')
:   nuke = nuke(:1) // char(ichar(nuke(2:2)) + 32) // nuke(3:7)

```

```

* ensure metastable notation, if present, is lower case.
*
do 30 j = 4, 7
  if (nuke(j:j) .ge. 'A' .and. nuke(j:j) .le. 'Z')
:   nuke = nuke(:j-1) // char(ichar(nuke(j:j)) + 32) // nuke(j+1:)
30 continue
  check = nuke
end

```

```

-----
* double precision function expfl (lm, t)
*

```

```

* author: k. f. eckerman
* date: 10/04/94
* purpose: routine to compute  $[1.0 - \exp(-lm * t)] / lm$ .
*
double precision lm, t, lmt, one, two, expfun, eps
logical first
parameter (one = 1.0d0, two = 2.0d0)
data first/.true./
if (first) then
  eps = one
10  eps = eps / two
  if (eps + one .gt. one) goto 10
  eps = dsqrt(eps)
  first = .false.
end if
lmt = lm * t
if (lmt .lt. eps) then
  expfl = t * (one - lmt / two)
else
  expfl = (one - expfun(-lmt)) / lm
end if
return
end

```

```

-----
* double precision function expfun (t)
*

```

```

* author: k. f. eckerman
* date: 10/04/94
* purpose: routine to compute  $\exp(t)$ .
*
double precision t, zero, upval
parameter(zero = 0.0d0, upval = 180.d0)
if (t .lt. -upval) then
  expfun = zero
else
  expfun = dexp(t)
end if
return
end

```

```

-----
* integer function ibinry ( target )
*

```

```

* function: ibinry
* author: k.f. eckerman
* date: 06/20/88
* purpose: locate record sort by target key
*
integer nstart, nlast, left, right, try
character*7 target, a1
logical first
save first, nstart, nlast
include 'iolist.cmn'
*
* initialization.
*
data first /.true./
if (first) then
  read (idex, '(214)', rec = 1) nstart, nlast
  first = .false.
end if
left = nstart
right = nlast
*
* begin attempts to find target.
*
10 try = int((left + right) / 2)
  read (idex, '(a7)', rec = try) a1
  if (a1 .lt. target) then
    left = try + 1
  elseif (a1 .gt. target) then
    right = try - 1
  else
    ibinry = try
    return
  end if
*
* continue search unless left > right then set ibinry to zero and
* let calling deal with the unidentified target.
*
if (left .lt. right + 1) then
  goto 10
else
  ibinry = 0
  return
end if
end
*
-----
* integer function icutoff(eat, ebt, egt, igamma, nspec)
*
dimension eat(*), ebt(*), egt(*)
ea = eat(nspec)

```

```

eb = ebt(nspec)
eg = egt(nspec)
if (ea .gt. 0. .and. igamma .eq. 0) then
  do 10 i = nspec-1, 1, -1
    if (eat(i) .lt. 0.99 * ea) then
      ia = i + 1
      goto 15
    end if
  10 continue
  ia = 1
else
  ia = 0
end if
15 if (eb .gt. 0.) then
  do 20 i = nspec-1, 1, -1
    if (ebt(i) .lt. 0.99 * eb) then
      ib = i + 1
      goto 25
    end if
  20 continue
  ib = 1
else
  ib = 0
end if
25 if (eg .gt. 0.) then
  do 30 i = nspec-1, 1, -1
    if (egt(i) .lt. 0.99 * eg) then
      ig = i + 1
      goto 35
    end if
  30 continue
  ig = 1
else
  ig = 0
end if
35 icutoff = max0(ig, max0(ia, ib))
return
end

```

```

-----
*
* character*(*) function lcase (a)
*
-----

```

```

*
* author: k. f. eckerman
* date: 10/04/94
* purpose: convert character variable a to lower case.
*
character*(*) a
lcase = a
do 10 i = 1, len_trim(lcase)
  ix = ichar(lcase(i:i))
  if (ix .gt. 64 .and. ix .lt. 91) then
    lcase(i:i) = char(ix + 32)
  end if
10 continue
return

```

