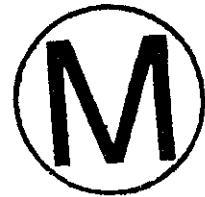
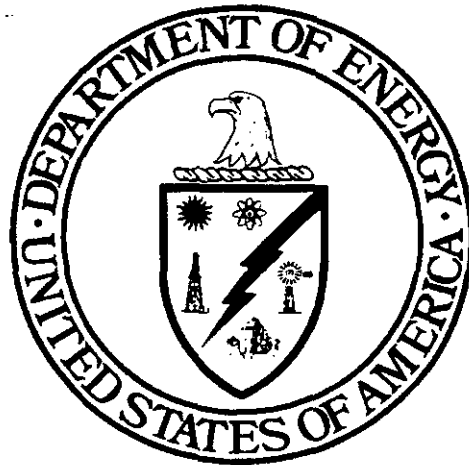

**Title 40 CFR Part 191
Compliance Certification
Application
for the
Waste Isolation Pilot Plant**

Appendix GENII



**United States Department of Energy
Waste Isolation Pilot Plant**

**Carlsbad Area Office
Carlsbad, New Mexico**

**WIPP PA User's Manual PREGENII,
WIPP User's Manual GENII**



WIPP PA
User's Manual
for
PREGENII, Version 6.21



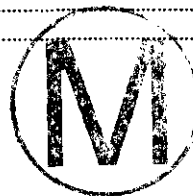
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1.0 INTRODUCTION

PREGENII creates input for the GENII-A code by translating data from CAMDAT and a user-supplied PREGENII text input file. PREGENII accesses a radionuclide database that provides information for converting solute concentrations to activity.

This document serves as a User's Manual for PREGENII, as used in the 1996 WIPP PA calculation. As such, it describes the code's purpose and function, the user's interaction with the code, and the models and methods employed by the code. Examples of user-accessible input and output files are included for the user's convenience.

1.1 Software Identifier

Code Name: PREGENII, A pre-processor for input to GENII-A

WIPP Prefix: G11

Version Number: 6.21, 4-22-96

Platforms: FORTRAN 77 for OpenVMS AXP, version 6.1, on DEC Alpha

1.2 Points of Contact

1.2.1 Code Sponsor

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2.0 FUNCTIONAL REQUIREMENTS

- R.1 PREGENII accurately transforms radionuclide inventories from input CDB files to desired GENII-A inventory.
- R.2 PREGENII produces an ASCII input file for the GENII-A computer code.

3.0 REQUIRED USER TRAINING AND/OR BACKGROUND

In order to run the PREGENII code successfully, the user will need a basic knowledge of

- undergraduate-level engineering, mathematics, and physics
- open VMS
- Digital Command Language
- Sandia's CAMDAT database.



To understand how PREGENII is used to configure and run GENII-A, the user should be familiar with the GENII-A code System (Radiation Shielding Information Center, 1995; Napier et al., 1988; WPO # 27751 [the GENII-A User's Manual produced for the WIPP PA QA project]) and the principal potential WIPP exposure routes to humans (which are explained below in Section 4.0).

4.0 DESCRIPTION OF THE MODELS AND METHODS

GENII-A is an implementation of the GENII 1.485 Environmental Radiation Dosimetry Software System (Radiation Shielding Information Center, 1995). PREGENII provides the necessary input to GENII-A so that GENII-A can compute resulting radiological effects on humans from a nuclear waste repository through the following six principal exposure routes or pathways through the biosphere:

1. **Contaminated stockpond, water-stock cattle, man (rancher).** Contaminated brine from an exploratory drillhole leaks into an aquifer and its groundwater is pumped into a stockpond. Livestock drink exclusively from this pond and ranchers consume the livestock.
2. **Contaminated cuttings, man (driller).** Individuals operating the exploratory drill that penetrates the WIPP repository are, because of their proximity to drilling operations, exposed externally to (1) contaminated soil from the drilling mud pit and (2) drilling samples that they examine.
3. **Contaminated stockpond, dust-air transport, man (farm family).** Contaminants from a dried stockpond (contaminated with radionuclides migrating through the groundwater, as explained in pathway 1) are suspended in an air plume that deposits the contamination onto a nearby farm. The contaminated crops and livestock from this farm are consumed by humans.
4. **Contaminated drilling-mud pit, dust-air transport, man (farm family).** Contaminants from a dried drilling-mud pit are suspended in an air plume that deposits the contamination onto a nearby farm. The contaminated crops and livestock from this farm are consumed by humans.

5. **Contaminated lake (drinking water, aquatic activities, fishing, irrigation).** Contaminated water from an exploratory drillhole leaks into an aquifer and its groundwater reaches a lake. Humans are contaminated by drinking water from the lake, fishing from the lake, aquatic activities in the lake, and by consuming crops irrigated by contaminated lake water.
6. **Contaminated well water (drinking water, irrigation).** Contaminated water from an exploratory drillhole leaks into an aquifer and its groundwater reaches a well. Humans are contaminated by drinking desalinated water from the well and consuming crops irrigated by contaminated well water.

While GENII-A models the above physical processes, PREGENII is predominantly a data formatting program. PREGENII is primarily a keyword-driven preprocessing program that creates an ASCII input control file that the GENII-A program can use to perform WIPP PA simulations of radionuclide exposure pathways to humans. Additionally, PREGENII reformulates concentrations from transport or cuttings calculations to make them compatible with GENII-A expectations; see the PREGENII RD/VVP documentation for details.

PREGENII also incorporates a suspension model that calculates how contaminated dust from either a dried stockpond or a dried drilling-mud pit is suspended in the air. The results of PREGENII's suspension calculation are treated as a source term by GENII, which calculates the transport of the suspended, contaminated dust from the source. PREGENII's suspension model is based on the following expression from US DOE (1980):

$$\hat{Q} = K_r \rho_s A_s \Delta x_s U \quad (1)$$

where

- \hat{Q} = the flux rate (kg/s)
- K_r = resuspension constant (s^2/m^3)
- ρ_s = density of surface soil available for resuspension (kg/m^3)
- A_s = surface area of soil available for resuspension (m^2)
- Δx_s = depth of soil available for resuspension (m)
- U = mean wind speed (m/s)



The resuspension factor K_r is taken to be 1.0×10^{-13} , which is applicable in semi-arid environments (US DOE, 1980).

The option also exists to use PREGENII to calculate χ/Q , the ratio of ground-level concentrations (Ci/m^3) to source strength (Ci/s) (US DOE, 1980):

$$\chi/Q = \frac{2.0}{3.0(2\pi)^{1/2} \sigma_y \sigma_z U} \quad (2)$$

$$\begin{aligned}\sigma_y &= 0.11D(1.0 + 10^{-4}D)^{-1/2} \text{ (dispersion coefficient)} \\ \sigma_z &= 0.08D(1.0 + 2.0 \times 10^{-4}D)^{-1/2} \text{ (dispersion coefficient)} \\ D &= \text{downwind transport distance (m)} \\ U &= \text{mean wind speed (m/s)}\end{aligned}$$



The expressions for σ_y and σ_z , provided above, represent slightly unstable lower atmospheric conditions typical of the desert in the southwestern United States and are, therefore, considered appropriate for this analysis (US DOE, 1980).

5.0 CAPABILITIES AND LIMITATIONS OF THE SOFTWARE

PREGENII processes input for the GENII-A version of GENII. Data for determining the biosphere inventory exists in a CAMDAT file. PREGENII expects this data to be located in specified analysis variables (specific units as described in Section 7.1). PREGENII does not give the user access to a complete set of GENII capabilities (e.g., scenarios involving stack release from nuclear power plants.) Instead, PREGENII gives the user the GENII-A capabilities required for performing WIPP PA calculations, as explained in Section 4.0. PREGENII expects the concentrations from the input CDBs to be located in specified analysis variables and to have specific units (see Section 7.1).

6.0 USER INTERACTIONS WITH THE SOFTWARE

The user runs PREGENII as a preprocessor for GENII-A to produce each of the GENII-A input control files corresponding to an n -vector sample space. As the computational flow diagram (Figure 1) shows, radionuclide concentration input to PREGENII can come from WIPP PA codes that simulate the direct route to the accessible environment (CUTTINGS code sequence), or from the WIPP PA codes that simulate the indirect route to the accessible environment (BRAGFLO, NUTS/PANEL, SECOFL, and SECOTP code sequences). (Pathways 2 and 4 listed in Section 4.0 use output from the CUTTINGS code sequence; pathways 1 and 3 listed in Section 4.0 use output from the BRAGFLO, NUTS/PANEL, SECOFL, and SECOTP code sequences. Calculations for pathways 5 and 6 are not shown in Figure 1 because they are not used in WIPP PA.)

6.1 Interactive Execution

The user can execute PREGENII interactively by typing the following line (followed by a carriage return) at the VMS "\$" prompt:

```
RUN WP$PRODROOT:[GI.EXE]PREGENII_PA96.EXE
```

A banner scrolls down the screen and then the following information describing the file definitions is printed on the screen:

PREGENII_TEST_NODBG expects the following files:

- 1) Input first CAMDAT File vector
- 2) Input Text File

- 3) Input Generic Radioisotope Database
- 4) Output GENII Input File
- 5) Output Diagnostics/Debug File (optional)

Subsequent questions in the procedure file request names for the above five files, described briefly below:

1. **Input computational database, CAMDAT, (.CDB) files.** These are the family of CAMDAT database files that contain, for each of the sampled vectors, the initial radionuclide (actinide) concentrations in either contaminated groundwater (output of ALGEBRACDB from the indirect-route-to-accessible-environment simulation shown in Figure 1) or from drilling operations (output of CUTTINGS from the direct-route-to-accessible-environment simulation shown in Figure 1). The name of the first .CDB file is specified. See Section 7.1 for more information on the input computational database files.
2. **PREGENII ASCII input control file.** This file, which contains the commands that establish how GENII-A will be run for the n -vector sample space corresponding to a given pathway, is the human interface to the GENII-A code sequence. This file is described extensively in Section 7.2.
3. **Input generic radioisotope database file.** This file contains information that characterizes the radionuclide isotopes, such as half-life, specific activity, and mass. The same input generic radioisotope database is used for all sample vector calculations. See Section 7.3 for more information on this file.
4. **GENII-A ASCII input control files.** These files, which are PREGENII output files, are the GENII-A ASCII input control files created by PREGENII to run GENII-A for each of the sampled vectors. There is a one-to-one correspondence between these files and the .CDB files. See Section 9.1 for more information on the GENII-A input control files.
5. **Output PREGENII diagnostics file.** This is a diagnostics/debug file containing information about the PREGENII run for the n -vector sample space. It is an optional file, but it must be specified if the user wants to take advantage of error reporting. See Section 9.2 for more information on this file.

6.2 Execution via Command File

Alternatively, the user may use a command file to execute PREGENII. A sample command file, `GI1_TEST_PCA.COM` in this example, follows:

```
----- GI1_TEST_PCA.COM follows -----  
$! -----  
$! MODULE:      GI1_TEST_PCA.COM  
$! PURPOSE:    RUN TEST CASES FOR PREGENII USING THE PRODUCTION EXE  
$! DATE:       15-JAN-1996  
$! AUTHOR:     E. J. DECOTEAU  
$! -----  
$ SET NOON  
$ START_DIR = F$ENVIRONMENT("DEFAULT")  
$ EXE_SRC   := $WP$PRODROOT:[GI.EXE]PREGENII_PA96.EXE  
$ SET DEFAULT WP$TESTROOT:[GI1.TEST]  
$! -----  
$ DEFINE GI1_CDB$INP GI1_TEST1_R001.CDB  
$ DEFINE GI1_UIF$INP GI1_TEST1_UIF.INP  
$ DEFINE GI1_RDB$INP GI1_TEST1_RDB.INP  
$ DEFINE GI1_TRN$OUT GI1_TEST1_TRN_R001.INP  
$ DEFINE GI1_DBG$OUT GI1_TEST1_DBG.OUT  
$ EXE_SRC GI1_CDB$INP GI1_UIF$INP GI1_RDB$INP GI1_TRN$OUT GI1_DBG$OUT  
$! -----  
$ SET DEFAULT 'START_DIR  
$ EXIT.
```



Note that the above command file specifies the names of Files 1 through 5 as `GI1_TEST1_R001.CDB`, `GI1_TEST1_UIF.INP`, `GI1_TEST1_RDB.INP`, `GI1_TEST1_TRN_R001.INP`, and `GI1_TEST1_DBG.OUT`, respectively. (For user's convenience, these filenames appear in bold type in the above sample command file.) Once the command file is written and stored, the user simply types an "@" followed by the name of the command file, which in this case would be:

```
@ GI1_TEST_PCA.COM
```

THIS SAMPLE COMPUTATIONAL FLOW DIAGRAM IS NOT NECESSARILY THE FLOW USED IN THE 1996 WIPP PA CALCULATION. IT IS INCLUDED SOLELY FOR ILLUSTRATIVE PURPOSES.

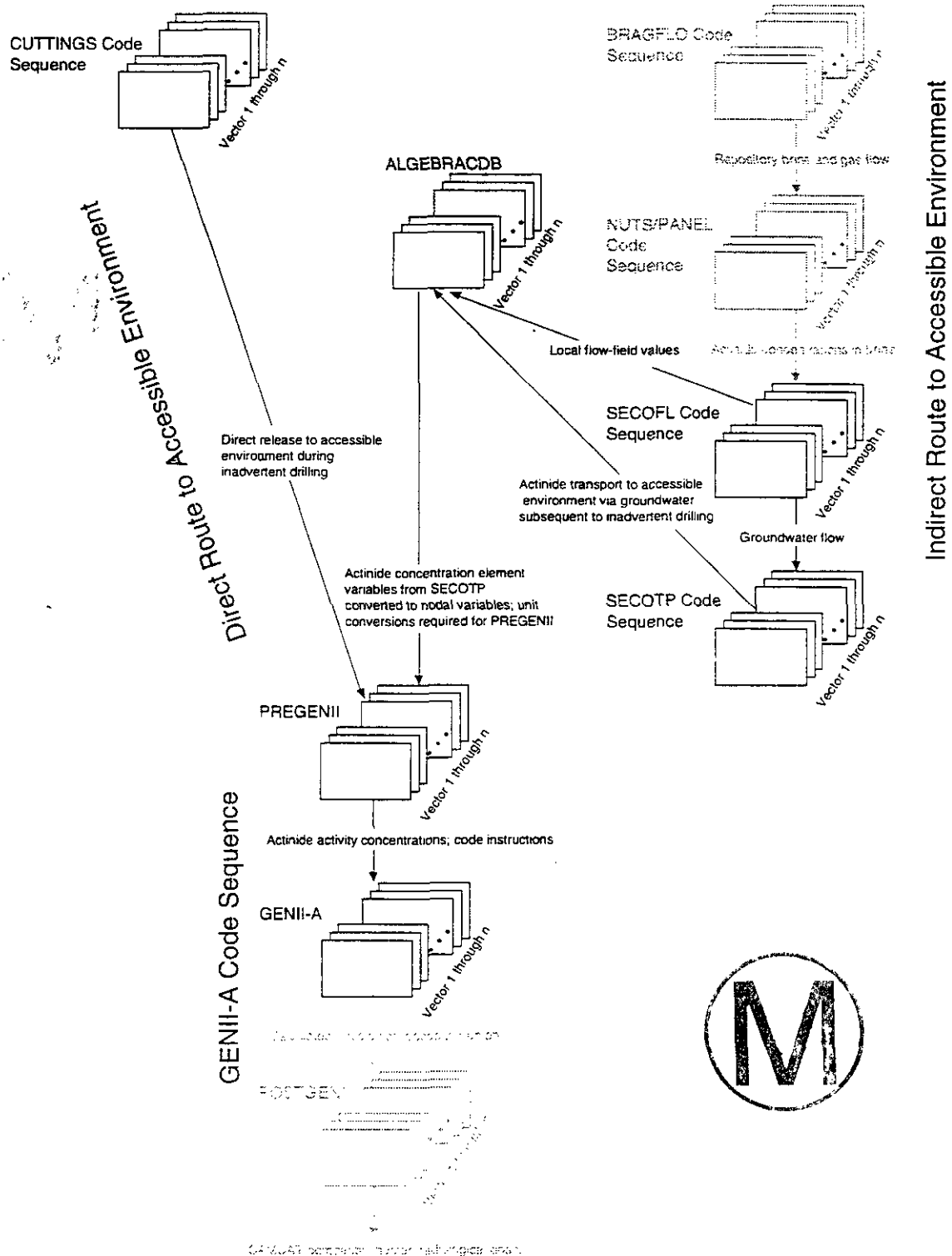


Figure 1. Sample computational flow diagram for PREGENII.

7.0 DESCRIPTION OF INPUT FILES

7.1 Input Computational Database File

The input computational database (.CDB) file follows the CAMDAT format. The CAMDAT format is described in detail in the *Programmer's Manual for CAMCON: Compliance Assessment Methodology Controller*, Sections 6.1 and 6.2 (Rechard et al., 1993). CAMDAT files are not user readable. Data from these files can be plotted using a compatible plotting package and examined using GROPE.

Data required to exist in the input computational database are listed below:

- radioisotopic concentrations saved as appropriate analysis variables (The groundwater concentrations must be nodal analysis variables using the units kg [solute]/m³ [fluid]; the excavated (drilling) concentrations must be global variables using the units total curies per radionuclide as provided by the CUTTINGS code.)
- the LHS-sampled biosphere-relevant parameters saved as material properties or attributes (e.g., brine concentration, contaminated fraction of animal drinking water, water drinking rates)
- flow field velocities nodal analysis variables as supplied by SECOFL2D.

7.2 PREGENII ASCII Input Control File

The PREGENII ASCII input control file consists of keywords that correspond to the exposure pathway explained in Section 4.0.

The format of the PREGENII input control file follows the standard format established for CAMCON input files as stated in the *User's Reference Manual for CAMCON: Compliance Assessment Methodology Controller*, Version 3.0, Section 2.9.4 (Rechard, 1992). The input file contains keywords, denoted by a leading asterisk (*), and parameters associated with the keywords that can function as secondary keywords or have input values associated with them.

User input must be read from the ASCII input control file. The general format for the PREGENII input control file is shown below. (Optional input is enclosed in square brackets ("[]").)

```
*major_keyword [keyword_flags], &  
[keyword-specific data, &  
.  
.  
]  
[*major_keyword, &
```

* Unless otherwise noted, ampersands (&s) should be provided at the end of each line.

```
]
```

Comments can be added to the ASCII input control file. Comments are preceded by an exclamation point (!), as illustrated below:

```
! list the variables which will be sampled, GENII name=CAMDAT name  
*LHS_SAMPLES, &
```

Sample input control files for three of the exposure pathways listed in Section 4.0 are provided in Appendix A (contaminated stockpond, water-stock cattle, man [rancher]), Appendix B (contaminated cuttings, man [driller]), Appendix C (contaminated drilling-mud pit, dust-air transport, man [farm family]), and Appendix D (contaminated dried stockpond, dust-air transport, man (farm family)). The user can refer to these sample input files to find out which keywords and parameter values should be specified for a given exposure pathway.

A description of the PREGENII keywords and their options follows.

