

US EPA ARCHIVE DOCUMENT

BACKGROUND DOCUMENT FOR THE HUMAN RISK MODULE FOR HWIR99 MULTIMEDIA, MULTIPATHWAY, AND MULTIRECEPTOR RISK ASSESSMENT (3MRA) MODEL

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DISCLAIMER

The work presented in this document has been funded by the U.S. Environmental Protection Agency. Mention of trade names or commercial products does not constitute endorsement or recommendation for use by the Agency.

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1.0 Module Overview and Summary of Functionality

The Human Risk Module is one of the component modules of the Multimedia, Multipathway, and Multireceptor Risk Assessment (3MRA) software system. The Human Risk Module processes modeled outputs from the Human Exposure Module (human receptor exposure estimates) and performs three major functions using these data:

1. *It calculates risk and/or hazard quotient (HQ) for each receptor, cohort, exposure pathway, exposure area, and year. Whether risk, HQ, or both are calculated is determined as a function of the chemical under consideration. For carcinogenic chemicals, risks are calculated as average risks over a 9-year exposure duration. For noncarcinogens, HQs are calculated as a 1-year average.*
2. *It constructs cumulative frequency histograms that quantify the distributions of receptor/cohort-specific populations among different levels of risk and/or HQ for each exposure pathway and aggregation of pathways,¹ and year. The populations consist of individual receptor/cohorts residing at the various exposure areas (residential areas and farms).*
3. *It determines and outputs that critical year during which the maximum cumulative risk and/or HQ occurs across the population for each receptor/cohort combination, for each exposure pathway and pathway aggregation.*

These functions are performed three times, once for each of three radial distances outward from the centroid of the waste management unit (WMU). The purpose of distance-specific results is to assess the sensitivity of risk results to distance from the chemical source.

These functions are performed by the Human Risk Module by a series of nested loops. Figures 1a through 1c illustrate the general looping structure used for a given radial distance. These illustrations are intended only to facilitate overall understanding of the module; the implementing computer code is significantly different to optimize performance.

¹ Aggregation of risks occurring simultaneously over multiple pathways is the essence of multipathway risk assessment. For example, if a receptor is exposed to chemicals from both ingestion of contaminated groundwater and ingestion of contaminated fish, then it is appropriate to estimate the cumulative risk that is incurred across these pathways. In some instances, it is appropriate to aggregate risk across portals of entry (i.e., ingestion and inhalation).

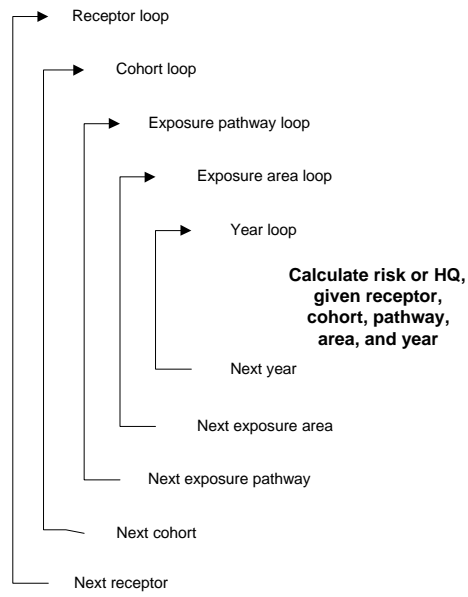


Figure 1a. Looping structure to calculate risk or HQ.

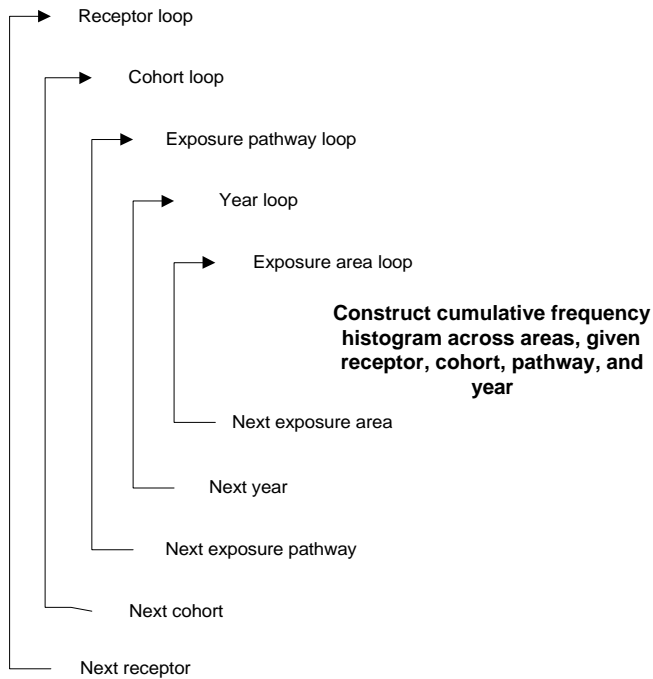


Figure 1b. Looping structure to build cumulative frequency histograms.