```

end
-----
*
* character*(*) function ltrim(a)
*
-----
*
* function: ltrim
* author: K.F. Eckerman
* date: 10/23/93
* purpose: trim leading blanks from string a
*
character*(*) a
logical ok
ok = .false.
10 if (a(1:1) .ne. ' ') ok = .true.
if (.not. ok) then
  n = len_trim(a) - 1
  do 20 i = 1, n
    a(i:i) = a(i+1:i+1)
  20 continue
  a(n+1:n+1) = ' '
  goto 10
end if
ltrim = a
return
end

```

```

-----
*
* double precision function timest (t, ix)
*
-----

```

```

*
* author: k. f. eckerman
* date: 10/04/94
* purpose: function returns time in days given time string t and its
* units ix.
* function arguments.
* character*2 ix
* character*8 t
* double precision tp
*
read(t, '(E8.0)') tp
if (ix .eq. 'us') then
  tp = tp / 8.64d+10
elseif (ix .eq. 'ms') then
  tp = tp / 8.64d+07
elseif (ix .eq. 's ') then
  tp = tp / 8.64d+04
elseif (ix .eq. 'm ') then
  tp = tp / 1.44d+03
elseif (ix .eq. 'h ') then
  tp = tp / 24.d0
elseif (ix .eq. 'y ') then
  tp = tp * 365.25d0
endif

```

```
timest = tp
return
end
```

```
-----
* character*(*) function ucase (a)
*
*-----
*
* author: k. f. eckerman
* date: 10/04/94
* purpose: convert character variable a to upper case.
*
* character*(*) a
* ucase = a
* do 10 i = 1, len_trim(ucase)
*   ix = ichar(ucase(i:i))
*   if (ix .gt. 96 .and. ix .lt. 123) then
*     ucase(i:i) = char(ix - 32)
*   end if
* 10 continue
* return
* end
```

```
-----
c integer function len_trim(a)
c
c-----
c
c author: k.f. eckerman
c date: 06/25/96
c purpose: determine the trim length of a character variable a
c           in the manner of Microsoft len_trim function. if the
c           len_trim function is not supported by the FORTRAN
c           compiler then active this routine by removal of the
c           'c's on the statements below and in the above name.
c
c character*(*) a
c n = len(a)
c do 10 i = n, 1, -1
c   if (a(i:i) .ne. ' ' .and. ichar(a(i:i)) .ne. 0) then
c     len_trim = i
c     return
c   end if
c 10 continue
c len_trim = 0
c end
```

A3. ILLUSTRATIVE PROGRAM READEM.FOR

program readem

```
*
* READEM illustrates the manner the electronic files of dose coefficients
* for Sandia National Laboratory can be accessed in FORTRAN. The procedure
* uses the index file DFEXTINT.NDX to coordinate the reading of the
* coefficients from their respective files.
* The coefficient files are:
* ICRPINGS.DAT - FGR 11/ICRP-30 ingestion intakes.
* ICRPINHS.DAT - FGR 11/ICRP-30 inhalation intakes.
* FGR12F31.DAT - FGR 12 Table III.1 for air submersion.
* FGR12F32.DAT - FGR 12 Table III.2 for water immersion.
* FGR12F33.DAT - FGR 12 Table III.3 for ground surface contamination.
* FGR12F34.DAT - FGR 12 Table III.4 contaminated soil slab 1 cm thick.
* FGR12F35.DAT - FGR 12 Table III.5 contaminated soil slab 5 cm thick.
* FGR12F36.DAT - FGR 12 Table III.6 contaminated soil slab 15 cm thick.
* FGR12F37.DAT - FGR 12 Table III.7 contaminated soil infinite thickness.
```