7.2.1 Keyword/Parameter Summary

The following summarizes use of all PREGENII keyword and parameter cards. Detailed descriptions of the keywords and their associated parameters, in the order presented in this listing, are found in Section 7.2.2.

```
-----  
*PATHWAY, &  
  PATH=[DRILL,FARM,LAKE,STOCK,WELL], SCENario=[E1,E2,E1E2] or [CH,RH], &  
  WASTE_forms=[value], VECTORS=[value], TIME_INT=[value], &  
  LOCations=[value], SOURCE=[WATER,CUTTINGS]
```

```
-----  
*ARRAY_CAMDAT, &  
  TYPE=[GLOBAL,NODE], ROOT=[array or variable name], &  
  LENGTH_root=[value], I_LOC=[value], J_LOC=[value], K_LOC=[value], &  
  NODE_loc=[value], TIME_SOLution=[value], TOLER=[value], &  
  UNITS_Time=[SECONDS,YEARS], INTERP=[LINEAR,NEAR], &  
  NUMBER_points=[value]
```



*STOCK_WELL, &
AQUIFER_AREA=[value], NUMBER_COWS=[value], RATE_DRINK=[value], &
POTABILITY=[value], PUMP_DURATION=[value], &
BRINE=[variable name or value], FLOW=[variable name or value]

*SUSPEND, &
DENSITY=[value], RATE_coeff=[value], AREA=[value], WIND=[value], &
DISTANCE_FARM=[value], RADIUS=[value], DEPTH=[value]

*NUCLEAR, &
CONC_cut=[value], NUM_nucs=[value], NUCLides={PU239,PA231,NP237...}

*DRILLer, &
DENSITY=[value], DEPTH_BOREhole=[value], &
RADIUS_Borehole=[value], RADIUS_Chip=[value]

*LAKE, &
VOLUME_LAKE=[value], DEPTH=[value], CATCH=[value], PRECIP=[value], &
TIME_FLOW=[value], UNITS_Time={SECONDS, YEARS}, &
FLOW=[variable name or value]

*WELL, &
AQUIFER_AREA=[value], TIME_FLOW=[value], UNITS_Time={SECONDS, YEARS}, &
FLOW=[variable name or value]

*REPORT, &
COMMITTED, ORGANS, NUCLIDES, PATHS

*SCENARIO, &
FAR_FIELD/NEAR_FIELD, CHRONIC/ACUTE, &
INDIVIDUAL/POPULATION={GRID or value}, &
TRANSPORT={GROUNDWATER, SURFACE, AIR, NONE}, INVENTORY={RELEASE, BASIC}

*TRANSPORT

AIR_TRANSPORT, OPTION={USE_CHI_OVER_Q, SELECT, SPECIFY}, JOINTFRE, &
USE_CHI_GRID, CHI_OVER_Q=[value], SECTOR=[value], RELEASE_DIST=[value], &
RELEASE_HEIGHT=[value]

SURFACE_WATER, MIX_MODEL={LAKE, RIVER, USER}

END_TRANSPORT

*EXPOSURE, &
DRINKING, ANIMAL_consumption, PLANT_consumption, AQUATIC_consumption, &
INHALATION, EXTERNAL_GROUND, FINITE_PLUME, INFINITE_PLUME, &
DOSE_PERIOD=[value], COMMIT_PERIOD=[value], INTAKE_PERIOD=[value], &
PERIOD_AIR_DEPosition=[value], &
UNITS_Activity={CURIES, MILLICURIES, MICROCURIES, PICOCURIES, BECQUERELS}, &
UNITS_SURFACE={CUBIC_METERS, SQUARE_METERS, KILOGRAMS}, &
PLUME_TIME_EXposure=[value], SOIL_TIME_EXposure=[value], &
SAMPLE_TIME_EXposure=[value], BOAT_TIME_EXposure=[value], &
SWIM_TIME_EXposure=[value], SHORE_TIME_EXposure=[value], &
TIME_IRRigation=[value], RATE_IRRigation=[value], &
TIME_INHALation=[value], AREA_EXTERNAL_source=[value] &
AREA_EXamination=[value]

*FLAGS, &
PRODUCTION={POPULATION, FOOD, GRID}, WATER_TREATMENT={YES, NO}, &
WATER_IRRigation={GROUNDWATER, SURFACE}, &
WATER_DRINK={GROUNDWATER, SURFACE}, RESIDENTIAL, GRID_POPulation

*SOIL_DATA, &
ROOTS_Upper_soil=[value], &
SOIL_Model= [MASS_LOAD, ANSPAUGH, NO_RESUSPENSION], &
SOIL_DILUTION_FACTOR=[value], DEPTH_TOP_Soil=[value], &
SOIL_OVER=[value], MASS_LOAD=[value], EXTERNAL_Source=[value]



*INGESTION

SOIL_INGESTION=[value]

WATER_consumption, TREAT={YES, NO}, HOLDup_time=[value], &
TRANSit_time=[value], CONsumption_rate=[value]

AQUATIC_consumption={FISH, MOLLus, CRUSt, PLANTs}, &
TRANSit_time=[value], PRODUCTION=[value], HOLDup_time=[value], &
CONsumption_rate=[value]

PLANT_consumption={FRUIT, GRAINS, LEAF, ROOTs}, &
GROW_time=[value], RATE_IRRigation=[value], TIME_IRRigation=[value], &
YIELD=[value], PRODUCTION=[value], HOLDup_time=[value], &
CONsumption_rate=[value]

ANIMAL_consumption={BEEF, EGGS, MILK, POULtry}, &
CONsumption=[value], HOLDup_time=[value], PRODUCTION=[value] , &
CONTAMINATED_H2O=[value]

FRESH_FEED={BEEF, MILK} FRACTION=[value], GROW_time=[value], &
RATE_IRRigation=[value], TIME_IRRigation=[value], YIELD=[value], &
STORAGE=[value]


```
STORED_FEED=[BEEF,POULTRY,MILK,EGGS], FRACTION=[value], &  
GROW_time=[value], RATE_IRRIGATION=[value], &  
TIME_IRRIGATION=[value], YIELD=[value], STORAGE=[value]
```

```
END_INGESTION_INPUT
```



```
-----  
*LHS_SAMPLES, &  
BIOSPHERE=[region name in CDB file], &  
HUMAN_DRINKING_WATER=H2O_DRNK, . . . *
```

```
-----  
*END
```

7.2.2 Keyword/Parameter Detailed Description

A complete listing and explanation of the keywords and associated parameters for PREGENII follows. Note that the user is required to type in only the uppercase letters. For example, the keyword *DRILLer can be specified by simply typing “*DRILL.”

UNLESS OTHERWISE NOTED, THE VALID RANGE FOR KEYWORD PARAMETERS THAT ARE ASSIGNED NUMERICAL VALUES IS ANY POSITIVE NUMBER GREATER THAN ZERO (i.e., RANGE > 0).

UNLESS OTHERWISE NOTED, ONLY ONE VALUE OR NAME CAN BE SPECIFIED FOLLOWING A PARAMETER= STATEMENT.

FOR PARAMETER STATEMENTS OF THE TYPE PARAMETER1/PARAMETER2, ONLY ONE PARAMETER CAN BE SPECIFIED.

FOR PARAMETER= STATEMENTS, DEFAULT VALUES ARE ENCLOSED IN GREATER THAN/LESS THAN BRACKETS (E.G., WASTE_forms=<1>). IF NO DEFAULT VALUE IS PROVIDED, THE WORD “NO DEFAULT” IS ENCLOSED IN GREATER THAN/LESS THAN BRACKETS (E.G., PATH=<no default>).

* List would include all PREGENII variables in CAMDAT that are LHS sampled.

FOR PARAMETER1/PARAMETER2 STATEMENTS, DEFAULT PARAMETERS ARE INDICATED WITHIN GREATER THAN/LESS THAN BRACKETS (E.G., CHRONIC/ACUTE <default=CHRONIC>). IF NO DEFAULT VALUE IS PROVIDED, NO TEXT FOLLOWS THE PARAMETER1/PARAMETER2 STATEMENT.

7.2.2.1 *PATHWAY

The *PATHWAY keyword defines an exposure pathway along with a PA scenario, intrusion time, and number of exposure locations, using the following parameters:

PATH=<no default>

Pathway descriptor for origin of contaminants: DRILL, FARM, LAKE, STOCK, WELL for drill cuttings, farm (atmospheric source), lake, stockpond, or water well, respectively. Only one pathway descriptor can be specified.

SCENario=<no default>

The WIPP PA scenario descriptor; used for informational purposes only. Example specifications include: intrusion through repository panel into an underlying pressurized brine pocket (E1), intrusion through repository into underlying dry rock (E2), or a combination of the two previous events (E1E2), or in the case of the drilling pathway, the waste type: contact handled waste (CH) or remote handled waste (RH).

WASTE_forms=<1>

The number of different waste-forms or parcels; range is any integer greater than 0.

VECTORS=<1>

The number of vectors (i.e., independent samples¹); range is any integer greater than 0.



TIME_INT=<no default>

Time of borehole intrusion, in years following decommissioning of repository.

LOCations=<no default>

Number of exposure locations; range is any integer greater than 0 up to a maximum value.

SOURCE=<no default>

How radionuclides transported: by water (WATER) or drilling cuttings (CUTTINGS).

¹ The Waste Isolation Pilot Plant performance assessments use Latin hypercube sampling methods to generate independent samples of parameter values from the distributions developed in the first step of a Monte Carlo analysis; see, for example, Section 4.2.2 of Rechar [1995] for details. Because each "independent sample" contains a complete set of parameter values required for running a single calculation, it is often referred to as a "vector" in the WIPP PA literature; hence, the parameter VECTORS=.

7.2.2.2 *ARRAY_CAMDAT

The *ARRAY_CAMDAT keyword specifies information about the location of concentration data in the CAMDAT database. A description of the parameters for this keyword follows.

TYPE=<no default>

The type of CAMDAT array; i.e., GLOBAL, or NODE, for global or nodal, respectively. NOTE: PREGENII expects groundwater concentrations to be nodal (analysis) variables where concentrations are expected to be kg/m³ per radionuclide; however, driller excavations come from global variables, where the units are curies per radionuclide released due to drilling events.

ROOT=<no default>

The root name of the CAMDAT array containing the concentrations.

LENGTH_root=<no default>

This is the character length of the ROOT described above. Its value is limited by the fact that CAMDAT names are limited to eight characters maximum. Because radioisotopes need six characters to uniquely identify them, LENGTH can be 0, 1, or 2, although 0 implies no other variables of that type exist in CAMDAT.

I_LOC=<no default>

The i-line locations of nodes where nodal array data reside.

J_LOC=<no default>

The j-line locations of nodes where nodal array data reside.

K_LOC=<no default>

The k-line locations of nodes where nodal array data reside.

NODE_loc=<no default>

The node index numbers of nodes where nodal array data reside. The location of nodal array data is specified using either NODE_loc or I_LOC, J_LOC, and K_LOC.

TIME_SOLution=<no default>

The time (at the time step) in the CAMDAT database that concentrations are retrieved. The units of time for TIME_SOLution are specified by UNITS_Time.

TOLER=<no default>

The time tolerance about TIME_SOLution values for including candidate CAMDAT analysis time steps.

UNITS_Time=<no default>

The units of time for TIME_SOLution values. The choices are SECONDS or YEARS.



INTERP=<no default>

Selects alternative interpolation schemes for times of CAMDAT analysis data that are within TOLER of TIME_SOLUTION; i.e., linear interpolation (LINEAR), or nearest point (NEAR). Note: If times are not within specified time tolerance value, no concentrations will be found.

NUMBER_points=<no default>

Number (maximum) of time points allowed for retrieval from CAMDAT that satisfy being within TOLER of TIME_SOLUTION. These points become candidates for use in interpolation. Note: First NUMBER_points encountered as time increases will be used.

7.2.2.3 *STOCK_WELL

A description of the parameters for specifying stockwell (i.e., stockpond) characteristics, which follow the *STOCK_WELL keyword, follows.

AQUIFER_AREA=<no default>

The cross-sectional area of the aquifer passing through the node where fluid (brine) flux is calculated. NOTE: the area specified by this parameter is normal to flow.

NUMBER_COWS=<no default>

The number of stock cattle supplied by the stockpond; range is any integer greater than 0.

RATE_DRINK=<no default>

The rate (cubic meters per year) at which the individual cattle drink from the stockpond.

POTABILITY=<no default>

Maximum acceptable specific density of brine for cattle drinking water; range is any real number equal to or greater than 1 (i.e., the specific density of pure water). This value corresponds to what is commonly called "minimum water potability."

PUMP_DURATION=<no default>

The fraction of a year that the stock pump is operating; range is any real positive number equal to or less than 1.

BRINE=<no default>

The name of the variable containing the specific density of brine found in the Culebra at the point of extraction; range is any real number equal to or greater than 1. (Must be a nodal analysis variable.) Alternatively, it can be a real value input by the user, which overrides the value in the CDB file.

FLOW =<no default>

The name of the variable containing the Darcy flow rate. (Must be a nodal analysis variable.) Alternatively, it can be a real value input by the user, which overrides the value in the CDB file.

7.2.2.4 *SUSPEND

A description of the parameters for suspension of particulates from soil to air, which follow the *SUSPEND keyword, follows.

DENSITY=<no default>

The mean density of the soil being resuspended (kg/m^3). This is ρ_s discussed in Equation 1.

RATE_coeff=<no default>

The coefficient for the resuspension rate. This is the resuspension constant K_r (s^2/m^3) discussed in Equation 1.

AREA=<no default>

Area over which suspension occurs (m^2).

WIND=<no default>

The mean wind speed (meters per second) over the area of suspension. This is U discussed in Equation 1.

DISTANCE_FARM=<no default>

Distance between the farm and the source (D for σ_y and σ_z in Equation 2).

RADIUS=<no default>

The radius (in meters) of a hypothetical borehole.

DEPTH=<no default>

The depth (in meters) of the soil which can be resuspended. This is Δx_s discussed in Equation 1.

7.2.2.5 *NUCLEAR

A description of the parameters for radionuclides, which follow the *NUCLEAR keyword, follows.

CONC_cut=<no default>

Minimum cutoff for concentrations of radionuclides used for creating GENII-A input (kg/m^3). (Used exclusive of NUM_NUCS, NUCLIDES=<no default>).

NUM_nucs=<no default>

Number of nuclides by explicit designation to use (no minimum cut-off); range is any integer greater than 0.

NUCLides=<no default>

Names of nuclides by explicit designation to use. Name is formed by concatenation of element symbol and nuclide atomic mass number followed by the letter M if it is a metastable state (no spaces); e.g., PU239, PA231, NP237 . . . The user should verify that the number of nuclides specified in the name list following NUCLides= agrees with the number specified by NUM_nucs=.



7.2.2.6 *DRILLer

A description of the parameters for the *DRILLer keyword, which indicates data specific to the driller pathway, follows.

DENSITY=<no default>

The mean density of the chip examined by the driller, in kg/m³.

DEPTH_BOREhole=<300.0>

The depth of the borehole, in meters. For WIPP PA calculations, the depth of the borehole is assumed to equal the depth of the repository.

RADIUS_Borehole=<no default>

The radius of the drilled borehole, in meters.

RADIUS_Chip=<no default>

The radius of a hypothetically spherical chip, in meters.



7.2.2.7 *LAKE

A description of the parameters for lake exposure scenarios, which follow the *LAKE keyword, follows.

VOLUME_LAKE=<no default>

The volume of the lake in cubic meters.

DEPTH=<no default>

The depth of the lake in meters.

CATCH=<no default>

The catchment area divided by lake area [unitless].

PRECIP=<no default>

Precipitation in meters per year.

TIME_FLOW=<no default>

The duration of flow into the lake from the contaminated aquifer, in the units specified by UNITS_Time.

UNITS_Time=<no default>

The units of time for TIME_FLOW values. The choices are SECONDS or YEARS.

FLOW=<no default>

The variable name containing the volumetric flow rate (m³/unit time specified by UNITS_Time) in CAMDAT. Alternatively, it can be a real value input by the user, which overrides the value in CAMDAT.

7.2.2.8 ***WELL**

A description of the parameters for farm-well exposure pathways, which follow the *WELL keyword, follows.

AQUIFER_AREA=<no default>

The cross-sectional area of the aquifer, in square meters, providing Darcy flow is being used (see FLOW=, below). NOTE: the area specified by this parameter is normal to flow. If flow is volumetric (see FLOW=, below), then AQUIFER_AREA=<1 . 0>.

TIME_FLOW=<no default> .

The duration of flow into the well from the contaminated aquifer, in the units specified by UNITS_Time.

UNITS_Time=<no default>

The units of time for TIME_FLOW values. The choices are SECONDS or YEARS.

FLOW=<no default>

The variable name containing either the volumetric flow rate (m³/unit time specified by UNITS_Time) in CAMDAT or Darcy flow rate (m/unit time specified by UNITS_Time) in CAMDAT. A real value can instead be input by the user, which overrides the value in CAMDAT. When flow is volumetric, AQUIFER_AREA=<1 . 0> (see AQUIFER_AREA=, above).

7.2.2.9 ***REPORT**

The *REPORT keyword is followed by one or more of the following parameters specifying how GENII-A outputs results:

COMMITTED

Indicates annual effective dose equivalent will be output from GENII-A run. This is a default setting that does not have to be explicitly specified.

ORGANS

Indicates dose by organ will be output from GENII-A run.

NUCLIDES

Indicates dose by nuclide (or radioisotope) will be output from GENII-A run.

PATHS

Indicates dose by various allowed paths (e.g., ingestion, inhalation, external) will be output from GENII-A run.

7.2.2.10 ***SCENARIO**

The *SCENARIO keyword is followed by the following parameters that characterize the exposure pathway to humans.

FAR_FIELD/NEAR_FIELD <default=FAR_FIELD>
Indicates whether far- or near-field exposure.

CHRONIC/ACUTE <default=CHRONIC>
Indicates whether exposure is chronic or acute.

INDIVIDUAL/POPULATION= <default=INDIVIDUAL>
Indicates whether exposure is to an individual (INDIVIDUAL) or a population (POPULATION=), where the choices for POPULATION are GRID (use a population grid) or the number of persons in the exposed population or critical group.

TRANSPORT=<GROUNDWATER>
Indicates the mode of transport to where exposure occurs; may be 1) groundwater (GROUNDWATER), 2) surface water (SURFACE), 3) air (AIR), or 4) NONE. Note: NONE indicates that the *TRANSPORT keyword is omitted. (*TRANSPORT parameters are not required when there is no transport; nor are they always required when the mode of transport is GROUNDWATER.)

INVENTORY=<BASIC>
Indicates whether radioisotope concentrations are transported (in GENII-A) to exposure location (RELEASE) or are assumed to be at exposure location (BASIC).

7.2.2.11 *TRANSPORT

The *TRANSPORT keyword is followed by the following parameters that characterize how radionuclides are transported.

AIR_TRANSPORT
Indicates air transport parameters, listed immediately below, follow.

OPTION=<no default>
Indicates which of the four air transport options are to be used by GENII-A, as specified in the AIR TRANSPORT section of the GENII-A input control file:

```
====AIR_TRANSPORT====,====SECTION 1=*  
0-Calculate PM  
Option: 1-Use chi/Q or PM value  
2-Select MI dist & dir  
3-Specify MI dist & dir
```

OPTION=USE_CHI_OVER_Q corresponds to Option 1; OPTION=SELECT corresponds to Option 2; OPTION=SPECIFY corresponds to Option 3. If OPTION= is not specified in the PREGENII input control file, Option 0 is selected, which means that the plume model is calculated by PREGENII.

JOINTFRE

If JOINTFRE is specified, then joint frequency meteorological data will be used in GENII-A to calculate the ratio of ground-level concentrations to the source strength. If JOINTFRE is not specified, then either USE_CHI_GRID or CHI_OVER_Q (described below) must be specified.

USE_CHI_GRID

If USE_CHI_GRID is specified, then a χ/Q grid provided by GENII-A will be used by GENII-A to calculate the above ratio.

CHI_OVER_Q=<0.0>

If CHI_OVER_Q is specified, the plume is semi-infinite. The value for χ/Q is either (1) directly calculated for GENII-A as explained in Section 4.0 (CHI_OVER_Q=CALCULATE), or (2) χ/Q is assigned a value greater than zero (CHI_OVER_Q=value).