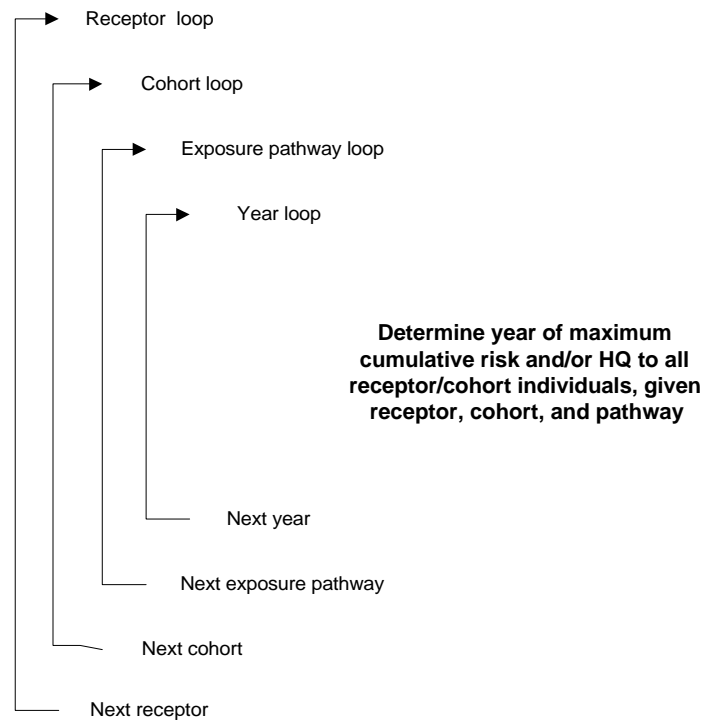


Figure 1c. Looping structure to determine critical year.

Section 2.0 summarizes assumptions and limitations. Section 3.0 discusses in detail the internal calculations and methodologies used to implement the basic functions described above. Inputs and outputs used are listed in Appendix A along with their input file names.

The following terms are defined for clarity.

Receptors. As described in the Human Exposure Module technical background document (US EPA, 1999a), two basic human receptor types are considered: residential receptors (residents and home gardeners) and farmers. Residential receptors may also be recreational fishers in addition to being a resident or home gardener. Farmers may be beef farmers or dairy farmers, and either type of farmer may also be a recreational fisher. These receptor categories were developed in consideration of exposure pathways, and the category names suggest the associated exposure pathway(s). For example, a residential resident is a receptor that is exposed only to the baseline exposure pathways, i.e., inhalation via air and shower and ingestion via soil and water. A resident gardener is a resident exposed through these exposure pathways plus ingestion of homegrown produce. At the highest level of receptor resolution, there are eight categories of human receptors: resident, resident gardener, resident fisher, resident gardener fisher, beef farmer fisher, dairy farmer fisher, beef farmer, and dairy farmer. These eight categories are each modeled for exposure by the Human Exposure Module, and the Human

Exposure Module's output has this eight-receptor resolution. The Human Risk Module then calculates risks and/or HQs for each of these eight receptor categories (Figure 1a). However, to maintain output storage at reasonable levels, the Human Risk Module then aggregates these eight categories into four² composite receptor categories: resident, resident gardener, fisher, and farmer, for purposes of developing the cumulative population³ frequency histograms (Figure 1b) and critical years (Figure 1c). For example, the composite "fisher" receptor population consists of subpopulations from the resident fisher, resident gardener fisher, beef farmer fisher, and dairy farmer fisher receptor categories. Similarly, beef farmers and dairy farmers are aggregated into a single, composite "farmer." A complete mapping of the eight receptor categories as output by the Human Exposure Module to their composited receptor categories as output by the Human Risk Module is presented in Table 1. Table 1 also shows the applicable exposure pathways for the receptor categories. In this document, the term "receptor" is used to mean either one of the eight most disaggregated receptor categories, or one of the four composited receptor categories, as appropriate to the context.

Cohorts. A cohort is a receptor subpopulation based on age. Five cohort classes are considered in the Human Risk Module⁴:

- # Child 1 (0 to 1 year old)
- # Child 2 (1 to 5 years old)
- # Child 3 (6 to 11 years old)
- # Child 4 (12 to 19 years old), and
- # Adult (greater than 19 years old).

Exposure Pathways. Nine individual exposure pathways are considered as indicated in Table 1. All exposure pathways do not apply to all receptors; those that are applicable are indicated by "yes" in the table. With respect to applicability among receptor cohorts, if a pathway applies to a receptor, then it applies to all cohorts of that receptor, with two exceptions: (1) shower inhalation applies only to Child 4 and Adult cohorts (younger children are assumed to bathe as opposed to shower), and (2) the infant breast milk pathway applies only to breastfeeding infants.⁵ (For the infant breast milk pathway, the margin of exposure [MOE] (mg/kg-d) is analogous to HQ for infant breast milk exposure. Hereinafter, HQ will be understood to mean "MOE" for the Child 1 cohort and breast milk pathway.)