```
*
* All files are formatted direct access files. The RECL specification in
* the FORTRAN open statement is read from the file DCFPAK.INI. See that file
* for further discussion regarding specifications for different compilers.
*
```

```
* The file FGR1112.IDX contains the following information:
* The first record gives the record numbers of the first and last data
* record, format (214) which are 2 and 839. The format of records 2 through
* 839 is (a7,a8,a2,a6,3i5,3(i4,e11.0),3f7.0,e11.0,ix,a9)
```

| Variable | Description | Format |
|-------------|-------------------------|--------|
| * nuke | Name of nuclide | a7 |
| * t12 | Halflife | a8 |
| * ix | Halflife units | a2 |
| * mode | Decay Modes | a6 |
| * inh | Record # for inhalation | 15 |
| * ing | Record # for ingestion | 15 |
| * iex | Record # for external | 15 |
| * id(1) | Record # of daughter | 14 |
| * f(1) | Branching fraction | e11 |
| * id(2) | Record # of daughter | 14 |
| * f(2) | Branching fraction | e11 |
| * id(3) | Record # of daughter | 14 |
| * f(3) | Branching fraction | e11 |
| * Ealpha | Emitted alpha energy | f7.0 |
| * Eelectron | Emitted electron energy | f7.0 |
| * Ephoton | Emitted photon energy | f7.0 |
| * AMU | Atomic mass | e11 |
| * ENDSF | Date of ENDSF | a9 |

```
*
* author: k.f. eckerman
* date: 06/04/96 : 06/27/96
*
```

```
include 'pakparm.for'
include 'dcfpak.cmn'
include 'batch.cmn'
character*7 nuke
character*5 amadx
```

```

character*1 class, ucase
logical ipath(9), ok
include 'iolist.cmn'
dbatch = .false.
numarg = nargs()
if (numarg .gt. 1) dbatch = .true.
*
* this loop sets all pathway flags to true; i.e., we want dose
* coefficients for all pathways.
*
do 1 i = 1, 9
1 ipath(i) = .true.
*
call cls
write(*, '(1x, ' View dose coefficients')')
write(*, '(3x, ' K.F. Eckerman and R.W. Leggett')')
write(*, '(3x, ' Oak Ridge National Laboratory')')
write(*, '(3x, ' Oak Ridge, TN 37831-6383', '/')')
*
open direct access files and write text to screen
call openem
*
label 10 is the subject of a backward pointing goto
10 write(*, '(a\)' )' Input nuclide (e.g.; Ba-137m or <Enter> to quit)-
.> '
read(*, '(bn, a7)' ) nuke
if (len_trim(nuke) .ne. 0) then
*
call nukeok to determine if nuke in data bases
call nukeok (nuke, ok)
*
if (.not. ok) then
write(*, '(1x, (a), ' is not in index file!')')
: nuke(:len_trim(nuke))
write(*, *)
write(*, *)
call pauseit
else
*
if no inhalation class is indicated then the class with the
highest effective dose will be assumed.
*
class = ' '
write(*, '(a\)' )' Clearance class (D, W, Y, V or " ")-> '
read(*, '(bn, a1)' ) class
class = ucase (class)
*
read in amad as a character and then do a internal read
*
write(*, '(a\)' )' Input AMAD (default 1 µm) -> '
read(*, '(bn, a5)' ) amadx
if (len_trim(amadx) .eq. 0) then
amad = 1.0
else

```