SECTOR=<no default>

Specifies the direction of the receptor. Can take on any value between 1 and 16; 1=south, 5=west, 9=north, 13=east, with other integers in this range representing intermediate directions. For example, 16=south-south-east.

RELEASE_DIST=<no default>

Distance from release point to receptor (m).

RELEASE_HEIGHT=<89.0>

For joint frequency data, indicates the height (m) above ground level where data taken.



SURFACE_WATER

Indicates surface water transport parameters, listed immediately below, follow.

MIX_MODEL=<no default>

Indicates the mix model, for surface water, to be used in GENII-A; choices are 1) lake (LAKE), 2) river (RIVER), or 3) user (USER).

END_TRANSPORT

Signifies the end of the *TRANSPORT parameters.

7.2.2.12 *EXPOSURE

A description of the parameters and values for exposure to radionuclides, which follow the *EXPOSURE keyword, follows.

DRINKING

Indicates exposure by drinking water.

ANIMAL_consumption

Indicates exposure by ingesting animal products.

PLANT_consumption

Indicates exposure by ingesting plant food (vegetables, fruits, grains, roots).

AQUATIC_consumption

Indicates exposure by eating aquatic food (e.g., fish).

INHALATION

Indicates exposure occurs from breathing.

EXTERNAL_GROUND

Indicates that groundshine (exposure to radiation coming directly from contaminated soil) occurs.

FINITE_PLUME

Indicates that there is exposure to (immersion in) a finite plume.

INFINITE_PLUME

Indicates that there is exposure to (immersion in) an infinite plume.

DOSE_PERIOD=<no default>

Period of dose due to exposure (years).

COMMIT_PERIOD=<50.0>

Period of dose commitment (years).

INTAKE_PERIOD=<1.0>

Period of intake of contaminated radionuclides (years).

PERIOD_AIR_DEPosition=<0.0>

Number of years of deposition from the air to the soil prior to exposure.

UNITS_Activity=<BECQUERELS>

Units of activity (CURIES, MILLICURIES, MICROCURIES, PICOCURIES, or BECQUERELS).

UNITS_Surface=<SQUARE_METERS>

Surface soil units (CUBIC_METERS, SQUARE_METERS, or KILOGRAMS).

PLUME_TIME_EXposure=<no default>

Time of exposure to radioactive plume in atmosphere (hours).

SOIL_TIME_EXposure=<no default>

Time of exposure to contaminated soil (hours).

SAMPLE_TIME_EXposure=<no default>

Time of exposure to contaminated sample (hours).

BOAT_TIME_EXposure=<no default>

Time of exposure to water while boating (hours).



SWIM_TIME_EXposure=<no default>
Time of exposure to water while swimming (hours).

SHORE_TIME_EXposure=<no default>
Time of exposure to water while on shore (hours).

TIME_IRRigation=<no default>
Time of irrigation (months).

RATE_IRRigation=<no default>
Rate of irrigation (inches per year).

TIME_INHALation=<no default>
Time of inhalation (hours).

AREA_EXTernal_source=<no default>
Total area of contaminated ground surface (square meters).

AREA_EXamination=<no default>
Cross-sectional area of contaminated sample examined (square meters).

7.2.2.13 *FLAGS

The user uses the *FLAGS keyword to set some of the flags (or switches) that are needed for the exposure configuration, as specified below.

PRODUCTION=<no specification>
Indicates atmospheric production option; choices are population weighted (POPULATION), food weighted (FOOD), or production grid (GRID). If none of the above are chosen, input defaults to uniform production.

WATER_TREATMENT=<NO>
Flag indicating whether water is treated before use (YES or NO).

WATER_IRRigation=<no default>
Source of the water used for irrigation (groundwater or surface water, GROUNDWATER or SURFACE, respectively).

WATER_DRINK=<no default>
Source of the water used for drinking (groundwater or surface water, GROUNDWATER or SURFACE, respectively).

RESIDENTial
Indicates residential irrigation.

GRID_POPulation
Indicates to use the population grid stored in FILENAMES.DAT.

7.2.2.14 *SOIL_DATA

A description of soil-related parameters, which follow the *SOIL_DATA keyword, follows.

ROOTS_Upper_soil=<no default>

This is the fraction of roots in the upper soil; range is any real positive number equal to or less than 1.

SOIL_Model=<NO_RESUSPENSION>

The soil model chosen for resuspension; may be MASS_LOAD, ANSPAUGH, or NO_RESUSPENSION. The factor for estimating the amount of resuspended material can be based on a time-dependent Anspaugh function (ANSPAUGH); alternatively, it can be calculated from atmospheric mass loading involving the mass loading of soil in air (MASS_LOAD) (g/m^3); NO_RESUSPENSION indicates that resuspension is not modeled.

SOIL_DILUTION_FACTOR=<no default>

This is the deep soil/surface soil dilution factor for manual redistribution due to farming activities.

DEPTH_TOP_Soil=<no default>

This is the depth of top soil available for resuspension (cm); this parameter must be specified if SOIL_Model=ANSPAUGH.

SOIL_OVER=<0.15>

Depth of overburden (m).

MASS_LOAD=<no default>

This is the mass load factor (g/m^3), this parameter must be specified if SOIL_Model=MASS_LOAD.

EXTERNAL_Source=<no default>

Area of external source surrounding soil (m^2).

7.2.2.15 *INGESTION

A description of ingestion-related parameters, which follow the *INGESTION keyword, follows.

SOIL_INGESTION Parameters

SOIL_INGESTION=<0.5>

Indicates amount of soil ingestion (kg/year).

WATER_consumption Parameters

WATER_consumption

Indicates that water consumption parameters, listed immediately below, follow.

TREAT=<NO>

Indicates whether drinking water treated (YES) or not (NO).

HOLDup_time=<no default>
Indicates holdup time (days) from source to consumption.

TRANSit_time=<no default>
Indicates transit time (days) from source to consumption.

CONSumption_rate=<730.0>
Indicates human consumption rate (liters/year).

AQUATIC_consumption Parameters

AQUATIC_consumption=<no default>
Indicates aquatic source of food is fish/mollusks/crustaceans/plants (FISH, MOLLus, CRUST, or PLANTs, respectively). Only one of these is indicated per input line. NOTE: Aquatic consumption parameters must be repeated for each aquatic food source.

TRANSit_time=<1.0 for FISH, MOLLus, CRUST; 24.0 for PLANTs>
Indicates transit time from aquatic source to consumption (hours).

PRODuction=<0.0>
Indicates production in kg/year.

HOLDup_time=<0.0>
Indicates holdup time from aquatic source to consumption (days).

CONSumption_rate=<0.0>
Indicates consumption rate in kg/year.

PLANT_consumption Parameters

PLANT_consumption=<no default>
Indicates terrestrial plant source of food is fruit/grain/leafy/root (FRUIT, GRAINs, LEAF, or ROOTs, respectively). Only one of these is indicated per input line. NOTE: Plant consumption parameters must be repeated for each plant type.

GROW_time=<90.0>
Indicates growing time before harvest (days).

RATE_IRRigation=<40.0>
Indicates rate of irrigation (inches/year).

TIME_IRRigation=<6.0>
Indicates duration of irrigation in months/year.

YIELD=<2.0, 0.8, 1.5, or 4.0 for FRUIT, GRAINs, LEAF, or ROOTs, respectively>
Indicates yield of crop in kg/m² of farmland.

PRODuction=<14.0 for FRUIT, LEAF, ROOTs; 180.0 for GRAINs>
Indicates production in kg/year.

HOLDup_time=<64.0, 72.0, 15.0, or 140.0 for FRUIT, GRAINS, LEAF, or ROOTS, respectively>

Indicates holdup time in days.

CONSumption_rate=<330, 80.0, 64., or 50.0 for FRUIT, GRAINS, LEAF, or ROOTS, respectively>

Indicates consumption rate in kg/year.

ANIMAL_consumption Parameters

ANIMAL_consumption=<no default>

Indicates terrestrial animal source of food is beef/poultry/milk/eggs (BEEF, EGGs, MILK, or POULtry, respectively.) Only one of these is indicated per input line. NOTE: Animal consumption parameters must be repeated for each animal food source.

CONSumption=<70.0, 20.0, 230.0, or 8.5 for BEEF, EGGs, MILK, or POULtry, respectively>

Indicates consumption rate in kg/year.

HOLDup_time=<34.0, 18.0, 4.0, or 34.0 for BEEF, EGGs, MILK, or POULtry, respectively>

Indicates holdup time in days.

PRODUCTION=<0.0>

Indicates production in kg/year.

CONTAMINATED_H2O=<0.5>

Amount of contaminated water consumed by animals as a fraction of total water consumed by animals.

FRESH_FEED Parameters

FRESH_FEED=<no default>

Indicates fresh feed for beef-producing (BEEF) or milk-producing (MILK) animals. NOTE: Fresh feed parameters must be repeated for each fresh food source.

FRACTION=<0.75>

Fraction of contaminated feed that is fresh; range is any value between 0 and 1.

GROW_time=<45.0 or 30.0 for BEEF or MILK, respectively>

Grow time for fresh animal feed (days).

RATE_IRRIGATION=<0.0>

Indicates rate of irrigation (inches/year) for fresh feed.

TIME_IRRIGATION=<0.0>

Indicates duration of irrigation (months/year) for fresh feed.

YIELD=<2.0 or 1.5 for BEEF or MILK, respectively>
Amount of fresh feed produced (kg/m²) per unit area of soil.

STORAGE=<100.0 or 0.0 for BEEF or MILK, respectively>
Storage time of fresh feed (days).

STORED_FEED Parameters

STORED_FEED=<no default>

Indicates stored feed for beef-producing (BEEF), poultry-producing (POULtry), milk-producing (MILK), or egg-producing (EGGs) animals. NOTE: Stored feed parameters must be repeated for each stored food type.

FRACTION=<0.25, 1.0, 0.25, or 1.0 for BEEF, POULtry, MILK, or EGGs, respectively>
Fraction of contaminated feed that is stored; range is any value between 0 and 1.

GROW_time=<90.0, 90.0, 45.0, or 90.0 for BEEF, POULtry, MILK, or EGGs, respectively>
Grow time for stored animal feed (days).

RATE_IRRIGATION=<40.0 for BEEF, 0.0 for POULtry, MILK, and EGGs>
Indicates rate of irrigation (inches/year) for stored feed.

TIME_IRRIGATION=<6.0 for BEEF, 0.0 for POULtry, MILK, and EGGs>
Indicates duration of irrigation (months/year) for stored feed.

YIELD=<0.8, 0.8, 2.0, or 0.8 for BEEF, POULtry, MILK, or EGGs, respectively>
Amount of stored feed produced (kg/m²) per unit area of soil.

STORAGE=<180.0, 180.0, 100.0, or 180.0 for BEEF, POULtry, MILK, or EGGs, respectively>
Storage time of stored feed (days).

END_INGESTION_INPUT Marker

END_INGESTION_INPUT

Signifies the end of the *INGESTION parameters.

7.2.2.16 *LHS_SAMPLES



BIOSPHERE=<biospher>

Biosphere name of region (block) in CDB file where sampled variables located.

Variables that are sampled in CAMDAT for the biosphere are listed following the BIOSPHERE= parameter statement.

The following format is used: {PREGENIIname=CAMDATname}.

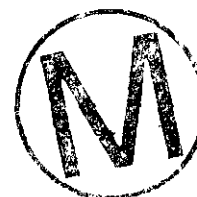
7.2.2.17 *END

The *END keyword indicates that this is the end of the input file.

7.3 Input Generic Radioisotope Database (.RDB) File

This input file contains the following generic information on the radionuclide isotopes that could reach man on an exposure pathway from the WIPP:

- daughter product
- half-life (seconds and years)
- atomic weight (grams per mole)
- activity conversion factor (Ci per kg)
- EPA release limit (in 10^6 curies or megacuries if half life > 20 years)
- waste unit (not used in WIPP PA)
- decay mode.



A listing of the input generic radioisotope database is provided in Appendix E.

8.0 ERROR MESSAGES

PREGENII aborts execution and outputs a variety of messages to the screen and/or the diagnostics/debug output file when input errors occur. A listing of these error messages follows.

- One of the following messages is output when memory errors are detected:

```
(ADDMEM) - REAL array size errors detected ***  
(ADDMEM2) - REAL array size errors detected ***  
(ADDMEM3) - REAL array size errors detected ***  
(ADDMEM) - REAL array memory errors detected ***  
(ADDMEM) - CHARACTER array size errors detected ***  
(ADDMEM1) - CHARACTER array size errors detected ***  
(MEMADJ) - REAL DYNAMIC MEMORY ALLOCATION ERRORS ***  
(MEMADJ) - Invalid REAL dynamic array indices detected ***  
(MEMADJ) - Invalid CHARACTER dynamic array indices detected ***  
(MEMADJ2) - REAL DYNAMIC MEMORY ALLOCATION ERRORS ***  
(MEMADJ3) - REAL DYNAMIC MEMORY ALLOCATION ERRORS ***  
(MEMADJC) - CHARACTER DYNAMIC MEMORY ALLOCATION ERRORS ***  
(MEMADJC2) - CHARACTER DYNAMIC MEMORY ALLOCATION ERRORS ***  
(MEMADJC3) - ### CHARACTER ### DYNAMIC MEMORY ALLOCATION ERRORS ***
```

If any of the above messages are displayed, the user should contact the code sponsor.

- The following messages are output when a required file cannot be found, opened, or closed:

```
Error calling DBSETUP
Error opening input CAMDAT file . . .
Error closing input CAMDAT file . . .
```

If any of the above messages are displayed, the user should verify that the required file names have been supplied and that the files are in the correct format.

- The following message is output if no brine concentration or fluid flow nodal variable is found:

```
WARNING, no BRINE CONCENTRATION nodal variable found'
WARNING, no FLUID FLOW nodal variable found'
```

If the above message is displayed, the user should supply this variable in the input CDB file or in the user input file.

- The following messages are output if there is an error in reading parameters supplied by the user in the PREGENII input-control file:

```
(RDAQUA) - Errors reading aquifer parameters ***
(RDNUCD) - Errors reading Nuclear (in air) parameters ***
(RDPATH) - Errors reading pathway parameters ***
(RDPGCD) - Read ERRORS encountered reading PREGENII input text file ***
(RDRILL) - Errors reading driller parameters ***
(RDSUSP) - Errors reading suspension (in air) parameters ***
(READ_EXPOSURE) - Errors reading exposure parameters ***
(READ_FLAGS) - Errors reading flags parameters ***
(READ_INGESTION) - Errors reading INGESTION input parameters ***
(READ_REPORT) - Errors reading Report definition ***
(READ_SCEN) - Errors reading Scenario definition ***
(READ_SOIL) - Errors reading SOIL input parameters ***
(READ_TRANSPORT) - Errors reading transport parameters ***
(RSTOCK) - Errors reading stockpond parameters ***
```

If any of the above messages are displayed, the user should check the indicated parameter specification in the PREGENII input control file.

- The following messages are output if there is an error in reading keywords supplied by the user in the PREGENII input-control file:

```
*** BAD AQUIFER KEYWORD = ...
*** MAY BE BAD CDB-array KEYWORD = ...
*** BAD CDB-array KEYWORD = ...
*** BAD NUCLEAR DATA KEYWORD = ...
*** POSSIBLE BAD PATHWAY KEYWORD = ...
*** BAD SUSPEND KEYWORD = ...
*** UNKNOWN KEYWORD = ...
*** BAD ingestion KEYWORD = ...
*** Unknown soil_data KEYWORD = ...
*** UNKNOWN TRANSPORT KEYWORD = ...
```

If any of the above messages are displayed, the user should check the indicated keyword specification in the PREGENII input control file.

- The following message is output when a problem is encountered reading a CDB-array parameter:

```
(RDARRD) - Errors reading CDB-array parameters in RDARRD***
```

If the above message is displayed, the user should check the input CDB file and the input control file for errors.

- The following messages are output if there is a problem with reading CAMDAT variables:

```
**** ERROR reading input CAMDAT time values ****  
*** ERROR reading input CAMDAT HISTORY variable values ***  
*** ERROR reading input CAMDAT GLOBAL variable values ***  
*** ERROR reading input CAMDAT NODAL variable values ***  
*** ERROR reading input CAMDAT ELEMENT variable values ***
```

If any of the above messages are displayed, there may be a problem with the input control file or the CDB file.

- The following message is output when PREGENII encounters problems with the generic nuclear database input file:

```
FINDFIT--too many nucs on curies data file  
FINDFIT - too many vectors read on file  
Isotopic name mismatch in FINDFIT  
Isotopic name mismatch in FINDFIT  
Can not find . . . in GENERIC NUCLEAR DATABASE  
Cannot find some radioisotopes in GENERIC library; see debug file
```

If the above message is displayed, the user should contact the person responsible for this database.

- If there is a problem with the LHS parameters, the following message is displayed:

```
Exceeded max number of LHS parameters, check LHS.INC
```

As the message indicates, the user should check the LHS include file.

- The following messages indicate problems with interpolation:

```
Warning, exceeding specified number of interpolation points  
inside range of specified times, may lead to poor  
interpolation, time= ...
```

```
Warning, insufficient number of interpolation points inside  
range of specified times, may lead to interpolation problems
```

Specified extraction time bracket is outside or excludes CDB analysis times

If these messages are encountered, the user should examine the time step and interpolation parameters following the *ARRAY_CAMDAT keyword in the PREGENII input control file.

9.0 DESCRIPTION OF OUTPUT FILES

9.1 GENII-A ASCII Input Control File

The GENII-A ASCII input control file, output by PREGENII, acts as an input control file for GENII-A. Appendices F, G, H, and I provide sample GENII-A ASCII input control files corresponding to the following exposure pathways²:

1. contaminated stockpond, water-stock cattle, man (rancher) (Appendix F)
2. contaminated cuttings, man (driller) (Appendix G)
3. contaminated drilling-mud pit, dust-air transport, man (farm family) (Appendix H)
4. contaminated dried stockpond, dust-air transport, man (farm family) (Appendix I).

The contents of the files in Appendices F, G, H, and I are specified by the PREGENII input control files contained in Appendices A, B, C, and D, respectively.

9.2 PREGENII Diagnostics/Debug File

The diagnostics/debug file contains run-time information for the run of PREGENII corresponding to the sampled vector. A listing of a sample diagnostics/debug file is provided in Appendix J.

10.0 REFERENCES

Napier, B.A., R.A. Peloquin, D.L. Strenge, and J.V. Ramsdell. 1988. *GENII - The Hanford Environmental Radiation Dosimetry Software System, Volume 1: Conceptual Representation and Volume 2: Users' Manual*. PNL-6584, Richland, Washington: Pacific Northwest Laboratory.

Radiation Shielding Information Center. 1995. *GENII 1.485 Environmental Radiation Dosimetry Software System, March 1995*. Oak Ridge, Tennessee: Oak Ridge National Laboratory.

² The sample files provided in this user's manual are not necessarily indicative of those used for the WIPP PA calculations.

Rechard, R.P. 1995. *An Introduction to the Mechanics of Performance Assessment Using Examples of Calculations Done for the Waste Isolation Pilot Plant Between 1990 and 1992*. SAND93-1378, Albuquerque, NM: Sandia National Laboratories.

Rechard, R.P., Ed. 1992. *User's Reference Manual for CAMCON: Compliance Assessment Methodology Controller, Version 3.0*. SAND90-1983, Albuquerque, NM: Sandia National Laboratories.

Rechard, R.P., A.P. Gilkey, H.J. Iuzzolino, D.K. Rudeen, K.A. Byle. 1993. *Programmer's Manual for CAMCON: Compliance Assessment Methodology Controller*. SAND90-1984, Albuquerque, NM: Sandia National Laboratories.