² The 3MRA Exit Level Processor I (ELP I) preserves this receptor resolution, but also aggregates these four receptors into a fifth, "all receptors" category.

³ Site-specific receptor populations were identified as part of the HWIR99 data collection activities and are specified by receptor category, exposure area (farm or census block), and distance ring. See US EPA (1999b) for discussion of the methodology.

⁴ For purposes of storage efficiency, the ELP I combines the Child 2 and 3 cohort classes as output by the Human Risk Module into a single composite cohort class (ages 1 to 11). Child 4 is also combined with the adult cohort class by the ELP I.

⁵ For HWIR99, the infant breast milk pathway is evaluated only for a single chemical, the dioxin species 2,3,7,8 -TCDD TEQ [CAS No. 1746-01-6]. (That is, the logical flag *ChemBreastMilkExp* will be set to "true" only for this chemical in the chemical properties input file, cp.ssf.)

Table 1. Applicable Receptor/Pathway Combinations

Pathway	Receptors (as output by Human Risk Module)							
	Resident	Resident Gardener	Fisher			Farmer		
	Receptors (as output by Human Exposure Module)							
	Resident	Resident Gardener	Resident Fisher	Resident Gardener Fisher	Beef Farmer Fisher	Dairy Farmer Fisher	Beef Farmer	Dairy Farmer
1. Air inhalation	yes	yes	yes	yes	yes	yes	yes	yes
2. Soil ingestion	yes	yes	yes	yes	yes	yes	yes	yes
3. Water ingestion	yes	yes	yes	yes	yes	yes	yes	yes
4. Crop ingestion	no	yes	no	yes	yes	yes	yes	yes
5. Beef ingestion	no	no	no	no	yes	no	yes	no
6. Milk ingestion	no	no	no	no	no	yes	no	yes
7. Fish ingestion	no	no	yes	yes	yes	yes	no	no
8. Shower inhalation^a	yes	yes	yes	yes	yes	yes	yes	yes
9. Infant breast milk^b	yes	yes	yes	yes	yes	yes	yes	yes

^a Shower inhalation applies only to Child 4 and Adult cohorts. All other pathways shown in Table 1 apply to all noninfant cohorts.

^b Applies only to Child 1 (infant) cohorts.

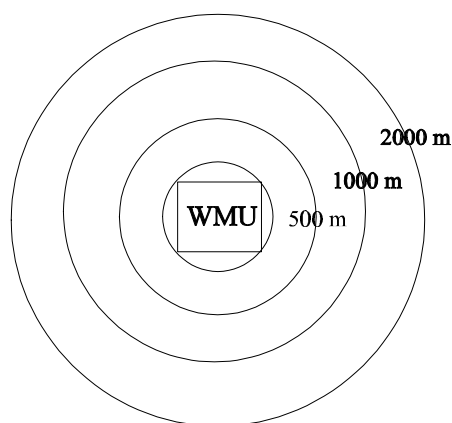
Multiple Exposure Pathways. The essence of a multipathway risk assessment is the evaluation of total risks incurred as a result of simultaneous exposure from different pathways. In the Human Risk Module, four different pathway aggregations are considered as shown in Table 2. The inhalation route aggregates over the two inhalation pathways. The ingestion route aggregates over all ingestion pathways. The groundwater aggregation includes the two groundwater-based pathways (drinking water ingestion and shower inhalation). Finally, the

Table 2. Pathway Aggregations

Pathway	Inhalation Route	Ingestion Route	Groundwater	Multipathway
1. Air inhalation	✓			✓
2. Soil ingestion		✓		✓
3. Water ingestion		✓	✓	✓
4. Crop ingestion		✓		✓
5. Beef ingestion		✓		✓
6. Milk ingestion		✓		✓
7. Fish ingestion		✓		✓
8. Shower inhalation	✓		✓	✓

multipathway aggregation includes all combinable⁶ pathways. (The infant breast milk pathway is a separate pathway that is not relevant to the route aggregations and is not included in the table.)

Distance Rings. The radial distance rings are set at 500 meters, 1,500 meters, and 2,000 meters from a circle circumscribing the (square) WMU (Figure 2). Thus, the first set of risk and/or HQ results is applicable only to those receptors residing within 500 meters of the WMU boundary. The second set applies to **all** receptors within 1,000 meters, including those previously considered within 500 meters. The third set applies to all receptors within 2,000 meters, which includes all receptors within the overall Area of Interest (AOI).

**Figure 2. WMU with three radial distance rings.**

⁶ The feasibility of pathway additivity is chemical-specific and is specified by the logical variables *ChemC_add* and *ChemNC_add* in the chemical properties input file.