```

read(amadx, '(f5.0)' ) amad
end if
*
lets get some factors
*
floral = 0.0
flinhi = 0.0
call dosecof(nuke, floral, class, flinhi, amad, ipath)
*
call tablem to print factors to screen
*
call tablem (amad)
*
endif
*
compute activity of chain members as at user specified times
*
call cls
write(*, *) ' Activity and Integrated Activity of Chain Members'
20 write(*, '(a\)' )
: ' Input time of interest (d); zero to quit --> '
read(*, '(bn, e10.0)' ) t
if (t .eq. 0.) goto 40
write(*, '(5x, 'Nuclide T1/2 A(t)/Ao intA/Ao(d)')')
*
do over the maximum length of the retained chain members
*
do 30 ispec = 1, max(nint, next)
call birch(ispec, t, a, aint)
write(*, '(5x, a7, 1x, a8, a2, 1p2e12.5)' ) nucnam(ispec),
: thalf(ispec), iu(ispec), a, aint
30 continue
goto 20
*
clear screen and goto 10 to get another nuclide.
*
40 call cls
go to 10
endif
*
close all files
*
call closem
end
*
-----
*
subroutine tablem (amad)
*
-----
*
routine: tablem
author: k.f. eckerman
data: 05/20/96
purpose: write dose coefficients to screen.
*
include 'pakparm.for'
include 'dcfpak.cmn'
character*60 head

```

```

character*20 titles(mfact)
character*18 units(mfact)
character*8 t, ltrim, buffer
character*5 buff5
data titles / 'Inhalation      ', 'Ingestion      ',
:             'Submersion      ', 'Immersion      ',
:             'Ground Surface   ', '1 cm Soil Slab ',
:             '5 cm Soil Slab   ', '15 cm Soil Slab',
:             'Infinite Thick Soil' /
data units / '(Sv/Bq)          ', '(Sv/Bq)          ',
:            '(Sv per Bq s m^-3)', '(Sv per Bq s m^-3)',
:            '(Sv per Bq s m^-2)', '(Sv per Bq s m^-3)',
:            '(Sv per Bq s m^-3)', '(Sv per Bq s m^-3)',
:            '(Sv per Bq s m^-3)' /
do 100 ifact = 1, mfact
  if (ifact .le. 2) then
    nupper = nint
  else
    nupper = next
  end if
  do 50 ispec = 1, nupper
    if (iflag(ispec, ifact)) then
      call cls
      head = ' Dose Coefficients ' // titles(ifact) (:len_trim(
:         titles(ifact))) // ' ' // units(ifact)
      ip = (80-len_trim(head))/2
      call curpos(2, ip)
      write(*,*) head(:len_trim(head))
      write(*,*)
      t = ltrim(Thalf(ispec))
      call currigh(6)
      if (ifact .eq. 1) then
        write(buffer, '(1pe8.1)') f1inh(ispec)
        write(buff5, '(f5.2)') amad
        write(*,*) nucnam(ispec) //
:         ' T1/2 = ' // t(:len_trim(t)) // ' ' //
:         iu(ispec) // ' Class: ' // classo(ispec)
:         // ' f_1 = ' // buffer // ' AMAD (um) = '
:         // buff5
      elseif (ifact .eq. 2) then
        write(buffer, '(1pe8.1)') f1orl(ispec)
        write(*,*) nucnam(ispec) //
:         ' T1/2 = ' // t(:len_trim(t)) // ' ' //
:         iu(ispec) // ' f_1 = ' // buffer
      else
        write(*,*) nucnam(ispec) //
:         ' T1/2 = ' // t(:len_trim(t)) // ' ' //
:         iu(ispec)
      end if