U.S. DOE (U.S. Department of Energy). 1980. *Final Environmental Impact Statement: Waste Isolation Pilot Plant*. DOE/EIS-0026. Washington, DC: U.S. Department of Energy.

11.0 APPENDICES

Note

The sample files and displays provided in the appendices that follow are examples *only*. They are not necessarily the files used for the 1996 WIPP PA regulatory calculation.



Appendix A: Sample PREGENII Input Control (.INP) File for Contaminated Stockpond, Water-Stock Cattle, Man (Rancher) Pathway

```
*PATHWAY, &
  VECTORS=2, PATH='STOCK', SCEN=E1E2, TIME_INT=1000.0, LOC=1, &
  SOURCE=WATER
*ARRAY_CAMDAT, &
  TYPE='NODE', ROOT='C_', LENGTH_ROOT=2, &
  I_LOC=10 J_LOC=10, K_LOC=7, &
  TIME_SOLUTION=3.157E11, &
  TOLER=1.0E9, UNITS_TIME=SECONDS, INTERP=NEAR, NUMBER_POINTS=1
*STOCK_WELL, &
  AQUIFER_AREA=1.0, &
  NUMBER_COWS=25, RATE_DRINK=10.0, POTABILITY=1.007, PUMP_DURATION=0.6, &
  BRINE=1.0, FLOW=1.0
*NUCLEAR, &
  NUM_NUCS=11, NUCLIDES=PU239, PA231, NP237, 'U233', 'U234', 'U235', &
  'U236', 'U238', SE79, TC99, 'I129'
*REPORT, &
  COMMITTED, NUCLIDES, PATHS
*SCENARIO, &
  FAR_FIELD, CHRONIC, INDIVIDUAL, TRANSPORT=GROUNDWATER, INVENTORY=BASIC
*EXPOSURE, &
  ANIMAL_INGESTION, &
  DOSE_PERIOD=1.0, COMMIT_PERIOD=50.0, INTAKE_PERIOD=1.0, &
  UNITS_ACTIVITY=PICOCURIES, UNITS_SURFACE=CUBIC_METERS
*FLAGS, &
  WATER_TREATMENT=NO, WATER_IRRIG=GROUNDWATER
*INGESTION
  ANIMAL_CONSUMPTION=BEEF, CONSUMPTION=100.0, HOLDUP=50.0, PRODUCTION=110.0, &
  CONTAMINATED_H2O=1.0
  ANIMAL_CONSUMPTION=POULTRY, CONSUMPTION=80.0, HOLDUP=10.0, &
  PRODUCTION=120.0, &
  CONTAMINATED_H2O=1.0
  ANIMAL_CONSUMPTION=MILK, CONSUMPTION=50.0, HOLDUP=10.0, PRODUCTION=120.0, &
  CONTAMINATED_H2O=1.0
  ANIMAL_CONSUMPTION=EGGS, CONSUMPTION=60.0, HOLDUP=10.0, PRODUCTION=120.0, &
  CONTAMINATED_H2O=1.0
  FRESH_FEED=BEEF, FRACTION=0.5, GROW_TIME=45, RATE_IRRIGATION=10.0, &
  TIME_IRRIGATION=6.0, YIELD=2.0, STORAGE=20.
  STORED_FEED=BEEF, FRACTION=0.5 GROW_TIME=45, RATE_IRRIGATION=10.0, &
  TIME_IRRIGATION=6.0, YIELD=2.0, STORAGE=100.
  END_INGESTION_INPUT
! list the variables which will be sampled, GENII name=CAMDAT name
*LHS_SAMPLES, &
  HUMAN_DRINKING_WATER=H2O_DRNK
*END
[End of file]
```



Appendix B: Sample PREGENII Input Control (.INP) File for Contaminated Cuttings, Man (Driller) Pathway

```
*PATHWAY, &
  WASTE_FORMS=1, VECTORS=1, PATH='DRILL', SCEN=E1E2, TIME_INT=1000.0, LOC=1, &
  SOURCE=CUTTINGS
*ARRAY_CAMDAT, &
  TYPE='GLOBAL', ROOT='C_', LENGTH_ROOT=2, &
  TIME_SOLUTION=7.25007E3, &
  TOLER=1.0E2, UNITS_TIME=YEARS, INTERP=NEAR, NUMBER_POINTS=1
*NUCLEAR, &
  NUM_NUCLS=11, NUCLIDES=PU239, PA231, NP237, U233, U234, U235, &
  U236, U238, SE79, TC99, I129
*DRILL, &
  DENSITY=1.4E3, RADIUS_CHIP=0.05, RADIUS_BOREHOLE=0.1775
*REPORT, &
  COMMITTED, NUCLIDES, PATHS
*SCENARIO, &
  NEAR_FIELD, CHRONIC, INDIVIDUAL, TRANSPORT=NONE, INVENTORY=BASIC
*EXPOSURE, &
  EXTERNAL_GROUND, &
  DOSE_PERIOD=1.0, COMMIT_PERIOD=50.0, INTAKE_PERIOD=1.0, &
  UNITS_ACTIVITY=PICOCURIES, UNITS_SURFACE=SQUARE_METERS, &
  PLUME_TIME_EXPOSURE=3700.0, SOIL_TIME_EXP=0.0, &
  SAMPLE_TIME_EXP=1.0, &
  AREA_EXTERNAL_SOURCE=0.0, AREA_EXAMINATION=7.854E-3
*SOIL_DATA, &
  SOIL_MODEL=NO_RESUSPENSION, SOIL_DILUTION_FACTOR=0.5, DEPTH_TOP_SOIL=10.0
! list the variables which will be sampled, GENII name=CAMDAT name
*LHS_SAMPLES, &
  HUMAN_DRINKING_WATER = H2O_DRNK
*END
[End of file]
```

Appendix C: Sample PREGENII Input Control (.INP) File for Contaminated Drilling-Mud Pit, Dust-Air Transport, Man (Farm Family) Pathway

```
*PATHWAY, &
  WASTE_FORMS=1, VECTORS=1, PATH='FARM', SCEN=E1E2, TIME_INT=1000.0, LOC=1, &
  SOURCE=CUTTINGS
*ARRAY_CAMDAT, &
  TYPE='GLOBAL', ROOT='C_', LENGTH_ROOT=2, &
  TIME_SOLUTION=7.25007E3, &
  TOLER=1.0E2, UNITS_TIME=YEARS, INTERP=NEAR, NUMBER_POINTS=1
*NUCLEAR, &
  NUM_NUCS=11, NUCLIDES=PU239, PA231, NP237, U233, U234, U235, &
  U236, U238, SE79, TC99, I129
*DRILL, &
  DENSITY=1.4E3, RADIUS_CHIP=0.05, RADIUS_BOREHOLE=0.1775
*REPORT, &
  COMMITTED, NUCLIDES, PATHS, ORGANS
*SCENARIO, &
  FAR_FIELD, CHRONIC, POPULATION=GRID, TRANSPORT=AIR, INVENTORY=RELEASE
*SUSPEND, &
  DENSITY=1.4E3, RATE_COEFF=1.0E-13, WIND_SPEED=3.7, DEPTH=.01, AREA=22.98
*TRANSPORT
! No continuation afer *TRANSPORT!!!
  AIR_TRANSPORT, JOINTFRE, SECTOR=16, &
  RELEASE_DIST=5.3E4, RELEASE_HEIGHT=1.0
END_TRANSPORT
*EXPOSURE, &
  EXTERNAL_GROUND, FINITE_PLUME, INHALATION, ANIMAL, PLANT, &
  DOSE_PERIOD=1.0, COMMIT_PERIOD=50.0, INTAKE_PERIOD=1.0, &
  UNITS_ACTIVITY=CURIES, UNITS_SURFACE=SQUARE_METERS, &
  PLUME_TIME_EXPOSURE=8766.0, &
  TIME_INHALATION=8766.0, &
  AREA_EXTERNAL_SOURCE=1000.0, AREA_EXAMINATION=7.854E-3
*FLAGS, &
  PRODUCTION=POPULATION
*SOIL_DATA, &
  SOIL_MODEL=ANSPAUGH, DEPTH_TOP=2.0
*INGESTION
  PLANT_CONSUMPTION=LEAF, GROW_TIME=60, RATE_IRRI=10.0, TIME_IRRI=6.0, &
  YIELD=50.0, PRODUCTION=120.0, HOLDUP=20.0, &
  CONSUMPTION=60.0
  PLANT_CONSUMPTION=ROOTS, GROW_TIME=70, RATE_IRRI=10.0, TIME_IRRI=6.0, &
  YIELD=50.0, PRODUCTION=100.0, HOLDUP=50.0, &
  CONSUMPTION=60.0
  PLANT_CONSUMPTION=FRUIT, GROW_TIME=80, RATE_IRRI=10.0, TIME_IRRI=6.0, &
  YIELD=60.0, PRODUCTION=130.0, HOLDUP=10.0, &
  CONSUMPTION=90.0
  PLANT_CONSUMPTION=GRAIN, GROW_TIME=90, RATE_IRRI=10.0, TIME_IRRI=6.0, &
  YIELD=40.0, PRODUCTION=110.0, HOLDUP=60.0, &
  CONSUMPTION=80.0
  ANIMAL_CONSUMPTION=BEEF, CONSUMPTION=100.0, HOLDUP=50.0, PRODUCTION=110.0, &
  CONTAMINATED_H2O=1.0
  ANIMAL_CONSUMPTION=POULTRY, CONSUMPTION=80.0, HOLDUP=10.0, &
  PRODUCTION=120.0, &
  CONTAMINATED_H2O=1.0
  ANIMAL_CONSUMPTION=MILK, CONSUMPTION=50.0, HOLDUP=10.0, PRODUCTION=120.0, &
  CONTAMINATED_H2O=1.0
```



```
ANIMAL_CONSUMPTION=EGGS, CONSUMPTION=60.0, HOLDUP=10.0, PRODUCTION=120.0, &  
CONTAMINATED_H2O=1.0  
FRESH_FEED=BEEF, FRACTION=0.5, GROW_TIME=45, RATE_IRRIGATION=10.0, &  
TIME_IRRIGATION=6.0, YIELD=2.0, STORAGE=20.  
STORED_FEED=BEEF, FRACTION=0.5 GROW_TIME=45, RATE_IRRIGATION=10.0, &  
TIME_IRRIGATION=6.0, YIELD=2.0, STORAGE=100.  
END_INGESTION_INPUT  
! list the variables which will be sampled, GENII name=CAMDAT name  
!*LHS_SAMPLES, &  
! HUMAN_DRINKING_WATER = H2O_DRNK  
*END  
[End of file]
```



Appendix D: Sample PREGENII Input Control (.INP) File for Contaminated Dried-Stockpond, Dust-Air Transport, Man (Farm Family) Pathway

```
*PATHWAY, &
  WASTE_FORMS=1, VECTORS=1, PATH='FARM', SCEN=E1E2, TIME_INT=1000.0, LOC=1, &
  SOURCE=WATER
*ARRAY_CAMDAT, &
  TYPE='NODE', ROOT='C_', LENGTH_ROOT=2, &
  I_LOC=10, J_LOC=10, K_LOC=7, &
  TIME_SOLUTION=3.157E11, &
  TOLER=1.0E9, UNITS_TIME=SECONDS, INTERP=NEAR, NUMBER_POINTS=1
*$STOCK_WELL, &
  AQUIFER_AREA=1.0, &
  NUMBER_COWS=25, RATE_DRINK=10.0, POTABILITY=1.007, PUMP_DURATION=0.6, &
  BRINE = 1.0, FLOW=1.0
*NUCLEAR, &
  NUM_NUCS=11, NUCLIDES=PU239, PA231, NP237, U233, U234, U235, &
  U236, U238, SE79, TC99, I129
*REPORT, &
  COMMITTED, NUCLIDES, PATHS, ORGANS
*SCENARIO, &
  FAR_FIELD, CHRONIC, TRANSPORT=AIR, INVENTORY=RELEASE
*SUSPEND, &
  DENSITY=1.5E3, RATE_COEFF=1.0E-13, WIND_SPEED=3.7, DEPTH=.01, AREA=728.5
*TRANSPORT
! No continuation afer *TRANSPORT!!!
  AIR_TRANSPORT, CHI_OVER_Q=CALCULATE, OPTION=USE_CHI_OVER_Q, RELEASE_DIST=5.3E4
END_TRANSPORT
*EXPOSURE, &
  EXTERNAL_GROUND, INFINITE_PLUME, INHALATION, ANIMALS, PLANTS, &
  DOSE_PERIOD=1.0, COMMIT_PERIOD=50.0, INTAKE_PERIOD=1.0, &
  UNITS_ACTIVITY=CURIES, UNITS_SURFACE=SQUARE_METERS, &
  PLUME_TIME_EXPOSURE=8766.0, SOIL_TIME_EXPOSURE=2920.0, &
  TIME_INHALATION=8766.0, PERIOD_AIR_DEP=100.0
*FLAGS, &
  PRODUCTION=POPULATION
*SOIL_DATA, &
  SOIL_MODEL=MASS_LOAD, MASS_LOAD=1.5E3, ROOTS_UPPER=0.5
*INGESTION
  PLANT_CONSUMPTION=LEAF, GROW_TIME=60, RATE_IRRI=10.0, TIME_IRRI=6.0, &
    YIELD=50.0, PRODUCTION=120.0, HOLDUP=20.0, &
    CONSUMPTION=60.0
  PLANT_CONSUMPTION=ROOTS, GROW_TIME=70, RATE_IRRI=10.0, TIME_IRRI=6.0, &
    YIELD=50.0, PRODUCTION=100.0, HOLDUP=50.0, &
    CONSUMPTION=60.0
  PLANT_CONSUMPTION=FRUIT, GROW_TIME=80, RATE_IRRI=10.0, TIME_IRRI=6.0, &
    YIELD=60.0, PRODUCTION=130.0, HOLDUP=10.0, &
    CONSUMPTION=90.0
  PLANT_CONSUMPTION=GRAIN, GROW_TIME=90, RATE_IRRI=10.0, TIME_IRRI=6.0, &
    YIELD=40.0, PRODUCTION=110.0, HOLDUP=60.0, &
    CONSUMPTION=80.0
  ANIMAL_CONSUMPTION=BEEF, CONSUMPTION=100.0, HOLDUP=50.0, PRODUCTION=110.0, &
    CONTAMINATED_H2O=1.0
  ANIMAL_CONSUMPTION=POULTRY, CONSUMPTION=80.0, HOLDUP=10.0, &
    PRODUCTION=120.0, &
    CONTAMINATED_H2O=1.0
  ANIMAL_CONSUMPTION=MILK, CONSUMPTION=50.0, HOLDUP=10.0, PRODUCTION=120.0, &
```



```
CONTAMINATED_H2O=1.0
ANIMAL_CONSUMPTION=EGGS, CONSUMPTION=60.0, HOLDUP=10.0, PRODUCTION=120.0, &
CONTAMINATED_H2O=1.0
FRESH_FEED=BEEF, FRACTION=0.5, GROW_TIME=45, RATE_IRRIGATION=10.0, &
TIME_IRRIGATION=6.0, YIELD=2.0, STORAGE=20.
FRESH_FEED=MILK, FRACTION=0.4, GROW_TIME=30, RATE_IRRIGATION=10.0, &
TIME_IRRIGATION=6.0, YIELD=5.0, STORAGE=10.
STORED_FEED=BEEF, FRACTION=0.5 GROW_TIME=45, RATE_IRRIGATION=10.0, &
TIME_IRRIGATION=6.0, YIELD=2.0, STORAGE=100.
STORED_FEED=POULTRY, FRACTION=0.6 GROW_TIME=20, RATE_IRRIGATION=10.0, &
TIME_IRRIGATION=6.0, YIELD=6.0, STORAGE=60.
STORED_FEED=MILK, FRACTION=0.6 GROW_TIME=30, RATE_IRRIGATION=10.0, &
TIME_IRRIGATION=6.0, YIELD=5.0, STORAGE=50.
STORED_FEED=EGGS, FRACTION=0.6 GROW_TIME=25, RATE_IRRIGATION=10.0, &
TIME_IRRIGATION=6.0, YIELD=3.0, STORAGE=40.
END_INGESTION_INPUT
! list the variables which will be sampled, GENII name=CAMDAT name
!*LHS_SAMPLES, &
! HUMAN_DRINKING_WATER = H2O_DRNK
*END
```