2.0 Assumptions and Limitations

Calculations performed by the Human Risk Module reflect a number of assumptions and/or limitations. These assumptions and limitations are

- # *2-km study area.* EPA assumed that all significant exposure and risk/HQ to human receptors occurs within 2 kilometers of the source boundary based on the types of waste management unit sources currently in the 3MRA model.
- # *Human receptors are stationary.* EPA assumed that human receptors both reside and work at the receptor location identified for them during site characterization. (Farmer receptors are on farms, and residential receptors are assumed to be at the centroid of census blocks within radial distance rings.) This assumption may overestimate or underestimate exposure, because it is possible that individuals may reside at the identified location within the study area but either commute to work outside of the study area or commute to more or less highly contaminated areas within the study area.
- # *Incremental risk is considered.* No provision is made for considering background exposures and their risks for the purpose of generating total risk estimates.
- # *Risk and HQ estimates are aggregated for certain receptors.* As mentioned, the four receptors considered—resident, residential gardener, farmer, and fisher—are fewer in number than the number of receptor categories output by the Human Exposure Module. Risks are aggregated for certain receptors to maintain output storage requirements at reasonable levels. Such aggregation results in some loss in risk resolution. For example, the risks specific to farmers who drink contaminated milk but do not ingest contaminated beef will not be available.
- # *Lifetime and exposure duration for carcinogens.* For carcinogenic risk calculations, receptors are assumed to live 76.5 years. Of this lifetime, the exposure duration is assumed to be 9 years.
- # *Carcinogenic risks are proportionately disaggregated from lifetime exposure to the assumed exposure duration.* Incurred risks are assumed to be lifetime risks that are reduced in direct proportion to the fraction of a lifetime actually exposed, i.e., 350 of 365 days per year (15 days away per year) for each year of exposure duration.

- # *Synergistic or antagonistic effects among multiple chemicals and individual chemical speciation on risk estimates are not considered.* The Human Risk Module is executed by the 3MRA system with a system-level chemical loop so that only one chemical is considered at any single execution. Chemicals are considered to be independent.
- # *Cancer slope factors do not vary with cohort age.* Age-specific differences in exposure responses are not available and consequently are not considered.
- # *Maximum HQ estimates are conservatively based on a single year of exposure.* Unlike carcinogenic risk estimates, which use a moving average over multiyear exposure periods (as discussed in the next section), HQ estimates treat each year independently, i.e., their time series reflects 1-year average values. Thus, a single high year of maximum exposure would not be “diluted” by a multiyear averaging period. This is a protective approach.
- # *If any residents in a census block group ingest ground water, all residents in the component census blocks are assumed to ingest ground water.* The census data report the number of households within a census block group that are served by ground water wells. However, this information is available only at the census block group level, and it is not possible to determine from census data alone whether individual census blocks within a block group with wells have wells or not. The Human Risk Module loops over census blocks when considering residential exposure areas. Consequently, the actual fraction of residents on wells for any individual residential exposure area is uncertain. To resolve this lack of information, the protective assumption is made that, if any residents in the block group containing the residential exposure area (or census block) under consideration are on wells, then all residents in the exposure area are on wells. That is not to say, of course, that all well water is contaminated. Only those wells lying within the ground water plume from the source are potentially contaminated.

3.0 Methodology

The three major functions of the Human Risk Module, illustrated in Figures 1a, 1b, and 1c, respectively, are discussed in this section. In addition, an overview of the module output format is provided.

3.1 Risk Calculations

If a receptor spent a lifetime exposed to a chemical at a given dose, the increased cancer risk over that lifetime would be estimated as

$$Risk = CSF \cdot Dose \quad (3-1)$$

where

- Risk = lifetime risk (probability units)
- CSF = chemical-specific cancer slope factor (mg/kg-d)⁻¹ (from the cp.ssf file)
- Dose = chemical dose (mg/kg-d).

Instead of a lifetime, consider now that the dose is only incurred for an exposure period of ExDur years (assumed to be 9 years for HWIR99). Further assume that the receptor is exposed only 350 days of each of those ExDur years. Assuming that cancer risk is linearly related to exposure period, the risk attributable to the exposure duration would then be

$$Risk = \left(\frac{ExDur \cdot 350}{LifeTime \cdot 365} \right) CSF \cdot Dose \quad (3-2)$$

where LifeTime is the receptor lifetime (yr).

Finally, assume that a different dose is incurred each year of the exposure duration. Let the subscript t denote year t. The risk over the exposure duration starting in year t is then

$$Risk_t = \left(\frac{350}{LifeTime \cdot 365} \right) CSF \sum_t^{t+ExDur-1} Dose_t \quad (3-3)$$

where $t+ExDur-1$ gives the length of the time series of risks.⁷

Consider now that a child cohort will age out of his or her initial cohort class as the exposure duration progresses. For example, a child beginning the exposure duration at age 3 will, over a 9-year exposure period, increase in age to 11 years old. Because the annual exposure doses are cohort class-specific, it is appropriate to consider these variable doses as the child ages through the exposure duration. The Human Risk Module performs this cohort aging as it is looping through the years in computing $Risk_t$ using Equation 3-3. To set an initial condition, children are assumed to begin each 9-year period at the midpoint of their respective age ranges (e.g., age 3 for Child 2). Thus, the age of a child cohort is monitored at each year t over the exposure duration, and $Dose_t$ is set in accordance with the relevant class.