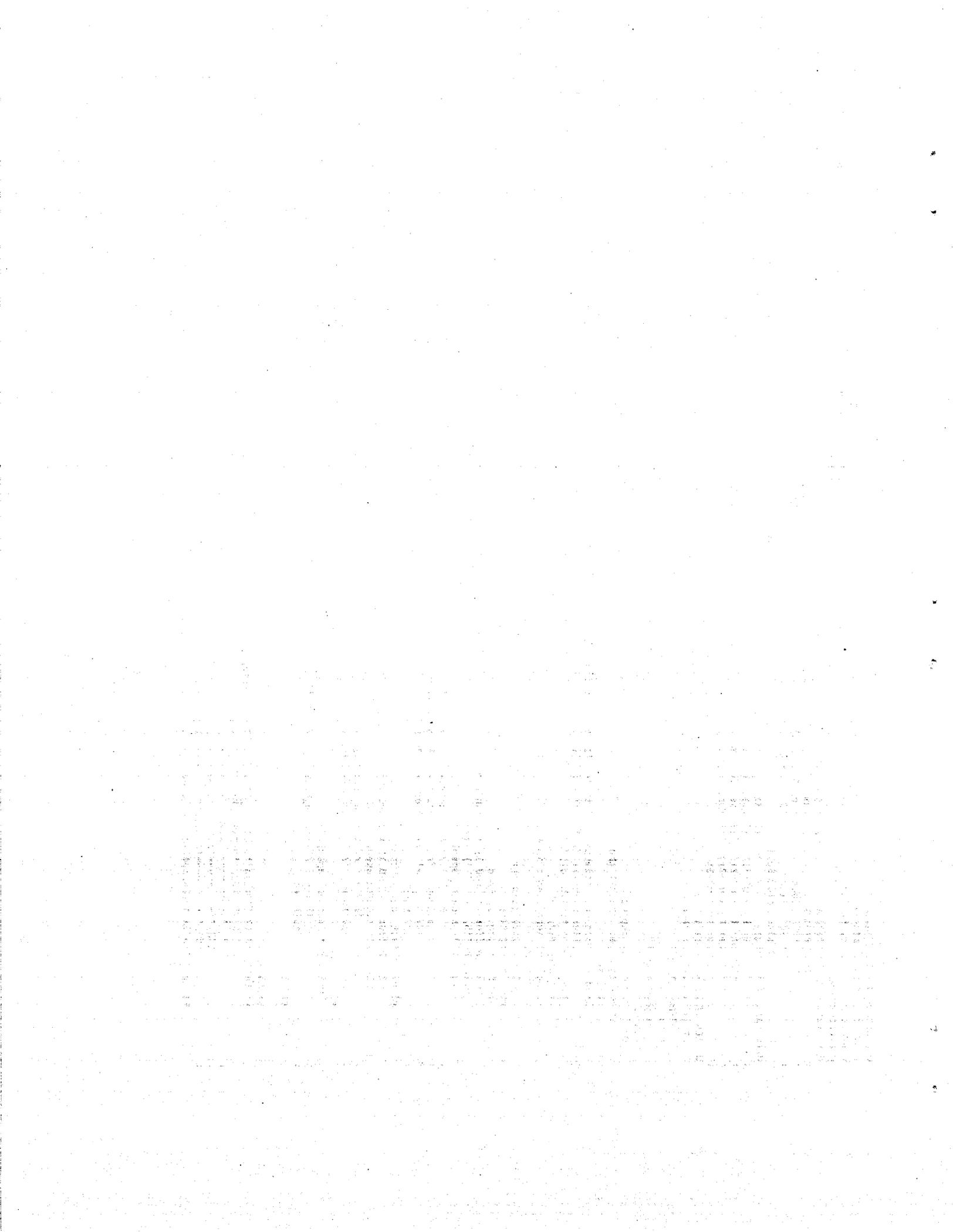
      write(*,*)
      write(*,*) (/,t7,'Organ',t20,'h T',t32,'Organ',t45,
:             'h T',t57,'Organ',t70,'h T',/,
:             t7,'-----',t10,'-----',
:             t32,'-----',t43,'-----',
:             t57,'-----',t68,'-----')
      write(*, '(3(6x,a9,2x,1pe8.2)') (organ(j),

```

```

:         df(ispec, ifact, j), j = 1, 25)
      call curpos(22, 60)
      write(*, ('Member: ',i2,' of ',i2)) ispec, nupper
      call pauseit
    end if
  50 continue
  100 continue
  return
end

```



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