PO216	FB212	1.5000E-01	4.7534E-09	2.1600E-01	3.4815E+14	10000000.	10000000.	ALPHA
PO218	FB214	1.8300E-02	5.7991E-06	2.1800E-01	2.8275E+11	10000000.	10000000.	ALPHA
AT217	BI213	3.2300E-02	1.0236E-09	2.1700E-01	1.6093E+15	10000000.	10000000.	ALPHA
AT218	BI214	2.0000E+00	6.3378E-08	2.1800E-01	2.5872E+13	10000000.	10000000.	ALPHA
RN219	PO215	3.9600E+00	1.2549E-07	2.1900E-01	1.3007E+13	10000000.	10000000.	ALPHA
RN220	PO216	5.5600E+01	1.7619E-06	2.2000E-01	9.2217E+11	10000000.	10000000.	ALPHA
RN222	PO218	3.3040E+05	1.0470E-02	2.2200E-01	1.5379E+08	10000000.	10000000.	ALPHA
FR221	AT217	2.8800E+02	9.1264E-06	2.2100E-01	1.7722E+11	10000000.	10000000.	ALPHA
FR223	RA223	1.3080E+03	4.1449E-05	2.2300E-01	3.8672E+10	10000000.	10000000.	BETA
RA223	RN219	9.8790E+05	3.1306E-02	2.2300E-01	5.1203E+07	10000000.	10000000.	ALPHA
RA224	RN220	3.1620E+05	1.0020E-02	2.2400E-01	1.5926E+08	10000000.	10000000.	ALPHA
RA225	AC225	1.2790E+06	4.0530E-02	2.2500E-01	3.9197E+07	10000000.	10000000.	BETA
RA226	FB210	5.0490E+10	1.6000E+03	2.2600E-01	9.8854E+02	1000.	10000000.	BETA
RA228	AC228	1.8150E+08	5.7516E-00	2.2800E-01	2.7258E+05	10000000.	10000000.	BETA
AC225	FR221	8.6400E+05	2.7379E-02	2.2500E-01	5.8025E+07	10000000.	10000000.	ALPHA
AC227	TH227	6.8710E+08	2.1774E+01	2.2700E-01	7.2321E+04	10000.	1000000000.	BETA
AC228	TH228	2.2070E+04	6.9938E-04	2.2800E-01	2.2417E+09	10000000.	10000000.	BETA
TH227	RA223	1.6170E+06	5.1241E-02	2.2700E-01	3.0731E+07	10000000.	10000000.	ALPHA
TH228	RA224	6.0370E+07	1.9131E-00	2.2800E-01	8.1951E+05	10000000.	10000000.	ALPHA
TH229	RA225	2.3160E+11	7.3392E+03	2.2900E-01	2.1268E+02	1000.	10000000.	ALPHA
TH230	RA226	2.4300E+12	7.7004E+04	2.3000E-01	2.0183E+01	100.	10000000.	ALPHA
TH231	PA231	9.1870E+04	2.9113E-03	2.3100E-01	5.3152E+08	100000000.	10000000.	BETA
TH232	RA228	4.4340E+17	1.4051E+10	2.3200E-01	1.0965E-04	100.	10000000.	ALPHA
TH234	PA234M	2.0820E+06	6.5977E-02	2.3400E-01	2.3153E+07	10000000.	10000000.	ALPHA
PA231	AC227	1.0340E+12	3.2766E+04	2.3100E-01	4.7225E+01	1000.	10000000.	ALPHA
PA233	U233	2.3330E+06	7.3930E-02	2.3300E-01	2.0751E+07	10000000.	10000000.	BETA
PA234	U234	2.4120E+04	7.6434E-04	2.3400E-01	1.9986E+09	10000000.	10000000.	BETA
PA234M	U234	7.0200E+01	2.2246E-06	2.3400E-01	6.8668E+11	10000000.	10000000.	BETA
U232	TH228	2.2710E+09	7.1966E-01	2.3200E-01	2.1409E+04	1000.	10000000.	ALPHA
U233	TH229	5.0020E+12	1.5851E+05	2.3300E-01	9.6785E+00	1000.	10000000.	ALPHA
U234	TH230	7.7160E+12	2.4451E+05	2.3400E-01	6.2474E+00	1000.	10000000.	ALPHA
U235	TH231	2.2210E+16	7.0381E-08	2.3500E-01	2.1612E-03	1000.	10000000.	ALPHA
U236	TH232	7.3890E+14	2.3415E-07	2.3600E-01	6.4666E-02	1000.	10000000.	ALPHA
U237	NP237	5.8320E+05	1.8481E-02	2.3700E-01	8.1610E+07	10000000.	10000000.	BETA
U238	TH234	1.4100E+17	4.4681E+09	2.3800E-01	3.3613E-04	1000.	10000000.	ALPHA
U240	NP240M	5.0760E+04	1.6085E-03	2.4000E-01	9.2593E+08	10000000.	10000000.	BETA
NP236	FU236	8.1000E+04	2.5668E-03	2.3600E-01	5.9008E+08	10000000.	10000000.	BETA
NP237	PA233	6.7530E+13	2.1400E-06	2.3700E-01	7.0480E-01	1000.	10000000.	ALPHA
NP238	FU238	1.8290E+05	5.7959E-03	2.3800E-01	2.5913E+08	10000000.	10000000.	BETA
NP239	FU239	2.0350E+05	6.4487E-03	2.3900E-01	2.3192E+08	10000000.	10000000.	BETA
NP240	FU240	3.9000E+03	1.2359E-04	2.4000E-01	1.2051E+10	10000000.	10000000.	BETA
NP240M	FU240	4.4400E+02	1.4070E-05	2.4000E-01	1.0586E+11	10000000.	10000000.	BETA
FU236	U232	8.9910E+07	2.8492E-00	2.3600E-01	5.3161E+05	10000000.	10000000.	ALPHA
FU237	NE237	3.9140E+06	1.2401E-01	2.3700E-01	1.2160E+07	10000000.	10000000.	ALPHA
FU238	U234	2.7690E+09	8.7747E+01	2.3800E-01	1.7116E+04	100.	10000000.	ALPHA
FU239	U235	7.5940E+11	2.4065E+04	2.3900E-01	6.2150E+01	100.	10000000.	ALPHA
FU240	U236	2.0630E+11	6.5374E+03	2.4000E-01	2.2782E+02	100.	10000000.	ALPHA
FU241	AM241	4.5440E+08	1.4399E-01	2.4100E-01	1.0300E+05	10000000.	10000000.	ALPHA
FU242	U238	1.1880E+13	3.7647E+05	2.4200E-01	3.9235E+00	100.	10000000.	ALPHA
FU243	AM243	1.7840E+04	5.6533E-04	2.4300E-01	2.6020E+09	10000000.	10000000.	ALPHA
FU244	U240	2.6070E+15	8.2613E-07	2.4400E-01	1.7733E-02	1000.	10000000.	ALPHA
FU246	AM246M	9.3740E+05	2.9705E-02	2.4600E-01	4.8916E+07	10000000.	10000000.	BETA
AM240	NP236	1.8288E+05	5.7953E-03	2.4000E-01	8.1105E+15	100000000.	10000000.	ALPHA
AM241	NP237	1.3640E+10	4.3224E+02	2.4100E-01	3.4314E+03	100.	10000000.	ALPHA
AM242	CM242	5.7670E+04	1.8275E-03	2.4200E-01	8.0825E+08	1000.	10000000.	ALPHA
AM242M	AM242	4.7930E+09	1.5189E-02	2.4200E-01	9.7249E+03	1000.	10000000.	ALPHA
AM243	NP239	2.3240E+11	7.3645E+03	2.4300E-01	1.9974E+02	100.	10000000.	ALPHA
AM246M	CM246	1.5000E+03	4.7534E-05	2.4600E-01	3.0569E+10	10000000.	10000000.	BETA
AM246	CM246	2.4300E+03	7.7004E-05	2.4600E-01	1.8870E+10	10000000.	10000000.	BETA
CM242	FU238	1.4070E+07	4.4586E-01	2.4200E-01	3.3128E+06	10000000.	10000000.	ALPHA
CM243	FU239	8.9880E+08	2.8482E+01	2.4300E-01	5.1646E+04	1000.	10000000.	ALPHA
CM244	FU240	5.7150E+08	1.8113E+01	2.4400E-01	8.0892E+04	10000000.	10000000.	ALPHA
CM245	FU241	2.6810E+11	8.4958E+03	2.4500E-01	1.7173E+02	1000.	10000000.	ALPHA
CM246	FU242	1.4920E+11	4.7280E+03	2.4600E-01	3.0733E+02	1000.	10000000.	ALPHA
CM247	AM243	4.9200E+14	1.5591E+07	2.4700E-01	9.2821E-02	1000.	10000000.	ALPHA
CM248	FU244	1.0700E+13	3.3907E+05	2.4800E-01	4.2508E+00	1000.	10000000.	ALPHA
CM250	FU246	2.1760E+11	6.8955E+03	2.5000E-01	2.0735E+02	1000.	10000000.	ALPHA
CF249	CM245	1.1060E+10	3.5048E+02	2.4900E-01	4.0959E+03	1000.	10000000.	ALPHA
CF250	CM246	4.1310E+08	1.3091E+01	2.5000E-01	1.0922E+05	10000000.	10000000.	ALPHA
CF251	CM247	2.8320E+10	8.9743E-02	2.5100E-01	1.5869E+03	1000.	10000000.	ALPHA
CF252	CM248	8.3250E+07	2.6381E+00	2.5200E-01	5.3768E+05	10000000.	10000000.	ALPHA
BK250	CF250	1.1600E+04	3.6759E-04	2.5000E-01	3.8897E+09	10000000.	10000000.	BETA

Appendix F: Sample GENII-A Input Control (.INP) File for Contaminated Stockpond, Water-Stock Cattle, Man (Rancher) Pathway

====GENII Input file=====8-Jul 88=====SECTION 2=====

Demonstration of CAMCON PREGENII/GENII interface
 This GENII-A input file was Created on 04/01/96 at 11:51:16

OPTIONS=====DEFAULT=====

P Near-field scenario?
 F Population dose?
 F Acute release?
 Maximum individual data set used
 Complete

TRANSPORT OPTIONS=====Section

F Air Transport
 F Surface Water Transport
 F Biotic Transport (near-field)
 F Waste Form Degradation (near)

REPORT OPTIONS=====

T Report AEDE only
 T Report by radionuclide
 T Report by pathway
 F Report debug diagnostics
 Complete

EXPOSURE PATHWAY OPTIONS===== Section

F Finite plume, external
 F Infinite plume, external
 F Ground, external
 F Recreation, external
 F Inhalation uptake
 F Drinking water ingestion
 F Aquatic foods ingestion
 F Terrestrial foods ingestion
 T Animal product ingestion
 F Inadvertent soil ingestion



INVENTORY *****

- 1 Inventory input activity units: (1-pCi 2-uCi 3-mCi 4-Ci 5-Bq)
- 2 Surface soil source units (1- m2 2- m3 3- kg)
- 11 Number of nuclides in source term

Use when	---Release Terms---			---Basic Concentrations---				
	transport selected			near-field scenario, optionally				
Release	Air	Surface	Buried	Air	Surface	Deep	Ground	Surface
Radio-	/yr	Water	Waste	/L	Soil	Soil	Water	Water
nuclide	/yr	/yr	/m3	/L	/unit	/m3	/L	/L
PU239							0.0E+00	
PA231							5.4E-25	
NP237							3.3E-23	
U 233							2.8E-24	
U 234							6.0E-22	
U 235							3.9E-29	
U 236							4.0E-25	
U 238							0.0E+00	
SE75							1.6E-24	
TC99							8.5E-04	
I 129							1.5E-06	

Use when	---Derived Concentrations---			
	measured values are known			
Release	Terres.	Animal	Drink	Aquatic
Radio-	Plant	Product	Water	Food
nuclide	/kg	/kg	/l	/kg

TIME *****

- 1. Intake ends after (yr)
- 50. Dose calc. ends after (yr)
- 1. Release ends after (yr)
- 0. No. of years of air deposition prior to the intake period
- 0. No. of years of irrigation water deposition prior to the intake period

FAR-FIELD SCENARIOS (IF POPULATION DOSE) *****

- 0 Definition option: 1-Use population grid in filePOP.IN
- 0 2-Use total entered on this line

NEAR-FIELD SCENARIOS *****

- 0 Prior to the beginning of the intake period: (yr)
- 0 When was the inventory disposed? (Package degradation starts)
- 0 When was LOIC? (Biotic transport starts)
- 0.0000 Fraction of roots in upper soil (top 15 cm)
- 0.0000 Fraction of roots in deep soil
- 0.0000 Manual redistribution: deep soil/surface soil dilution factor

.000E+00 Source area for external dose modification factor (m2)
 .000E+00 Source area for close examination dose factor (m2)
 TRANSPORT *****
 =====AIR TRANSPORT=====SECTION 1=====
 0 Calculate PM
 0 Option: 1-Use chi/Q or PM value
 2-Select MI dist & dir
 3-Specify MI dist & dir
 .000E+00 Chi/Q or PM value
 0 MI sector index (1=S)
 .000E+00 MI distance from release point (m)
 89.00 Release height (m)
 T Use jf data, (T/F) else chi/Q grid

====SURFACE WATER TRANSPORT=====SECTION 2=====
 0 Mixing ratio model: 0-use value, 1-river, 2-lake
 0.00 Mixing ratio, dimensionless
 .000E+00 Average river flow rate for: MDXFLG=0 (m3/s) MDXFLG=1,2 (m/s)
 0.00 Transit time to irrigation withdrawal location (hr)
 If mixing ratio model > 0:

EXPOSURE*****
 =====EXTERNAL EXPOSURE=====SECTION 5=====
 Exposure time (Hours):
 0.0 Plume (hr)
 0.0 Surrounding soil contamination duration (hr)
 0.0 Examined soil contamination duration (hr)
 0.150 Soil overburden depth (m)
 0.0 Swimming (hr)
 0.0 Boating (hr)
 0.0 Shoreline activities (hr)
 0 Shoreline type: (1-river, 2-lake, 3-ocean, 4-tidal basin)
 0.0 Transit time for release to reach aquatic recreation (hr)
 0.0 Average fraction of time submersed in acute cloud (hr/person hr)

Residential irrigation:
 F Consider: (T/F)
 1 Source: 1-ground water
 2-surface water; 3-derived
 0.0 Application rate (in/yr)
 0.0 Duration (mo/yr)

====INHALATION=====SECTION 6=====
 0.0 Hours of exposure to contamination per year
 0 0-No resus- 1-Use Mass Loading 2-Use Anspaugh model
 .000E+00 persion Mass loading factor (g/m^3) Top soil available (cm)

====INGESTION POPULATION=====SECTION 7=====
 2 Atmospheric production option
 .000E+00 0-Use food-weighted chi/Q, (kg-sec/m^3), enter value on this line
 1-Use population-weighted chi/Q
 2-Use uniform production
 3-Use chi/Q and production grids (PRODUCTION will be overridden)
 0 Population ingesting aquatic foods, 0 defaults to total (person)
 0 Population ingesting drinking water, 0 defaults to total (person)
 F Consider dose from food exported out of region (default=F)

Note below: S* or Source: 0-none, 1-ground water, 2-surface water
 3-Derived concentration entered above

==== AQUATIC FOODS / DRINKING WATER INGESTION=====SECTION 8=====

F Salt water? (default is fresh)

DRINKING WATER (Humans)

1 SOURCE (see above)
 F TREATMENT? T/F
 0.0 HOLDUP/TRANSIT(da)
 730.0 CONSUMPTION (L/yr)

USE	TRAN-	PROD-	-CONSUMPTION-	
? FOOD	SIT	DUCTION	HOLDUP	RATE
T/F TYPE	hr	kg/yr	da	kg/yr
F FISH	1.0	0.0E+00	0.00	0.0
F MOLLUS	1.0	0.0E+00	0.00	0.0
F CRUSTA	1.0	0.0E+00	0.00	0.0
F PLANTS	1.0	0.0E+00	0.00	0.0

====TERRESTRIAL FOOD INGESTION=====SECTION 9=====

USE	GROW	--IRRIGATION--		PROD-	--CONSUMPTION--			
? FOOD	TIME	S RATE	TIME	YIELD	DUCTION	HOLDUP	RATE	
T/F TYPE	da	* in/yr	mo/yr	kg/m2	kg/yr	da	kg/yr	
T LEAF V	90.00	1	40.0	6.0	1.5	0.0	14.0	15.0
T ROOT V	90.00	1	40.0	6.0	4.0	0.0	14.0	140.0
T FRUIT	90.00	1	40.00	6.0	2.0	0.0	14.0	64.0
T GRAIN	90.00	1	40.0	6.0	0.8	0.0	180.0	72.0



====ANIMAL PRODUCTION CONSUMPTION====SECTION 10====

USE T/F	FOOD TYPE	---HUMAN---		TOTAL PROD- UCTION kg/yr	DRINK WATER CONSUM FRACT.	DIET FRAC- TION	GROW TIME da	-----STORED FEED-----		STOR- YIELD kg/m3	AGE da	
		CONSUMPTION RATE kg/yr	HOLDUP da					-IRRIGATION-- S RATE in/yr	TIME mo/yr			
T	BEEF	100.0	50.0	110.00	1.00	0.50	45.00	1	10.0	6.0	2.00	100.0
T	POULTRY	80.0	10.0	120.00	1.00	1.00	90.00	1	0.0	0.0	0.80	180.0
T	MILK	50.0	10.0	120.00	1.00	0.25	45.00	1	0.0	0.0	2.00	100.0
T	EGG	60.0	10.0	120.00	1.00	1.00	90.00	1	0.0	0.0	0.80	180.0
-----FRESH FORAGE-----												
	BEEF					0.50	45.00	1	10.0	6.0	2.00	20.0
	MILK					0.75	30.00	1	0.0	0.0	1.50	0.0

 [End of file]

Appendix G: Sample GENII-A Input Control (.INP) File for Contaminated Cuttings, Man (Driller) Pathway

===GENII Input file=====8-Jul 88=====SECTION 2=====

Demonstration of CAMCON PREGENII/GENII interface
 This GENII-A input file was Created on 04/01/96 at 11:51:16

OPTIONS=====DEFAULT=====

T Near-field scenario?
 F Population dose?
 F Acute release?
 Maximum Individual data set used
 Complete

TRANSPORT OPTIONS=====Section

F Air Transport
 F Surface Water Transport
 F Biotic Transport (near-field)
 F Waste Form Degradation (near)

REPORT OPTIONS=====

T Report AEDE only
 T Report by radionuclide
 T Report by pathway
 F Report debug diagnostics
 Complete

EXPOSURE PATHWAY OPTIONS===== Section

F Finite plume, external
 F Infinite plume, external
 T Ground, external
 F Recreation, external
 F Inhalation uptake
 F Drinking water ingestion
 F Aquatic foods ingestion
 F Terrestrial foods ingestion
 F Animal product ingestion
 F Inadvertent soil ingestion

INVENTORY =====

- 1 Inventory input activity units: (1-pCi 2-uCi 3-mCi 4-Ci 5-Bq)
- 1 Surface soil source units (1- m2 2- m3 3- kg)
- 11 Number of nuclides in source term

Use when	---Release Terms---			---Basic Concentrations---				
	transport selected			near-field scenario, optionally				
Release	Air	Surface	Buried	Air	Surface	Deep	Ground	Surface
Radio- nuclide	/yr	Water /yr	Waste /m3	/L	Soil /unit	Soil /m3	Water /L	Water /L
PU239						2.7E+07		
PA231						5.2E+07		
NP237						2.5E+06		
U 233						6.5E+08		
U 234						8.8E+07		
U 235						4.0E+05		
U 236						7.8E+06		
U 238						9.2E+03		
SE79						4.2E+06		
TC99						1.1E+08		
I 129						3.4E+05		

Use when	---Derived Concentrations---			
	measured values are known			
Release	Terres.	Animal	Drink	Aquatic
Radio- nuclide	Plant /kg	Product /kg	Water /l	Food /kg

TIME =====

- 1. Intake ends after (yr)
- 50. Dose calc. ends after (yr)
- 1. Release ends after (yr)
- 0. No. of years of air deposition prior to the intake period
- 0. No. of years of irrigation water deposition prior to the intake period

FAR-FIELD SCENARIOS (IF POPULATION DOSE) =====

- 0 Definition option: 1-Use population grid in filePOP.IN
- 0 2-Use total entered on this line

NEAR-FIELD SCENARIOS =====

- 0 Prior to the beginning of the intake period: (yr)
- 0 When was the inventory disposed? (Package degradation starts)
- 0 When was LOIC? (Biotic transport starts)
- 0.0000 Fraction of roots in upper soil (top 15 cm)
- 0.0000 Fraction of roots in deep soil
- 0.5000 Manual redistribution: deep soil/surface soil dilution factor

```
.000E+00 Source area for external dose modification factor (m2)
.785E+02 Source area for close examination dose factor (m2)
TRANSPORT *****
====AIR TRANSPORT====SECTION 1====
0 0-Calculate PM
Option: 1-Use chi/Q or PM value
2-Select MI dist & dir
3-Specify MI dist & dir
.000E+00 Chi/Q or PM value
0 MI sector index (1=S)
.000E+00 MI distance from release point (m)
89.00 Release height (m)
T Use jf data. (T/F) else chi/Q grid

====SURFACE WATER TRANSPORT====SECTION 2====
0 Mixing ratio model: 0-use value, 1-river, 2-lake
0.00 Mixing ratio, dimensionless
.000E+00 Average river flow rate for: MDPLG=0 (m/s) MDPLG=1,2 (m/s)
0.00 Transit time to irrigation withdrawal location (hr)
If mixing ratio model > 0:
```

EXPOSURE*****

```
====EXTERNAL EXPOSURE====SECTION 5====
Exposure time (hours):
3700.0 Plume (hr)
0.0 Surrounding soil contamination duration (hr)
1.0 Examined soil contamination duration (hr)
0.150 Soil overburden depth (m)
0.0 Swimming (hr)
0.0 Boating (hr)
0.0 Shoreline activities (hr)
0 Shoreline type: (1-river, 2-lake, 3-ocean, 4-tidal basin)
0.0 Transit time for release to reach aquatic recreation (hr)
0.0 Average fraction of time submerged in acute cloud (hr/person hr)
```

```
Residential irrigation:
F Consider: (T/F)
0 Source: 1-ground water
2-surface water; 3-derived
0.0 Application rate (in/yr)
0.0 Duration (mo/yr)
```

```
====INHALATION====SECTION 6====
0.0 Hours of exposure to contamination per year
0 0-No resus- 1-Use Mass Loading 2-Use Anspaugh model
.000E+00 pension Mass loading factor (g/m^3) Top soil available (cm)
```

```
====INGESTION POPULATION====SECTION 7====
2 Atmospheric production option
.000E+00 0-Use food-weighted chi/Q. (kg-sec/m^3), enter value on this line
1-Use population-weighted chi/Q
2-Use uniform production
3-Use chi/Q and production grids (PRODUCTION will be overridden)
0 Population ingesting aquatic foods. 0 defaults to total (person)
0 Population ingesting drinking water. 0 defaults to total (person)
F Consider dose from food exported out of region (default=F)
```