3.2 Hazard Quotient Calculations

For noncarcinogenic chemicals, annual hazard quotients are calculated in lieu of risks. These are calculated as

$$HQ_t = \frac{Dose_t}{RfD} \quad \text{for ingestion pathways} \quad (3-4)$$

$$HQ_t = \frac{C_t}{RfC} \quad \text{for inhalation pathways} \quad (3-5)$$

where

- HQ_t = hazard quotient for year t (unitless)
- $Dose_t$ = chemical dose (mg/kg-d)
- RfD = reference dose (mg/kg-d) (from the cp.ssf file)
- C_t = air concentration (mg/m³)
- RfC = reference air concentration (mg/m³) (from the cp.ssf file).

For infant breast milk, the margin of exposure in year t (MOE_t) is similarly calculated as

$$MOE_t = \frac{Dose_t}{BM} \quad (3-6)$$

where BM (mg/kg-d) is the chemical-specific benchmark based on background exposure levels.

⁷ As t is incremented from year 1 of the simulation to the last year, $Risk_t$ is in fact a *moving* average risk. For example, for a T -year time series of doses ($t = 1, \dots, T$), the resulting time series of moving average risks will be $t = 1, \dots, T-ExDur+1$. For example, for $T = 100$ years and $ExDur = 9$ years, 92 9-year moving average risks would be calculated.

3.3 Cumulative Frequency Histograms of Receptors at Various Risk Levels

The second major function performed by the Human Risk Module is to construct cumulative frequency histograms of the receptor/cohort population across exposure areas that incurs various risk or HQ levels. The basic structure of the looping to accomplish this is shown in Figure 1b. For any given year t , a set of risk and/or HQ histograms is constructed. The set of histograms at any year t consists of **conditional** histograms, that is, one histogram for each combination of receptor, cohort, exposure pathway⁸ (or pathway aggregation), and distance ring. Thus, the full collection of cumulative histograms is a time series of conditional histograms for risk and/or HQ.

A risk cumulative histogram is defined by a set of six class intervals or “bins.” The risk ranges defining those bins are: Bin 1 = 0 to 10^{-8} ; Bin 2 = 10^{-8} to 10^{-7} ; Bin 3 = 10^{-7} to 10^{-6} ; Bin 4 = 10^{-6} to 10^{-5} ; Bin 5 = 10^{-5} to 10^{-4} ; and Bin 6 = 10^{-4} to 0. An HQ (or MOE) cumulative histogram is defined by four bins: Bin 1 = 0 to 0.1; Bin 2 = 0.1 to 1.0; Bin 3 = 1.0 to 10.0; and Bin 4, greater than 10.0. At any year t , and given a receptor, cohort, pathway/pathway aggregation, and ring, a cumulative risk histogram contains the cumulative population corresponding to the receptor/cohort combination, across all exposure areas from the WMU out to the distance ring, that incurs risks falling within each risk range. A cumulative HQ histogram is similarly constructed.

As an example, suppose 150 adult residents reside collectively at all residential exposure areas (census block centroids) within the first ring. Furthermore, for a given pathway for, e.g., year 1, assume that 25 of them incur HQs within the first HQ bin, 50 within the second, 25 within the third, and the remaining 50 within the fourth bin. For year 2, assume that exposures change such that the resulting distribution is 10 in bin 1, 40 in bin 2, 30 in bin 3, and 70 in bin 4. The conditional, cumulative histograms for these two example years would then be:

HQ Range:	0 to 0.1	0.1 to 1.0	1.0 to 10.0	> 10.0
Year 1 Cumulative Population:	25	75	100	150
Year 2 Cumulative Population:	10	50	80	150

3.4 Application of *RegPercentile* Criterion and Determination of Maximum Risk/HQ Years

As illustrated in Figure 1c, the time series of conditional frequency histograms is analyzed to determine that year in which a prespecified percentage of the population has the

⁸ As an option, the module can either include in the histograms **all** receptor/cohort individuals, i.e., whether incurring a positive dose or not, or only those individuals that incur a nonzero dose. In the latter case, the risk and/or HQ histograms would be interpreted as further conditioned on positive exposure. The option is set by the logical flag *DoExposed*. *DoExposed* was set to “true” for HWIR99, meaning all individuals are included in the histograms, whether exposed or not.

maximum total risk and/or HQ over all years. The prespecified percentage criterion is the parameter RegPercentile⁹, and the year at which the maximum is attained is the variable Tcrit. For each year of a time series, the following steps are performed to determine Tcrit for a given ring, receptor/cohort, pathway/pathway aggregation:

1. Beginning with the first bin (corresponding to the lowest risk/HQ range), loop across bins accumulating individuals until that bin is reached in which the RegPercentile of the population is attained. For purposes of this discussion, denote this bin as $BIN_{RegPercentile}$.
2. Estimate the total risk/HQ to all individuals in bins 1 through $BIN_{RegPercentile}$ by multiplying each bin's population by the mid-range risk/HQ value for that bin and accumulating over bins. For purposes of this discussion, denote that total risk/HQ as $TOTAL_t$, where t represents the current year.
3. Compare $TOTAL_t$ to the maximum total risk/HQ previously calculated across all prior years, denoted as $TOTAL_{max}$. If $TOTAL_t$ is greater than $TOTAL_{max}$, then replace $TOTAL_{max}$ with $TOTAL_t$ and update Tcrit to year t.
4. Repeat Steps 1 to 3 for all years. Upon completion, Tcrit will be that year with maximum total risk to RegPercentile of the population for a given ring, receptor/cohort, or pathway/pathway aggregation.