Note below: S* or Source: 0-none, 1-ground water, 2-surface water
 3-Derived concentration entered above

==== AQUATIC FOODS / DRINKING WATER INGESTION====SECTION 8====

F Salt water? (default is fresh)

DRINKING WATER (Humans)

```
0 SOURCE (see above)
F TREATMENT? T/F
0.0 HOLDUP/TRANSIT(da)
0.0 CONSUMPTION (L/yr)
```

USE ?	FOOD TYPE	TRAN- SIT hr	PROD- UCTION kg/yr	-CONSUMPTION- HOLDUP da	RATE kg/yr
F	FISH	1.0	0.0E+00	0.00	0.0
F	MOLLUS	1.0	0.0E+00	0.00	0.0
F	CRUSTA	1.0	0.0E+00	0.00	0.0
F	PLANTS	1.0	0.0E+00	0.00	0.0

====TERRESTRIAL FOOD INGESTION====SECTION 9====

USE ?	FOOD TYPE	GROW TIME da	--IRRIGATION-- S RATE in/yr	TIME mo/yr	YIELD kg/m2	PROD- UCTION kg/yr	--CONSUMPTION-- HOLDUP da	RATE kg/yr
T	LEAF V	90.00	0	40.0	6.0	1.5	0.0	14.0
T	ROOT V	90.00	0	40.0	6.0	4.0	0.0	140.0
T	FRUIT	90.00	0	40.00	6.0	2.0	0.0	14.0
T	GRAIN	90.00	0	40.0	6.0	0.8	0.0	180.0



====ANIMAL PRODUCTION CONSUMPTION=====SECTION 10=====

USE ? T/F	FOOD TYPE	---HUMAN---		TOTAL	DRINK	DIET GROW		-STORED FEED-		STOR-		
		CONSUMPTION RATE	HOLDUP da	PROD- DUCTION kg/yr	WATER CONSUM FRACT.	FRAC- TION	TIME da	S RATE * in/yr	IRRIGATION TIME mo/yr	YIELD kg/m3	AGE da	
T	BEEF	70.0	34.0	0.00	0.50	0.25	90.00	0	40.0	6.0	0.80	180.0
T	POULTRY	8.5	34.0	0.00	0.50	1.00	90.00	0	0.0	0.0	0.80	180.0
T	MILK	230.0	4.0	0.00	0.50	0.25	45.00	0	0.0	0.0	2.00	100.0
T	EGG	20.0	18.0	0.00	0.50	1.00	90.00	0	0.0	0.0	0.80	180.0
						-----FRESH FORAGE-----						
	BEEF					0.75	45.00	0	0.0	0.0	2.00	100.0
	MILK					0.75	30.00	0	0.0	0.0	1.50	0.0

 [End of file]



Appendix H: Sample GENII-A Input Control (.INP) File for Contaminated Drilling-Mud Pit, Dust-Air Transport, Man (Farm Family) Pathway

====GENII Input file=====8-Jul 88=====SECTION 2=====

Demonstration of CAMCON PREGENII/GENII interface
 This GENII-A input file was Created on 04/01/96 at 11:51:16

OPTIONS=====DEFAULT=====

F Near-field scenario?
 T Population dose?
 F Acute release?
 Maximum individual data set used

Complete
 TRANSPORT OPTIONS=====Section
 T Air Transport
 F Surface Water Transport
 F Biotic Transport (near-field)
 F Waste Form Degradation (near)

REPORT OPTIONS=====Section
 T Report AEDE only
 T Report by radionuclide
 T Report by pathway
 F Report debug diagnostics

Complete
 EXPOSURE PATHWAY OPTIONS===== Section
 T Finite plume, external
 F Infinite plume, external
 T Ground, external
 F Recreation, external
 T Inhalation uptake
 F Drinking water ingestion
 F Aquatic foods ingestion
 T Terrestrial foods ingestion
 T Animal product ingestion
 F Inadvertent soil ingestion

INVENTORY *****

4 Inventory input activity units: (1-pCi 2-uCi 3-mCi 4-Ci 5-Bq)
 1 Surface soil source units (1- m2 2- m3 3- kg)
 11 Number of nuclides in source term

Use when	Release Terms			Basic Concentrations			
	transport selected			near-field scenario, optionally			
Release	Surface	Buried	Surface	Deep	Ground	Surface	
Radio-	Water	Waste	Air	Soil	Soil	Water	Surface
nuclide	/yr	/m3	/L	/unit	/m3	/L	/L
PU239	1.4E-06						
PA231	2.7E-06						
NP237	1.3E-07						
U 233	1.3E-05						
U 234	4.5E-06						
U 235	2.1E-08						
U 236	4.0E-07						
U 238	4.7E-10						
SE79	2.2E-07						
TC99	5.7E-06						
I 129	1.8E-08						

Use when	Derived Concentrations			
	measured values are known			
Release	Terres.	Animal	Drink	Aquatic
Radio-	Plant	Product	Water	Food
nuclide	/kg	/kg	/l	/kg

TIME *****

- 1. Intake ends after (yr)
- 50. Dose calc. ends after (yr)
- 1. Release ends after (yr)
- 0. No. of years of air deposition prior to the intake period
- 0. No. of years of irrigation water deposition prior to the intake period

FAR-FIELD SCENARIOS (IF POPULATION DOSE) *****

1 Definition option: 1-Use population grid in filePOP.IN
 0 2-Use total entered on this line

NEAR-FIELD SCENARIOS *****

Prior to the beginning of the intake period: (YT)
 0 When was the inventory disposed? (Package degradation starts)
 0 When was LOIC? (Biotic transport starts)
 0.0000 Fraction of roots in upper soil (top 15 cm)
 0.0000 Fraction of roots in deep soil
 0.0000 Manual redistribution: deep soil/surface soil dilution factor

```
.100E+04 Source area for external dose modification factor (m2)
.785E+02 Source area for close examination dose factor (m2)
TRANSPORT *****
====AIR TRANSPORT====SECTION 1====
0          Option: 1-Use chi/Q or PM value
              2-Select MI dist & dir
              3-Specify MI dist & dir
.000E+00 Chi/Q or PM value
16         MI sector index (1=S)
.530E+05 MI distance from release point (m)
1.00      Release height (m)
T         Use jf data, (T/F) else chi/Q grid
```

```
====SURFACE WATER TRANSPORT====SECTION 2====
0          Mixing ratio model: 0-use value, 1-river, 2-lake
0.00      Mixing ratio, dimensionless
.000E+00 Average river flow rate for: MDXFLG=0 (m3/s) MDXFLG=1,2 (m/s)
0.00      Transit time to irrigation withdrawal location (hr)
          If mixing ratio model > 0:
```

EXPOSURE*****

```
====EXTERNAL EXPOSURE====SECTION 5====
Exposure time (hours):
8766.0    Plume (hr)
0.0       Surrounding soil contamination duration (hr)
0.0       Examined soil contamination duration (hr)
0.150    Soil overburden depth (m)
0.0       Swimming (hr)
0.0       Boating (hr)
0.0       Shoreline activities (hr)
0         Shoreline type: (1-river, 2-lake, 3-ocean, 4-tidal basin)
0.0       Transit time for release to reach aquatic recreation (hr)
0.0       Average fraction of time submersed in acute cloud (hr/person hr)
```

```
Residential irrigation;
F         Consider: (T/F)
0         Source: 1-ground water
              2-surface water; 3-derived
0.0       Application rate (in/yr)
0.0       Duration (mo/yr)
```

```
====INHALATION====SECTION 6====
8766.0    Hours of exposure to contamination per year
2         0-No resus- 1-Use Mass Loading 2-Use Anspaugh model
.200E+00  pension      Mass loading factor (g/m^3) Top soil available (cm)
```

```
====INGESTION POPULATION====SECTION 7====
1         Atmospheric production option
.000E+00  0-Use food-weighted chi/Q, (kg-sec/m^3), enter value on this line
          1-Use population-weighted chi/Q
          2-Use uniform production
          3-Use chi/Q and production grids (PRODUCTION will be overridden)
0         Population ingesting aquatic foods, 0 defaults to total (person)
0         Population ingesting drinking water, 0 defaults to total (person)
F         Consider dose from food exported out of region (default=F)
```

```
Note below: S* or Source: 0-none, 1-ground water, 2-surface water
                3-Derived concentration entered above
==== AQUATIC FOODS / DRINKING WATER INGESTION====SECTION 8====
```

F Salt water? (default is fresh)

DRINKING WATER (Humans)

```
0         SOURCE (see above)
F         TREATMENT? T/F
0.0       HOLDUP/TRANSIT(da)
730.0     CONSUMPTION (L/yr)
```

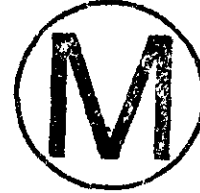
USE	FOOD	TRAN-	PROD-	-CONSUMPTION-
T/F	TYPE	hr	kg/yr	da kg/yr
F	FISH	1.0	0.0E+00	0.00 0.0
F	MOLLUS	1.0	0.0E+00	0.00 0.0
F	CRUSTA	1.0	0.0E+00	80.00 0.0
F	PLANTS	1.0	0.0E+00	80.00 0.0

====TERRESTRIAL FOOD INGESTION====SECTION 9====

USE	FOOD	GROW	--IRRIGATION--	PROD-	--CONSUMPTION--	
T/F	TYPE	da	S RATE	YIELD	HOLDUP	RATE
		da	* in/yr	kg/m2	da	kg/yr
T	LEAF V	60.00	0 10.0	6.0 50.0	120.0	20.0 60.0
T	ROOT V	70.00	0 10.0	6.0 50.0	100.0	50.0 60.0
T	FRUIT	80.00	0 10.00	6.0 60.0	130.0	10.0 90.0
T	GRAIN	90.00	0 10.0	6.0 40.0	110.0	60.0 80.0

====ANIMAL PRODUCTION CONSUMPTION=====SECTION 10=====

USE ? T/F	FOOD TYPE	---HUMAN---		TOTAL PROD- UCTION	DRINK WATER CONSUM	DIET FRAC- TION	GROW TIME da	--STORED FEED--		STOR- YIELD AGE			
		CONSUMPTION RATE kg/yr	HOLDUP da					IRRIGATION S RATE in/yr	TIME mo/yr				
T	BEEF	100.0	50.0	110.00	1.00	0.50	45.00	0	10.0	6.0	2.00	100.0	
T	POULTRY	80.0	10.0	120.00	1.00	1.00	90.00	0	0.0	0.0	0.80	180.0	
T	MILK	50.0	10.0	120.00	1.00	0.25	45.00	0	0.0	0.0	2.00	100.0	
T	EGG	60.0	10.0	120.00	1.00	1.00	90.00	0	0.0	0.0	0.80	180.0	
								---FRESH FORAGE---					
	BEEF						0.50	45.00	0	10.0	6.0	2.00	20.0
	MILK						0.75	30.00	0	0.0	0.0	1.50	0.0



 [End of file]

Appendix I: Sample GENII-A Input Control (.INP) File for Contaminated Dried Stock Pond, Dust-Air Transport, Man (Farm Family) Pathway

====GENII Input file=====8-Jul 88=====SECTION 2=====

Demonstration of CAMCON PREGENII/GENII interface
 This GENII-A input file was Created on 04/01/96 at 11:51:16

OPTIONS=====DEFAULT=====

F Near-field scenario?
 F Population dose?
 F Acute release?
 Maximum Individual data set used
 Complete

TRANSPORT OPTIONS=====Section

T Air Transport
 F Surface Water Transport
 F Biotic Transport (near-field)
 F Waste Form Degradation (near)

REPORT OPTIONS=====

T Report AEDE only
 T Report by radionuclide
 T Report by pathway
 F Report debug diagnostics
 Complete

EXPOSURE PATHWAY OPTIONS===== Section

F Finite plume, external
 T Infinite plume, external
 T Ground, external
 F Recreation, external
 T Inhalation uptake
 F Drinking water ingestion
 F Aquatic foods ingestion
 T Terrestrial foods ingestion
 T Animal product ingestion
 F Inadvertent soil ingestion



INVENTORY =====

4 Inventory input activity units: (1-pCi 2-uCi 3-mCi 4-Ci 5-Bq)
 1 Surface soil source units (1- m2 2- m3 3- kg)
 11 Number of nuclides in source term

Use when	---Release Terms---			-----Basic Concentrations-----				
	transport selected			near-field scenario, optionally				
Release	Surface	Buried		Surface	Deep	Ground	Surface	
Radio- nuclide	Air	Water	Waste	Air	Soil	Soil	Water	Surface
	/yr	/yr	/m3	/L	/unit	/m3	/L	/L
PU239	0.0E+00							
PA231	3.8E-35							
NP237	2.3E-33							
U 233	2.0E-34							
U 234	4.2E-32							
U 235	0.0E+00							
U 236	2.8E-35							
U 238	0.0E+00							
SE79	1.1E-34							
TC99	6.0E-14							
I 129	1.0E-16							

Use when	-----Derived Concentrations-----			
	measured values are known			
Release	Terres.	Animal	Drink	Aquatic
Radio- nuclide	Plant	Product	Water	Food
	/kg	/kg	/l	/kg

TIME =====

1. Intake ends after (yr)
 50. Dose calc. ends after (yr)
 1. Release ends after (yr)
 100. No. of years of air deposition prior to the intake period
 0. No. of years of irrigation water deposition prior to the intake period

FAR-FIELD SCENARIOS (IF POPULATION DOSE) =====

0 Definition option: 1-Use population grid in filePOP.IN
 0 2-Use total entered on this line

NEAR-FIELD SCENARIOS =====

Prior to the beginning of the intake period: (yr)
 0 When was the inventory disposed? (Package degradation starts)
 0 When was LOIC? (Biotic transport starts)
 0.5000 Fraction of roots in upper soil (top 15 cm)
 0.0000 Fraction of roots in deep soil


```

0.0000 Manual redistribution: deep soil/surface soil dilution factor
.000E+00 Source area for external dose modification factor (m2)
.000E+00 Source area for close examination dose factor (m2)
TRANSPORT *****
====AIR TRANSPORT====SECTION 1====
      0-Calculate PM
1      Option: 1-Use chi/Q or PM value
          2-Select MI dist & dir
          3-Specify MI dist & dir
.249E-07 Chi/Q or PM value
0      MI sector index (1=S)
.530E+05 MI distance from release point (m)
89.00 Release height (m)
T      Use jf data, (T/F) else chi/Q grid
  
```

```

====SURFACE WATER TRANSPORT====SECTION 2====
0      Mixing ratio model: 0-use value, 1-river, 2-lake
0.00 Mixing ratio, dimensionless
.000E+00 Average river flow rate for: MIXFLG=0 (m3/s) MIXFLG=1.2 (m/s)
0.00 Transit time to irrigation withdrawal location (hr)
      If mixing ratio model > 0:
  
```

EXPOSURE*****

```

====EXTERNAL EXPOSURE====SECTION 5====
Exposure time (hours):
8766.0 Plume (hr)
2920.0 Surrounding soil contamination duration (hr)
0.0 Examined soil contamination duration (hr)
0.150 Soil overburden depth (m)
0.0 Swimming (hr)
0.0 Boating (hr)
0.0 Shoreline activities (hr)
0 Shoreline type: (1-river, 2-lake, 3-ocean, 4-tidal basin)
0.0 Transit time for release to reach aquatic recreation (hr)
0.0 Average fraction of time submersed in acute cloud (hr/person hr)
  
```

```

Residential irrigation:
F      Consider: (T/F)
0      Source: 1-ground water
          2-surface water; 3-derived
0.0 Application rate (in/yr)
0.0 Duration (mo/yr)
  
```

```

====INHALATION====SECTION 6====
8766.0 Hours of exposure to contamination per year
1      0-No resus- 1-Use Mass Loading 2-Use Anspaugh model
.150E+04 pension Mass loading factor (g/m^3) Top soil available (cm)
  
```

```

====INGESTION POPULATION====SECTION 7====
1      Atmospheric production option
.000E+00 0-Use food-weighted chi/Q, (kg-sec/m^3), enter value on this line
          1-Use population-weighted chi/Q
          2-Use uniform production
          3-Use chi/Q and production grids (PRODUCTION will be overridden)
0      Population ingesting aquatic foods, 0 defaults to total (person)
0      Population ingesting drinking water, 0 defaults to total (person)
F      Consider dose from food exported out of region (default=F)
  
```

Note below: S* or Source: 0-none, 1-ground water, 2-surface water
 3-Derived concentration entered above

==== AQUATIC FOODS / DRINKING WATER INGESTION====SECTION 8====

F Salt water? (default is fresh)

DRINKING WATER (Humans)

```

0      SOURCE (see above)
F      TREATMENT? T/F
0.0 HOLDUP/TRANSIT(da)
730.0 CONSUMPTION (L/yr)
  
```

USE ?	FOOD TYPE	TRAN-SIT hr	PROD-UCION kg/yr	-CONSUMPTION- HOLDUP da	RATE kg/yr
F	FISH	1.0	0.0E+00	0.00	0.0
F	MOLLUS	1.0	0.0E+00	0.00	0.0
F	CRUSTA	1.0	0.0E+00	0.00	0.0
F	PLANTS	1.0	0.0E+00	0.00	0.0

====TERRESTRIAL FOOD INGESTION====SECTION 9====

USE ?	FOOD TYPE	GROW TIME da	--IRRIGATION-- S RATE in/yr	TIME mo/yr	YIELD kg/m2	PROD-UCION kg/yr	--CONSUMPTION-- HOLDUP da	RATE kg/yr
T	LEAF V	60.00	0	10.0	6.0	50.0	120.0	20.0
T	ROOT V	70.00	0	10.0	6.0	50.0	100.0	50.0
T	FRUIT	80.00	0	10.00	6.0	60.0	130.0	10.0



T GRAIN 90.00 0 10.0 6.0 40.0 110.0 60.0 80.0

====ANIMAL PRODUCTION CONSUMPTION=====SECTION 10====

T/F	TYPE	---HUMAN---		TOTAL CONSUMPTION	PROD- UCTION	DRINK WATER	DIET FRAC-	GROW TIME	---STORED FEED---		YIELD	AGE
		RATE	HOLDUP						IRRIGATION	STOR-		
		kg/yr	da	kg/yr	FRACT.	TION	da	* in/yr	mo/yr	kg/m3	da	
T	BEEF	100.0	50.0	110.00	1.00	0.50	45.00	0	10.0	6.0	2.00	100.0
T	POULTRY	80.0	10.0	120.00	1.00	0.60	20.00	0	10.0	6.0	6.00	60.0
T	MILK	50.0	10.0	120.00	1.00	0.60	30.00	0	10.0	6.0	5.00	50.0
T	EGG	60.0	10.0	120.00	1.00	0.60	25.00	0	10.0	6.0	3.00	40.0
-----FRESH FORAGE-----												
	BEEF					0.50	45.00	0	10.0	6.0	2.00	20.0
	MILK					0.40	30.00	0	10.0	6.0	5.00	10.0

Appendix J: Sample Diagnostics/Debug File

PREGENII C-2.10VV (06/28/95)

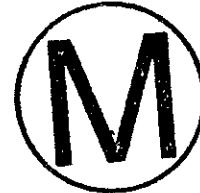
12/05/95 11:44:24

```
PPPPPP RRRRRR EEEEEEE GGGGG EEEEEEE N NN IIII IIII
PP PP RR RR EE GG GG EE NN NN NN NN II II
PP PP RR RR EE GG EE NNN NN II II
PPPPPP RRRRRR EEEEE GG EEEEE NN N NN II II
PP RRRRR EE GG GGG EE NN NNN II II
PP RR RR EE GG GG EE NN NN II II
PP RR RR EEEEE GGGGG EEEEE NN N IIII IIII
```

A pre-processor program for input to GENII

PREGENII Version 2.10VV
Version Date 06/28/95 QA Level C
Written by Ron D. McCurley
Sponsored by Ron D. McCurley

Run on 12/05/95 at 11:44:24
Run on ALPHA AXP BEATLE OpenVMS V6.1



.....
Prepared for
Sandia National Laboratories
Albuquerque, New Mexico 87185-5800
for the United States Department of Energy
under Contract DE-AC04-76DP00789
.....

Disclaimer

This computer program was prepared as an account of work sponsored by an agency of the United States Government. Neither the United States Government nor any agency thereof, nor any of their employees, nor any of their contractors, subcontractors, or their employees, makes any warranty, express or implied, or assumes any legal liability or responsibility for the accuracy, completeness, or usefulness of any information, apparatus, product, or process disclosed or represents that its use would not infringe privately owned rights. Reference herein to any specific commercial product, process, or service by trade name, trademark, manufacturer, or otherwise, does not necessarily constitute or imply its endorsement, recommendation, or favoring by the United States Government, any agency thereof or any of their contractors or subcontractors. The views and opinions expressed herein do not necessarily state or reflect those of the United States Government, any agency thereof or any of their contractors or subcontractors.
.....

.....
FILE ASSIGNMENTS:

Input first CANDAT File vector:
U1:[RDMCCUR.PREGENII.TEST]TEST_R001.CDB;3
Written on 08/24/95 12:20:19
Input Text File:
U1:[RDMCCUR.PREGENII.TEST]PREGENII_STOCK.INP;9
Written on 12/05/95 11:43:41
Input Generic Radioisotope Database:
C3:[CAMCON.CUTTINGS]GENERIC.RDB;1
Written on 07/29/94 16:01:40
Output GENII Input File:
U1:[RDMCCUR.PREGENII.TEST]GENII_STOCK_R001.INP
Output Diagnostics/Debug File:
U1:[RDMCCUR.PREGENII.TEST]PREGENII.DBG
Read report specifications
Read scenario specifications
Reading exposure parameters
*** UNKNOWN KEYWORD = 1.0 ***
*** UNKNOWN KEYWORD = 50.0 ***
*** UNKNOWN KEYWORD = 1.0 ***
*** UNKNOWN KEYWORD = PICOGRAYS ***
*** UNKNOWN KEYWORD = CUBIC_METERS ***
*** UNKNOWN KEYWORD = IRRIGATION_DURATION ***
*** UNKNOWN KEYWORD = 6.0 ***
*** UNKNOWN KEYWORD = NO ***

*** UNKNOWN KEYWORD = GROUNDWATER ***

268507 more words allocated by DYNMEM
Total allocated is 268507

NVARI = 0
NVARGL = 0
NVARND = 12
NVAREL = 4
NVAERI = 0
NVARGL = 0
NVARND = 12
NVAREL = 4
NVAERI = 0
NVARGL = 0
NVARND = 12
NVAREL = 4
NVAERI = 0
NVARGL = 0
NVARND = 12
NVAREL = 4



599958 more words allocated by DYNMEM
Total allocated is 868465

Specified number of interpolation times and extraction time are not compatible with CDB times--automatically reducing number of interpolation times to 1

300120 more words allocated by DYNMEM
Total allocated is 1168585

.....
(RGRDB)

Solution interpolated to value at nearest time 3.1560401E+11

CONCENTRATION DATA AT NODE 5761

U1:[RDMCCUR.PREGENII.TEST]TEST_R001.CDB

UNITS= PICOCURIES/LITER (DRINKING WATER)

Radioisotope with name PU239 has negligible concentration in CAMDAT CDB

Radioisotope with name U238 has negligible concentration in CAMDAT CDB

Specified number of interpolation times and extraction time are not compatible with CDB times--automatically reducing number of interpolation times to 1

Solution interpolated to value at nearest time 3.1560401E+11

CONCENTRATION DATA AT NODE 5761

U1:[RDMCCUR.PREGENII.TEST]TEST_R002.CDB

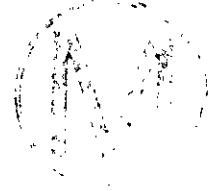
UNITS= PICOCURIES/LITER (DRINKING WATER)

Radioisotope with name PU239 has negligible concentration in CAMDAT CDB

Radioisotope with name U 238 has negligible concentration in CAMDAT CDB

Appendix K: Review Forms

This appendix contains review forms for the PREGENII User's Manual.

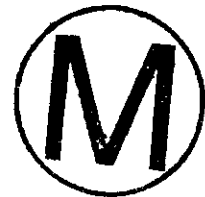


NOTE: Copies of the User's Manual Reviewer's Forms are available in the Sandia WIPP Central Files.

**WIPP PA
User's Manual**

for

GENII-A, Version 2.10



Document Version 1.00

WPO # 27751

November 13, 1995

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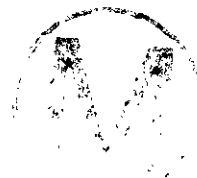
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1.0 INTRODUCTION

1.1 Document Purpose

This document serves as a user's manual for GENII-A, as used in the 1996 WIPP PA calculation. As such, it describes the code's purpose and function, the user's interaction with the code, and the models and methods employed by the code. Examples of user-accessible input and output files are included for the user's convenience.

The GENII-A code, which runs on a DEC Alpha platform, duplicates a subset of the executables from the original GENII program (Radiation Shielding Information Center, 1995). Because a published conceptual representation and user's manuals for GENII already exist (Napier et al., 1988 [Volumes 1 and 2]), an important purpose of this user's manual (WPO # 27751) is to point the user to the discussions in Napier et al. pertinent to the 1996 WIPP PA calculation. It is recommended that the user have a copy of Napier et al., available from the Sandia WIPP Central Files, while reading this user's manual (WPO # 27751).

1.2 Software Identifier

Code Name: GENII-A, a DEC Alpha-platform implementation of GENII, the second generation of the Hanford environmental dosimetry computer codes compiled in the Hanford Environmental Dosimetry System.

WIPP Prefix: GI2

Version Number: 2.10, 1/16/96

Platforms: FORTRAN 77 for OpenVMS AXP, version 6.1, on DEC Alpha

1.3 Points of Contact

1.3.1 Code Sponsor

Leo J. Rahal
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2201 Buena Vista Drive, S.E.
Albuquerque, NM 87106
Voice: (505) 766-9629
Fax: (505) 766-9125

1.3.2 Code Consultant

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Albuquerque, NM 87106
Voice: (505) 766-9629
Fax: (505) 766-9125

2.0 FUNCTIONAL REQUIREMENTS

The functional requirements for GENII-A are listed below:

- R.1 GENII-A reads pathway and nuclide inventory input data.
- R.2 GENII-A calculates doses for acute releases.
- R.3 GENII-A calculates doses for chronic releases.
- R.4 GENII-A calculates doses for air transport of radionuclides with or without meteorological input data.
- R.5 GENII-A calculates doses for finite plume air immersion.
- R.6 GENII-A calculates doses for infinite plume air immersion.
- R.7 GENII-A calculates doses for external ground exposure.
- R.8 GENII-A calculates doses for animal product ingestion with or without irrigation option.
- R.9 GENII-A calculates doses for terrestrial food ingestion with or without irrigation option.
- R.10 GENII-A calculates doses from dairy product ingestion with or without irrigation option.
- R.11 GENII-A calculates doses from aquatic food ingestion.
- R.12 GENII-A calculates doses from drinking water ingestion.
- R.13 GENII-A calculates doses for far-field release.
- R.14 GENII-A calculates doses for near-field release.
- R.15 GENII-A calculates doses for lake or river surface water transport.
- R.16 GENII-A calculates doses from external recreational exposure including boating, swimming, and external shoreline exposure.
- R.17 GENII-A calculates doses from handling radioactive samples.
- R.18 GENII-A calculates individual dose.
- R.19 GENII-A calculates population dose using population distribution data.
- R.20 GENII-A calculates doses from inhalation of airborne radionuclides.

3.0 REQUIRED USER TRAINING AND/OR BACKGROUND

In order to run the GENII-A code successfully, the user will need a basic knowledge of

- Open VMS
- Digital Command Language
- Sandia's CAMDAT database.

To understand the theoretical portions of this manual (and the theoretical portions of the user manual by Napier et al. [1988]) and understand and interpret the results of GENII-A, the user should have a working knowledge of

- scenario development
- biosphere transport of radionuclides
- some knowledge of radionuclide decay processes and
 - radionuclide/organ interactions
 - radiation interactions with organic matter

An undergraduate degree in science or engineering is also recommended. The user should also have some knowledge of the original GENII program and its user manuals (Napier et al., 1988; Radiation Shielding Information Center, 1995). (The original GENII program, because it can run on an IBM PC platform, is sometimes called PC-GENII.)

4.0 DESCRIPTION OF THE MODELS AND METHODS

4.1 Program Modules

While GENII is composed of seven linked computer codes and their associated data libraries, GENII-A makes use of only five of them, as Figure 1 shows. Note that the ENVIN module has been renamed GENII¹ and that GENII calls ENV and DOSE.

Aside from the above name and hierarchy changes, a minor modification was made to the GENII code allowing a combined dose calculation from a spherical radioactive source (hand-held by the driller) and the ground surface exposure dose from a nearby source of radionuclides spread over a

¹ This program module should not be confused with GENII, GENII-A's predecessor. To prevent confusion, this program module (and all program modules) are written in a Courier font: GENII.

specified surface area. This capability is an option and can be selected through appropriate input data.

The following should also be noted:

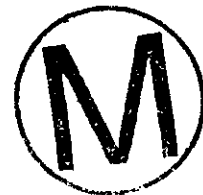
- Only static outputs from EXTDF and INTDF are used by GENII-A; in other words, the boxes labeled EXTDF and INTDF in Figure 1 represent static data files, not program modules that are exercised when GENII-A is run. (EXTDF and INTDF are described in Sections 3.5 and 3.6 of Volume 1 of Napier et al., 1988 and Sections 3.3 and 3.4 of Volume 2 of Napier et al., 1988.) These modules are discussed below.
- Some modification to input formatting was made along with the deletion of unused parameters and the addition of new parameters for the sample exposure option mentioned above.
- Another addition was the inclusion of the requirement to indicate the number of nuclides in the GENII-A input file.

4.1.1 GENII

The ENVIN portion of GENII

- controls the reading of the input control text (.INP) file prepared by PREGENII (see computational flow discussion in Section 6.0 and input control file discussion in Section 7.2)
- organizes the input for the environmental transport and exposure module, ENV
- prepares the data transfer files that are used as input by ENV
- outputs the run input parameters report (i.e., the output input echo file) (Section 9.3).

Details on ENVIN are provided in Volume 1 of Napier et al. (Section 3.2).



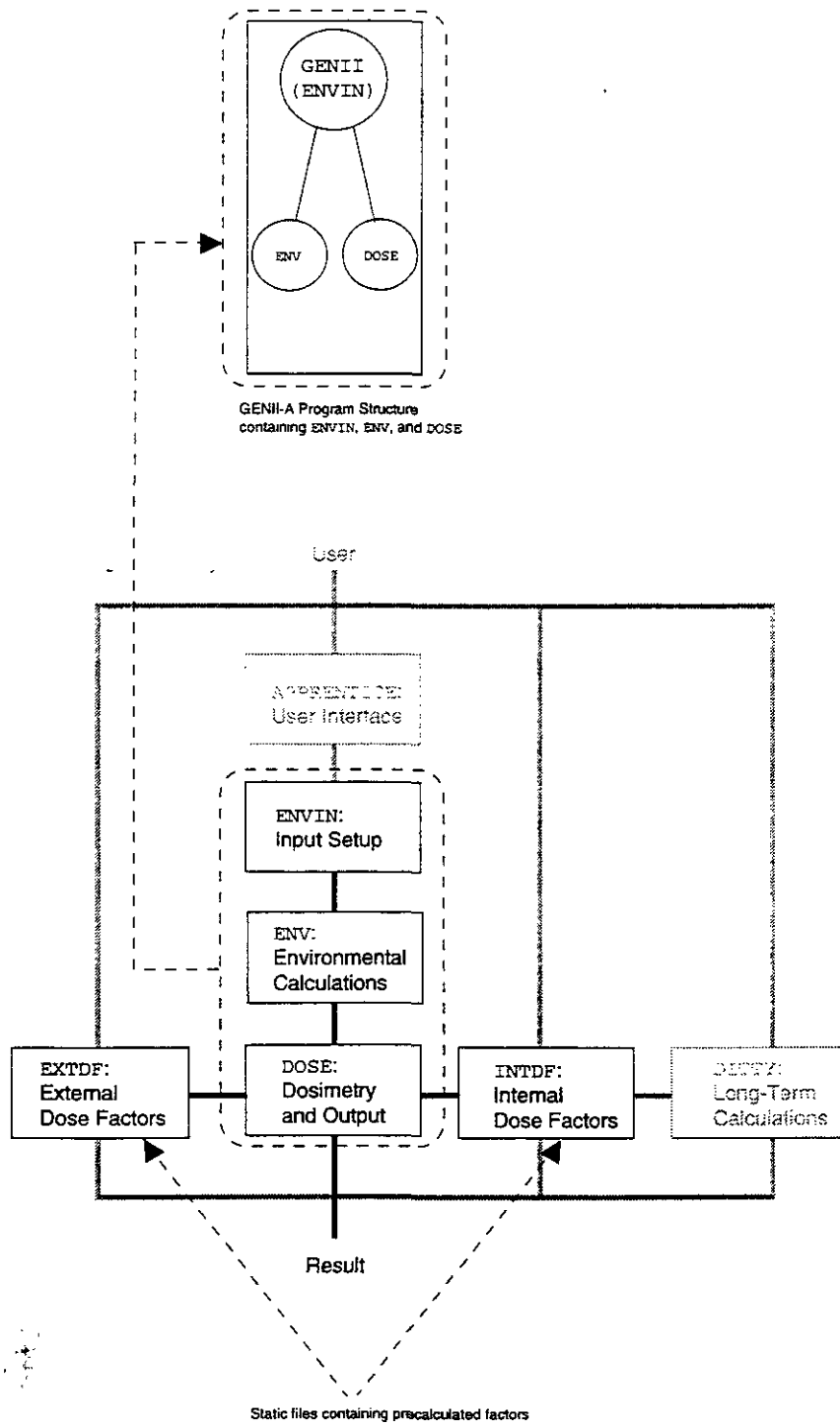


Figure 1. GENII-A implementation of GENII. (Faded portions of figure not used by GENII-A.)

4.1.2 ENV

ENV calculates environmental transfer, uptake, and human exposure to radionuclides that result from the chosen pathway for the defined source terms, as described in Volume 1 of Napier et al. (1988) (Section 3.3). The intermediate information that ENV calculates on annual media concentrations and intake rates are written to data transfer files that are input to DOSE.

4.1.3 DOSE

GENII-A uses DOSE to compute concentrations and intake through the following six principal exposure routes or pathways through the biosphere:

1. **Contaminated stockpond, water-stock cattle, man (rancher).** Contaminated brine from an exploratory drillhole leaks into an aquifer and its groundwater is pumped into a stockpond. Livestock drink exclusively from this pond and ranchers consume the livestock.
2. **Contaminated cuttings, man (driller).** Individuals operating the exploratory drill that penetrates the WIPP repository are, because of their proximity to drilling operations, exposed externally to (1) contaminated soil from the drilling mud pit and (2) drilling samples that they examine.²
3. **Contaminated stockpond, dust-air transport, man (farm family).** Contaminants from a dried stockpond (contaminated with radionuclides migrating through the groundwater, as explained in pathway 1) are suspended in an air plume that deposits the contamination onto a nearby farm. The contaminated crops and livestock from this farm are consumed by humans.
4. **Contaminated drilling-mud pit, dust-air transport, man (farm family).** Contaminants from a dried drilling-mud pit are suspended in an air plume that deposits the contamination onto a nearby farm. The contaminated crops and livestock from this farm are consumed by humans.
5. **Contaminated lake (drinking water, aquatic activities, fishing, irrigation).** Contaminated water from an exploratory drillhole leaks into an aquifer and its groundwater reaches a lake. Humans are contaminated by drinking water from the lake, fishing from the lake, aquatic activities in the lake, and by consuming crops irrigated by contaminated lake water.

² It is to be noted that this option will not be exercised for the WIPP PA calculations since it was not included in the test cases for the QA series. The exposure of the driller will be determined from two separate calculations, one involving exposure from a ground plane source (mud pit) and the second from handling the spherical source. In this way each contribution can be examined separately. These test cases have been included in the QA series.

6. **Contaminated well water (drinking water, irrigation).** Contaminated water from an exploratory drillhole leaks into an aquifer and its groundwater reaches a well. Humans are contaminated by drinking desalinated water from the well and consuming crops irrigated by contaminated well water.

The 1996 WIPP PA calculation is limited to the above six principal exposure routes.

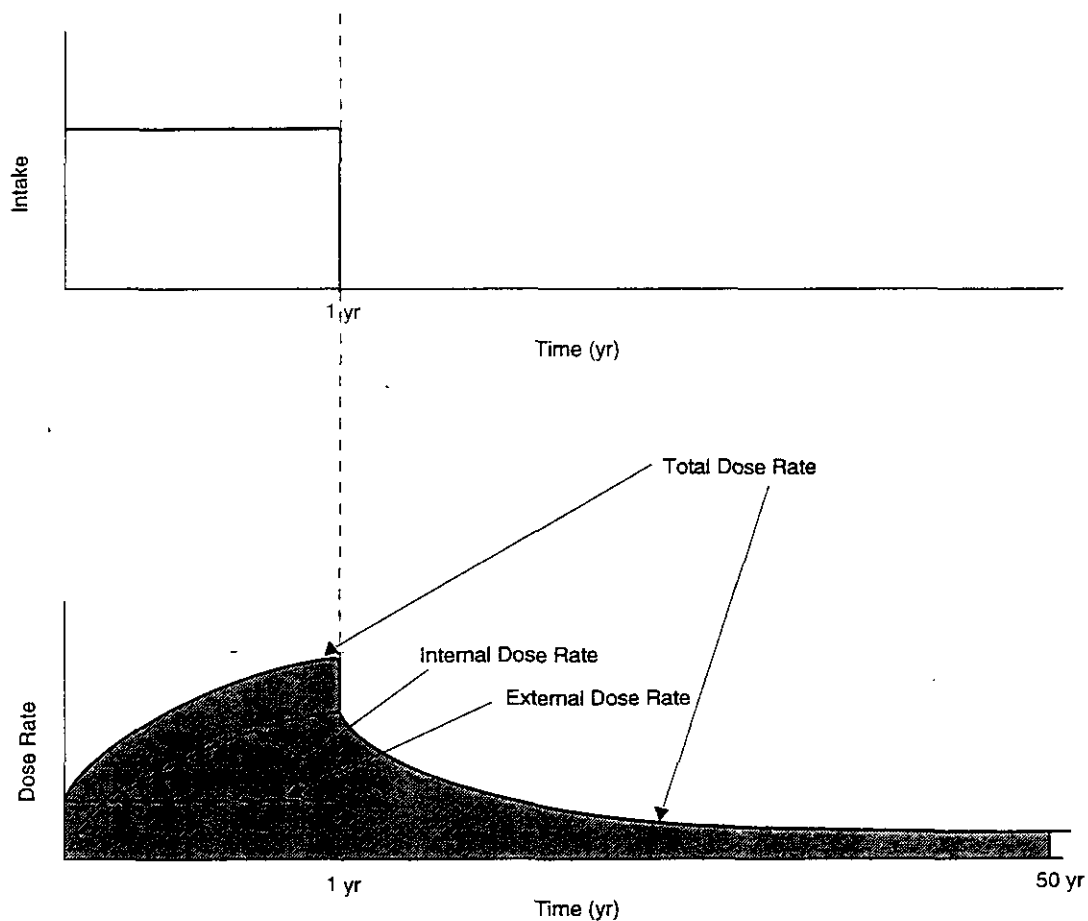
DOSE reads the annual intake and exposure rates defined by ENV and converts them to radiation dose. The calculation of external dose is done with precalculated factors from EXTDF, and the calculation of internal dose is done with precalculated factors from INTDF.