3.5 Outputs

Of the complete time series of conditional, cumulative histograms, only those associated with Tcrit years are written to the human risk module's output file, hr.grf. Specifically, for each ring, receptor/cohort, and pathway/pathway aggregation (for which an entire time series of histograms has been developed), the histogram associated with the Tcrit year for that pathway/pathway aggregation is output. **In addition**, however, the histograms associated with all other pathways/pathway aggregation routes at that same Tcrit year are also output. These other histograms will not necessarily be the histograms corresponding to their own Tcrit years. However, it is of interest to examine risk distributions for other pathways during the critical year for a given pathway, because this presents information on the contribution of these pathways to the total risk or HQ. Thus, for example, if there are M receptor/cohort/ring combinations for each of N pathways or pathway aggregations (N is 9 for individual pathways), then M*N sets of histograms are output. For pathway "i" corresponding to Tcrit_i, there are M histograms, one of which is the histogram for which year Tcrit_i was the year of maximum risk/HQ across all years.

⁹ The RegPercentile parameter can vary between 0 and 100 percent. For HWIR99, it is specified as 100 percent.

4.0 References

U.S. EPA (Environmental Protection Agency). 1999a. Human Exposure Module for HWIR99 Multimedia, Multipathway, and Multireceptor Risk Assessment (3MRA) Model. Office of Solid Waste, Washington, DC.

U.S. EPA (Environmental Protection Agency). 1999b. Data Collection for the Hazardous Waste Identification Rule. Section 9: Human Receptor Data. Office of Solid Waste, Washington, DC.

Appendix A

Inputs and Outputs

Appendix A

Inputs and Outputs

The Human Risk Module receives inputs from its module-specific input file, hr.ssf, the generic site layout file (sl.ssf), the generic chemical properties file (cp.ssf), and modeled inputs from the Human Exposure Module's output file, he.grf. Human Risk Module outputs are written to hr.grf. These variables are listed and described in Tables A-1 through A-5.

Table A-1. Hr.ssf Input Parameters (Module-Specific Inputs)

Input Parameter	Units	Description
<i>LifeTime</i>	years	Human lifetime used in carcinogenic risk calculation
<i>ExDur_Car_Farm</i>	years	Exposure duration used for modeling carcinogenic risk for all farming receptor populations
<i>ExDur_Car_Block</i>	years	Exposure duration used for modeling carcinogenic risk for all residential receptor populations
<i>ExDur_NCar_Farm</i>	years	Exposure duration used for modeling noncarcinogenic HQ/MOE for all farming receptors.
<i>ExDur_NCar_Block</i>	years	Exposure duration used for modeling noncarcinogenic HQ/MOE for all residential receptors.
<i>RegPercentile</i>	percent	Regulatory criterion used in calculating total risk incurred by a given percentage of the population. <i>RegPercentile</i> is the percentage.
<i>DoExposed</i>	unitless	Logical flag indicating whether the output CDFs comprise (1) only actually exposed receptors (true), or (2) all receptors (false).

Table A-2. Sl.ssf Input Parameters (Module-Specific Site Layout Inputs)

Input Parameter	Units	Description
<i>BinRange_Min_C</i>	unitless	Carcinogenic risk values used to define the minimum value for each of the carcinogenic risk bins.
<i>BinRange_Min_NC</i>	unitless	Noncarcinogenic HQ values used to define the minimum value for each of the noncarcinogenic HQ bins.
<i>NumBinC</i>	unitless	Number of bins used in reporting cancer risk (i.e., number of bins used to define the cumulative risk distribution)
<i>NumBinNC</i>	unitless	Number of bins used in reporting noncancer HQs (i.e., number of bins used to define the cumulative HQ distribution)
<i>NumHumRcp</i>	unitless	Number of residential locations (i.e., number of human receptor points excluding farms)
<i>NumFarm</i>	unitless	Number of beef and/or dairy farms
<i>NumRing</i>	unitless	Number of concentric rings used to subdivide the site for purposes of estimating risk or HQ/MOE distributions conditional on distance from the source.
<i>FarmPopulation</i>	unitless	Number of farmers associated with each of the farms/crop areas identified for a given site. These population estimates are farmer-, type-, and cohort-specific.
<i>HumRcpPopulation</i>	unitless	Number of residents (nonfarmers) associated with each of the residential locations identified for a given site. These population estimates are receptor population- and cohort-specific.
<i>RingFarmFrac</i>	fraction	The fraction of a given farm that is located within a given ring. This variable is used to allocate farm population into different rings for purposes of ring-specific risk or HQ/MOE estimates when the farm occurs in multiple rings.