GENII-A uses DOSE to calculate the following for each radionuclide:

- inhalation effective dose equivalent
- ingestion effective dose equivalent
- external dose
- internal effective dose equivalent
- annual effective dose equivalent.

All values are reported in dose equivalent units of rem. A 50-year dose commitment is assumed. The effective dose equivalent (EDE) combines the 1-year external dose and the internal dose over a 50-year period with an assumed 1-year intake period, as shown in Figure 2, multiplied by appropriate weighting factors for nuclides and organs. The internal effective dose equivalent equals the sum of the ingestion and inhalation dose. Further details on DOSE are provided in Volume 1 of Napier et al., 1988 (Section 3.4).

Note that an additional dose calculation capability has been added to GENII-A: the spherical source exposure calculation, which utilizes the external exposure algorithm provided in DOSE with the appropriate dose convergence factors. See Section 7.1.5 for details.



$$\text{Committed Dose} = \int_{0 \text{ yr}}^{50 \text{ yr}} (\text{Total Dose Rate}) dt$$

Figure 2. Committed dose from 1-year internal and external exposure plus extended internal dose (from Figure 3.2 of Volume 1 of Napier et al., 1988)

4.2 Mathematical Representations

The mathematical models and algorithms used by GENII are discussed in detail in Chapter 4.0 of Volume 1 of Napier et al. (1988). To understand the theory upon which GENII-A is based, the reader should read the following portions of Chapter 4.0 of Napier et al.:

- Section 4.1, Internal Dosimetry
- Section 4.2, External Dosimetry
- Section 4.3, Atmospheric Dispersion
- Section 4.4, Air Submersion
- Section 4.5, Surface Water Transport Models
- Section 4.6, Soil Contamination Model
- The following subsections in Section 4.7, Terrestrial Exposure Pathways:
 - Subsection 4.7.1, Inhalation
 - Subsection 4.7.2, Drinking Water Ingestion
 - Subsection 4.7.4, Crop Ingestion — Chronic Exposures
 - Subsection 4.7.5, Animal Product Ingestion — Chronic Exposures
 - Subsection 4.7.7, External Exposure

4.3 Solution Techniques

The GENII package of computer codes is written in standard FORTRAN 77 using a Lahey compiler. Most routines are simple algebraic solutions, and no special logic is employed. One exception is the set of Bateman differential equations used by DOSE to calculate radioactive decay and generation of daughter products; the Bateman equations are solved in subroutine CHAIN using a chain decay solver. Another exception is INTDF, which is not run when GENII-A is exercised. (The same static output from INTDF is used for all GENII-A runs; see Section 4.1.)

5.0 CAPABILITIES AND LIMITATIONS OF THE SOFTWARE

5.1 Capabilities

GENII-A, as used for the 1996 WIPP PA calculation,

- calculates radiation doses for chronic releases
- evaluates the following exposure pathways—soil (surface source), air (semi-infinite cloud and finite cloud geometries), inhalation pathways, and ingestion pathways
- inputs measured concentrations of the source term in specified environmental media
- provides an interface for external calculation of atmospheric dispersion
- identifies target populations by distance and direction for individuals and populations.



5.2 Limitations

The following limitations and assumptions are discussed in the noted parts of Napier et al., 1988:

- The internal dosimetry model does not account for elimination of material leaving a target organ (Volume 1, Subsection 4.1.1).
- All iodine decay products (isotopes of the noble gas xenon) are assumed to be stable or to escape the body before decaying (Volume 1, Subsections 4.1.3 and 4.1.4).
- Tritiated water is assumed to be uniformly distributed among the soft tissues at any time following intake, where it is retained with a biological half time of 10 days (Volume 1, Subsection 4.1.6).
- All intakes of carbon-14 are assumed to be completely and instantaneously absorbed (Volume 1, Subsection 4.1.6).
- For chains with daughters with very short half-lives, the decay energy is assigned to the parent (Volume 1, Subsection 4.1.7).
- Simple atmospheric dispersion modeling is used (Volume 1, Section 4.3 and Subsection 4.3.7).
- The derivation of the atmospheric dispersion models explicitly includes the assumptions that the release is from a point source and that the effluent travels in a straight line once it is released (Volume 1, Subsection 4.3.7).
- The surface water models make the following limiting assumptions: constant flow depth; constant downstream or longshore velocity; straight river channel; constant lateral dispersion coefficient; continuous point discharge release of effluents; constant river width (Volume 1, Section 4.5).
- The quantity of activity from contaminated soil brought to the surface by animals is assumed to be uniformly distributed in the surface soil and available for entry into plant and animal product pathways in subsequent years (Volume 1, Section 4.6.3).

- There is no measurable decrease in the the Anspaugh resuspension factor (used for calculating inhalation exposure) after about 17 years (Volume 1, Subsection 4.7.1).
- Inadvertent ingestion of water during bathing is neglected (Volume 1, Subsection 4.7.2).
- Because interception of materials in irrigation water (i.e., the fraction of radionuclides deposited within a unit area that ends up on vegetation surfaces) is not well understood, a default value of 0.25 is used (Volume 1, Subsection 4.7.4).
- The concentrations of tritium or carbon-14 in environmental media (soil, plants, and animal products) are assumed to have the same specific activity as the contaminating medium (Volume 1, Subsection 4.7.9).

6.0 USER INTERACTIONS WITH THE SOFTWARE



GENII-A is run for each input control file generated by PREGENII corresponding to a n -vector sample space. As the computational flow diagram (Figure 3) shows, radionuclide concentration processed by PREGENII can originate from WIPP PA codes that simulate the direct route to the accessible environment (CUTTINGS code sequence), or from the WIPP PA codes that simulate the indirect route to the accessible environment (BRAGFLO, NUTS/PANEL, SECOFL, and SECOTP code sequences). (Pathways 2 and 4 listed in Subsection 4.1.3 use output from the CUTTINGS code sequence; pathways 1 and 3 listed in Subsection 4.1.3 use output from the BRAGFLO, NUTS/PANEL, SECOFL, and SECOTP code sequences.)

6.1 Interactive Execution

The user can execute GENII-A interactively by typing the following two lines (each followed by a carriage return) at the VMS "\$" prompt:

```
DEFINE GI2_DFL$DEF WP$TESTROOT:[GI2.DAT]
RUN WP$PRODROOT:[GI.EXE]GENII-A.EXE
```

A banner scrolls down the screen and then the following information describing the file definitions is printed on the screen:

GENII-A expects the following files:

- 1) Input Text File
- 2) Input Filenames File
- 3) Output dose file
- 4) Output input echo file
- 5) Output Diagnostics/Debug File (optional)

THIS SAMPLE COMPUTATIONAL FLOW DIAGRAM IS NOT NECESSARILY THE FLOW USED IN THE 1996 WIPP PA CALCULATION. IT IS INCLUDED SOLELY FOR ILLUSTRATIVE PURPOSES.

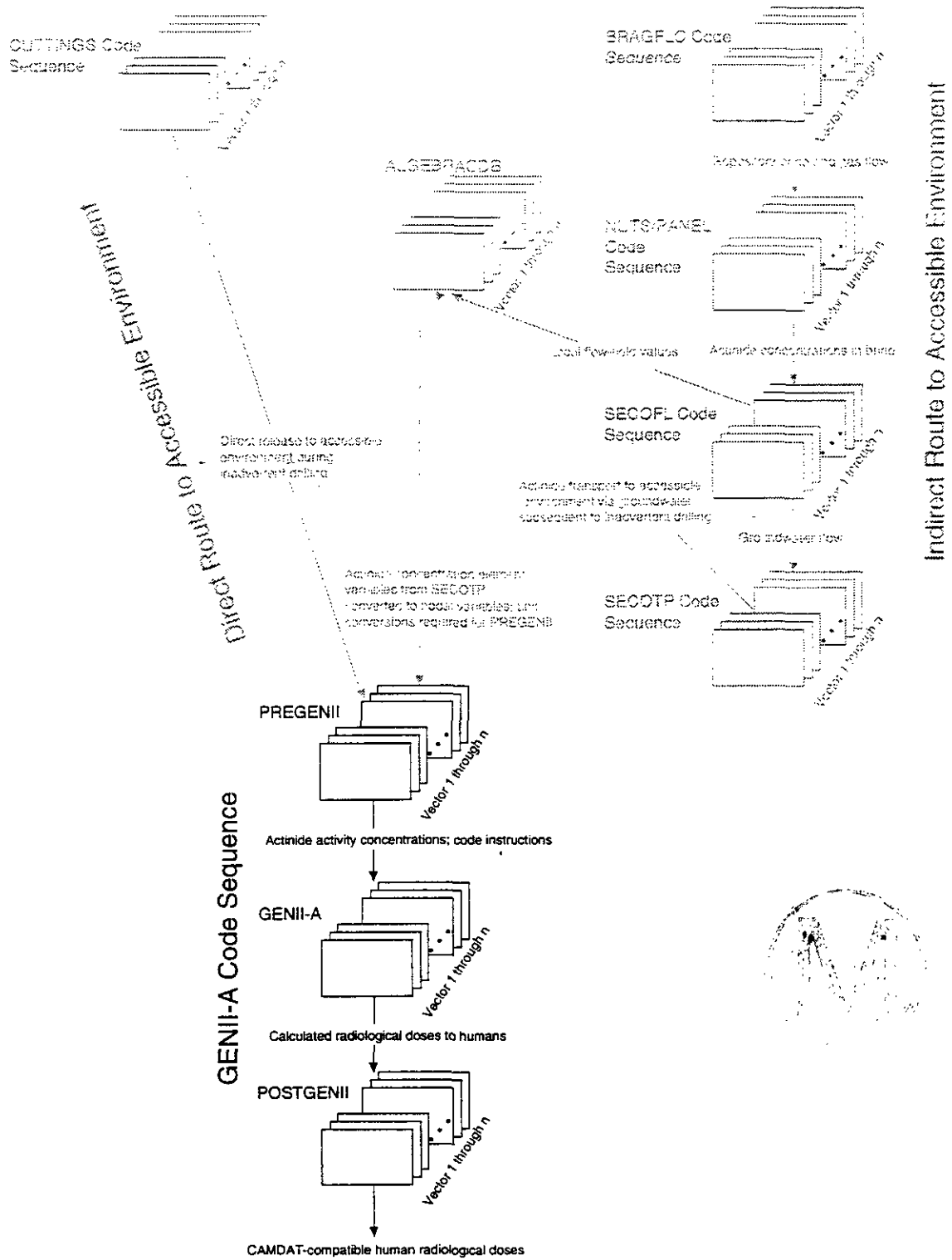


Figure 3. Sample computational flow diagram for GENII-A.

Subsequent questions in the procedure file request names for the above five files, described briefly below:

1. **Input text (.INP) file.** This is the ASCII input control file output by PREGENII (Figure 3) to run GENII-A for the sampled vector. See Section 7.1 for more information on this file.
2. **Input filenames (.DAT) file.** This file contains the names of the data files, input files, output files, and buffers required to run GENII-A. See Section 7.2 for more information on this file.
3. **Output dose (.OUT) file.** This file contains the results of the GENII-A calculation for the sampled vector; it is read by POSTGENII (see Figure 3). See Section 9.1 for more information on this file.
4. **Output input echo (.OUT) file.** This file, referred to in Napier et al. (1988) as the run input parameters report, contains a listing of parameters input to GENII-A for the sampled vector. See Section 9.2 for more information on this file.
5. **Output diagnostics/debug (.OUT) file.** This output file contains information about the GENII-A run for the sampled vector. It is an optional file, but it must be specified if the user wants to take advantage of error reporting. See Section 9.3 for more information on this file.

6.2 Execution via Command File

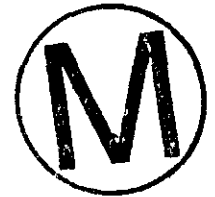
Alternatively, the user may use a command file to execute GENII-A. A sample command file (SAMPLE.COM) follows:

```
! ----
! MODULE:          SAMPLE.COM
! PURPOSE:         RUN A CASE THROUGH GENII-A USING A COM FILE
! DATE:           22-DEC-1995
! AUTHOR:         USER NAME
! ----
SET NOON
START_DIR = F$ENVIRONMENT("DEFAULT")
EXE_SRC := $WP$PRODROOT:[GI.EXE]GENII-A.EXE
DEFINE GI2_DFL$DEF WP$TESTROOT:[GI2.DAT]
DEFINE GI2_FND$INP GI2_DFL$DEF:GI2_FILENAME.DAT
SET DEFAULT WP$TESTROOT:[GI2.TEST]
! ----
DEFINE GI2_TRN$INP GI2_TEST1_TRN.INP
DEFINE GI2_TRN$OUT GI2_TEST1_TRN.OUT
DEFINE GI2_ECO$OUT GI2_TEST1_ECO.OUT
DEFINE GI2_DBG$OUT GI2_TEST1_DBG.OUT
EXE_SRC GI2_TRN$INP GI2_FND$INP GI2_TRN$OUT GI2_ECO$OUT GI2_DBG$OUT
! ----
SET DEFAULT `START_DIR
```

EXIT

Note that the the above command file specifies the names of Files 1 through 5 as **GI2_TEST1_TRN.INP**, **GI2_FILENAME.DAT**, **GI2_TEST1_TRN.OUT**, **GI2_TEST1_ECO.OUT**, and **GI2_TEST1_DBG.OUT**, respectively. (For user's convenience, these filenames appear in bold type in the above sample command file.) Once the command file is written and stored, the user simply types an "@" followed by the name of the command file, which in this case would be:

@SAMPLE.COM



7.0 DESCRIPTION OF INPUT FILES

7.1 ASCII Input Control (.INP) File

The GENII-A ASCII input control file (File 1 introduced in Section 6.1) contains the input specifications required to exercise GENII-A. This input file is referred to as GENII.IN by Napier et al. (1988) and is described line by line in Volume 2 (Section 3.2) of that publication.

A higher-level description of the GENII-A ASCII input control file, as used for the 1996 WIPP PA calculation, follows. In addition, a sample input control file, along with a detailed line-by-line description of the sample file, is provided in Appendix A.

By examining the sample input control file in Appendix A, one can see that the GENII-A input control file consists of seven major fields:

- options
- inventory
- time
- far-field scenarios
- near-field scenarios
- transport
- exposure.

A description of these fields follows. The sample input control file provided in Appendix A can be used as a guide while reading this description. This sample input control file is not necessarily indicative of one which will be used for the 1996 WIPP PA calculation.

7.1.1 Options

7.1.1.1 General



GENII-A allows for either near- or far-field scenarios. Far-field scenarios are for processes involving release of radioactive material into a wide environment. Near-field scenarios focus on possible doses to an individual at a particular location. For the 1996 WIPP PA calculation, the contaminated cuttings, man (driller) exposure pathway (described in Subsection 4.1.3 of this user's manual) is near-field; the remaining five pathways (also described in Subsection 4.1.3) are far-field.

GENII-A can be commanded to calculate either individual doses (for representative members of a critical group) or population doses (collective doses to regional populations or subpopulations). For the 1996 WIPP PA calculation, individual doses are calculated for all pathways.

For the 1996 WIPP PA calculation, GENII-A is limited to chronic releases; acute releases are not modeled.

"Maximum Individual data set used" indicates a conservative approach to selection of individual dose calculation parameters used for inhalation, ingestion, and external exposure. These conservative parameters are in line with the "critical group" requirement.

7.1.1.2 Transport

For the 1996 WIPP PA calculation, only one of the four transport options is ever invoked: the air transport option, which is used for the two dust-air transport pathways. As Figure 3 shows, groundwater transport for the stockpond pathway is handled by the SECO family of WIPP PA codes, and transport up the borehole to the drilling site is handled by the CUTTINGS family of WIPP PA codes. Sources from these calculations are deposited at the location of the scenario as basic concentrations.

7.1.1.3 Report

For all pathways considered for the 1996 WIPP PA calculation, the following report options are used:

- Dose is reported as committed dose equivalent (CDE), the committed dose from one year of exposure over a 50-year period (see Figure 2), appropriately weighted for each organ.
- Dose is reported for each radionuclide.
- Dose is reported by exposure pathway.
- The debug report is not printed on the screen.

7.1.1.4 Exposure Pathway

The following exposure pathways are exercised for the 1996 WIPP PA calculation:

- finite plume, external
- infinite plume, external
- ground, external
- inhalation uptake
- terrestrial foods ingestion
- animal product ingestion
- sample exposure.

7.1.2 Inventory

The inventory field specifies the input activity units, surface soil units, and the number of nuclides in the source term.

The inventory field also requires specification of the source term as a release term, basic concentration, or derived concentration. Release terms are sources to air or water or concentrations in buried wastes. The WIPP dust-air transport pathways specify an air release term. Basic concentrations can be entered when the transport steps are calculated outside of GENII-A. Basic concentrations are used for the WIPP groundwater and drilling cuttings pathways.

7.1.3 Time

Values provided to the time field allow specification of length of exposure, period for which dose commitment is calculated, length of time during which release occurs, and the time of air or irrigation water deposition prior to the intake period. For the 1996 WIPP PA calculation, the intake and release times are typically assumed to be one year, the dose calculation covers a 50-year period, and no air or irrigation water deposition is assumed to occur before the intake period.

7.1.4 Far-Field Scenarios

For the 1996 WIPP PA calculation, the dust-air pathways are considered far-field scenarios. Only individual doses are calculated.

7.1.5 Near-Field Scenarios

For the 1996 WIPP PA calculation, values can be provided for the following parameters in the near-field scenarios input field:

- “Manual redistribution: deep soil/surface soil dilution factor.” A value is specified for the drilling cuttings pathway because drilling a borehole involves physical disruption that mixes deeply buried waste.
- “Source area for external dose modification factor.” The value corresponding to this parameter is the area of the contaminated surface; a value is required for the dust-air transport pathways.
- “Source area for close examination dose factor.” The GENII-A code has the capability to calculate exposure from a spherical hand-held source and a ground plane. The user has the option to implement either or both of these capabilities:
 - In order to implement the spherical source exposure option, the following input parameters are needed: The “Source area for close examination dose factor” should be set equal to 1250 square meters, and the soil overburden depth should be set to 0.15 meters in the “External Exposure” input field in order to flag within the code the appropriate area modification factor and dose calculation factor, respectively. Additionally, a value must be set for the “Examined soil contamination duration” (hours).
 - The input for the ground plane exposure consists of the area over which the radionuclides are spread in addition to the exposure time to the ground plane area and the distance from that source.

The exposure times may not necessarily be equal for the two sources (spherical source and ground plane). When the selection is made to calculate exposure from a ground plane together with that from the spherical source, the program combines the two exposures into one and outputs the result as the external dose. If only one pathway is selected (spherical or ground plane), then the external exposure for that pathway will appear as the external dose. When the combined calculation is made, the basic concentration is input in the “Deep Soil” column under “Basic Concentrations.”

7.1.6 Transport

7.1.6.1 Air Transport

The 1996 WIPP PA calculation requires that the plume model be calculated by PREGENII, meaning that the “0=Calculate PM” model is selected. When the pathway is dust-air, PREGENII can provide either

- a grid of precalculated χ/Q values and a matching grid of population that GENII-A cross-multiplies to create a population-weighted χ/Q
- joint frequency distribution in place of the χ/Q grid.