Table A-3. Cp.ssf Input Variables (Module-Specific Chemical Properties)

Input Parameter	Units	Description
<i>ChemC_Add</i>	unitless	Identifies whether carcinogenic risk for a given chemical can be added across routes.
<i>ChemNC_Add</i>	unitless	Identifies whether noncarcinogenic HQ/MOEs for a given chemical can be added across routes.
<i>ChemBreastMilkExp</i>	unitless	Identifies whether a given chemical should be assessed for breast milk exposure (i.e., does it bioconcentrate in breast milk)
<i>ChemCSFinhal</i>	(mg/kg-d) ⁻¹	Inhalation cancer slope factor
<i>ChemCSFfood</i>	(mg/kg-d) ⁻¹	Cancer slope factor used to evaluate dietary exposure and incidental soil ingestion (excluding drinking water)
<i>ChemCSFwater</i>	(mg/kg-d) ⁻¹	Cancer slope factor used to evaluate ingestion of drinking water
<i>ChemRFC</i>	mg/m ³	Inhalation reference concentration
<i>ChemRFDfood</i>	mg/kg-d	Reference dose used to evaluate dietary exposure and incidental soil ingestion (excluding drinking water and fish)
<i>ChemRFDwater</i>	mg/kg-d	Reference dose used to evaluate ingestion of drinking water
<i>ChemRFDfish</i>	mg/kg-d	Reference dose used to evaluate dietary exposure to fish
<i>ChemBM</i>	mg/kg-d	Background-driven breast milk exposure value used in generating margin of exposure estimate for breast milk consumption in infants

Table A-4. He.grf Input Variables (Module-Specific Modeled Inputs)

Input Parameter	Units	Description
<i>IngBM<pathway>H</i>	mg/kg-d	Chemical- and pathway- specific average daily dose for the nonfarmer infant resulting from breast milk ingestion. (Note: "<pathway>" denotes the actual pathway name in the variables generated by the human exposure module.)
<i>IngBM<pathway>HYR</i>	unitless	Time series of years corresponding to this variable.
<i>IngBM<pathway>HNY</i>	unitless	Number of years in the time series corresponding to this variable.
<i>IngBM<pathway>F</i>	mg/kg-d	Chemical- and pathway- specific average daily dose for the farmer infant resulting from breast milk ingestion. (Note: "<pathway>" denotes the actual pathway name in the variables generated by the human exposure module.)
<i>IngBM<pathway>FYR</i>	unitless	Time series of years corresponding to this variable.
<i>IngBM<pathway>FNY</i>	unitless	Number of years in the time series corresponding to this variable.
<i>Cambient_Farm</i>	mg/m ³	Farm-specific modeled ambient air concentration used in evaluating inhalation risk. Separate estimates are generated for each modeled year.
<i>Cambient_FarmYR</i>	unitless	Time series of years corresponding to this variable.
<i>Cambient_FarmNY</i>	unitless	Number of years in the time series corresponding to this variable.
<i>Cambient_HumRcp</i>	mg/m ³	Residential location-specific modeled ambient air concentration used in evaluating inhalation risk. Separate estimates are generated for each modeled year.
<i>Cambient_HumRcpYR</i>	unitless	Time series of years corresponding to this variable.
<i>Cambient_HumRcpNY</i>	unitless	Number of years in the time series corresponding to this variable.
<i>Csb_Farm</i>	mg/m ³	Farm/crop area-specific modeled shower/bath air concentration used in evaluating inhalation risk. Separate estimates are generated for each modeled year.
<i>Csb_FarmYR</i>	unitless	Time series of years corresponding to this variable.

(continued)

Table A-4. (continued)

Input Parameter	Units	Description
<i>Csb_FarmNY</i>	unitless	Number of years in the time series corresponding to this variable.
<i>Csb_HumRcp</i>	mg/m ³	Residential location-specific modeled shower/bath air concentration used in evaluating inhalation risk. Separate estimates are generated for each modeled year.
<i>Csb_HumRcpYR</i>	unitless	Time series of years corresponding to this variable.
<i>Csb_HumRcpNY</i>	unitless	Number of years in the time series corresponding to this variable.
<i>Ing<pathway>_Farm</i>	mg/kg-d	Chemical- and pathway-specific average daily dose for the farmer resulting from ingestion of the dietary item identified as the “pathway” by the variable. (Note: “<pathway>” denotes the actual pathway name in the variables generated by the human exposure module.)
<i>Ing<pathway>_FarmYR</i>	unitless	Time series of years corresponding to this variable.
<i>Ing<pathway>_FarmNY</i>	unitless	Number of years in the time series corresponding to this variable.
<i>Ing<pathway>_HumRcp</i>	mg/kg-d	Chemical- and pathway-specific average daily dose for the nonfarmer resulting from ingestion of the dietary item identified as the “pathway” by the variable. (Note: “<pathway>” denotes the actual pathway name in the variables generated by the human exposure module.)
<i>Ing<pathway>_HumRcpYR</i>	unitless	Time series of years corresponding to this variable.
<i>Ing<pathway>_HumRcpNY</i>	unitless	Number of years in the time series corresponding to this variable.

Table A-5. Hr.grf Output Variables (Human Risk Module Outputs)

Output Parameter	Units	Description
<i>Risk_1_Index;</i> <i>Risk_2_Index;</i> <i>Risk_3_Index</i>	unitless	Number of exposure pathway-specific (<i>Risk_1_Index</i>), exposure route-specific (<i>Risk_2_Index</i>), or total (<i>Risk_3_Index</i>) carcinogenic risk estimates generated for each receptor population/age cohort combination. Separate exposure pathway-, exposure route-, and total risk estimates are generated for each ring modeled. Risk results for each of these three categories are only reported for Tcrit (i.e., for the maximum risk year) and not for all modeled years.
<i>HQ_1_Index;</i> <i>HQ_2_Index;</i> <i>HQ_3_Index</i>	unitless	Number of exposure pathway-specific (<i>HQ_1_Index</i>), exposure route-specific (<i>HQ_2_Index</i>), or total (<i>HQ_3_Index</i>) non-carcinogenic HQ estimates generated for each receptor population/age cohort/chemical combination. Separate exposure pathway-, exposure route-, and total HQ estimates are generated for each ring modeled. HQ results for each of these three categories are only reported for Tcrit (i.e., for the maximum risk year) and not for all modeled years.
<i>Risk_1;</i> <i>Risk_2;</i> <i>Risk_3</i>	unitless	CDFs of population in risk bins for exposure pathway-specific (<i>Risk_1</i>), exposure route-specific (<i>Risk_2</i>), and total (<i>Risk_3</i>) carcinogenic risk. Separate CDFs are generated for each receptor/cohort/ring combination. These estimates are only reported for Tcrit.
<i>HQ_1;</i> <i>HQ_2;</i> <i>HQ_3</i>	unitless	CDFs of population in HQ bins for exposure pathway-specific (<i>HQ_1</i>), exposure route-specific (<i>HQ_2</i>) and total (<i>HQ_3</i>) non-carcinogenic HQ estimate. Separate CDFs are generated for each receptor population/cohort/ring combination. These estimates are only reported for Tcrit.
<i>Risk_1_TcrIndex;</i> <i>Risk_2_TcrIndex;</i> <i>Risk_3_TcrIndex</i>	years	Tcrit (critical year or maximum risk year) for carcinogenic risk. Separate Tcrits are identified for exposure pathways (<i>Risk_1_TcrIndex</i>), exposure routes (<i>Risk_2_TcrIndex</i>), and for total risk (<i>Risk_3_TcrIndex</i>).
<i>Risk_1_RingIndex;</i> <i>Risk_2_RingIndex;</i> <i>Risk_3_RingIndex</i>	unitless	The specific ring associated with each of the Tcrit values identified through the <i>Risk_#_TcrIndex</i> variables (i.e., <i>Risk_1_RingIndex</i> , <i>Risk_2_RingIndex</i> , and <i>Risk_3_RingIndex</i>).
<i>Risk_1_PathIndex;</i> <i>Risk_2_PathIndex;</i> <i>Risk_3_PathIndex</i>	unitless	The specific exposure pathway associated with each of the Tcrit values identified through the <i>Risk_#_TcrIndex</i> variables (i.e., <i>Risk_1_RingIndex</i> , <i>Risk_2_RingIndex</i> , and <i>Risk_3_RingIndex</i>).
<i>HQ_1_TcrIndex;</i> <i>HQ_2_TcrIndex;</i> <i>HQ_3_TcrIndex</i>	years	Tcrit (critical year or maximum HQ year) for noncarcinogenic HQ. Separate Tcrit values are identified for exposure pathways (<i>HQ_1_TcrIndex</i>), exposure routes (<i>HQ_2_TcrIndex</i>), and for total HQ (<i>HQ_3_TcrIndex</i>).

(continued)

Table A-5. (continued)

Output Parameter	Units	Description
<i>HQ_1_RingIndex;</i> <i>HQ_2_RingIndex;</i> <i>HQ_3_RingIndex</i>	unitless	The specific ring associated with each of the Tcrit values identified through the HQ_#_TcrIndex variables (i.e., HQ_1_RingIndex, HQ_2_RingIndex, and HQ_3_RingIndex).
<i>HQ_1_PathIndex;</i> <i>HQ_2_PathIndex;</i> <i>HQ_3_PathIndex</i>	unitless	The specific exposure pathway associated with each of the Tcrit values identified through the HQ_#_TcrIndex variables (i.e., HQ_1_RingIndex, HQ_2_RingIndex, and HQ_3_RingIndex).